

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 23:37:38 ; Search time 14585 Seconds
(without alignments)
19967.524 Million cell updates/sec

Title: US-10-005-469-1

Perfect score: 7992

Sequence: 1 gccagcccccgtattgggggc.....ctctctgcagatcaagtact 7992

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_huc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsl1:*

9: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 795.4 | 10.0 | 935 | 7 | CK284786 EST747508 |
| 2 | 794 | 9.9 | 804 | 7 | CK291519 EST754233 |
| 3 | 794 | 9.9 | 856 | 7 | CK287297 EST750019 |
| 4 | 794 | 9.9 | 910 | 7 | CK287930 EST750652 |
| 5 | 794 | 9.9 | 933 | 7 | CK291799 EST754513 |
| 6 | 794 | 9.9 | 936 | 7 | CK256977 EST740614 |
| 7 | 794 | 9.9 | 947 | 7 | CK288208 EST760922 |
| 8 | 794 | 9.9 | 954 | 7 | CK283361 EST746083 |
| 9 | 778.8 | 9.7 | 811 | 7 | CK288185 EST750907 |
| 10 | 587 | 7.3 | 878 | 7 | CK288711 EST751433 |
| 11 | 577.4 | 7.2 | 789 | 8 | AQ361914 mgxb0005K |
| 12 | 559.8 | 7.0 | 620 | 8 | AQ398387 mgxb0009J |
| 13 | 542.4 | 6.8 | 549 | 7 | CK801630 NF32C08f4 |
| 14 | 514.8 | 6.4 | 561 | 8 | AQ447874 mgxb0012I |
| 15 | 508 | 6.4 | 509 | 8 | AQ447775 mgxb0011E |
| 16 | 505.4 | 6.3 | 637 | 8 | AQ447230 mgxb0006O |
| 17 | 503.8 | 6.3 | 592 | 8 | AQ449162 mgxb0023E |
| 18 | 499 | 6.2 | 499 | 8 | AQ398880 mgxb0006P |
| 19 | 496.4 | 6.2 | 498 | 8 | AQ398730 mgxb0009G |
| 20 | 477.4 | 6.0 | 586 | 7 | CK801096 NF15h06f4 |
| 21 | 475.8 | 6.0 | 857 | 8 | AQ875013 V12088 mt |
| 22 | 474.8 | 5.9 | 710 | 8 | BH972732 odj46h10. |
| 23 | 469.8 | 5.9 | 473 | 8 | AQ397768 mgxb0001J |
| 24 | 468.8 | 5.9 | 594 | 8 | AQ397253 mgxb0003C |

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|------|-------|-----|-----|---|----------|---------------------|
| C 25 | 465.2 | 5.8 | 850 | 8 | AQ875052 | AQ875052 V120F5 mt |
| C 26 | 463.4 | 5.8 | 798 | 8 | AQ876139 | AQ876139 V133G10 m |
| C 27 | 458.8 | 5.7 | 482 | 1 | AL449872 | AL449872 AL449872 |
| C 28 | 456.8 | 5.7 | 861 | 8 | AQ875040 | AQ875040 V120E4 mt |
| C 29 | 455.6 | 5.7 | 815 | 8 | AQ876134 | AQ876134 V133F5 mt |
| C 30 | 451.2 | 5.6 | 799 | 8 | AQ876220 | AQ876220 V152G7 mt |
| C 31 | 450 | 5.6 | 784 | 8 | AQ876152 | AQ876152 V133H11 m |
| C 32 | 444.6 | 5.6 | 790 | 8 | AQ875904 | AQ875904 V153G3 mt |
| C 33 | 437.2 | 5.5 | 797 | 7 | CK283362 | CK283362 EST746084 |
| C 34 | 434.6 | 5.4 | 765 | 7 | CK283362 | AQ876080 V133AA mt |
| C 35 | 426.8 | 5.3 | 804 | 8 | AQ876080 | AQ876080 EST760923 |
| C 36 | 422.8 | 5.3 | 759 | 7 | CK298209 | AQ876019 V132C3 mt |
| C 37 | 414.6 | 5.2 | 791 | 8 | AQ876019 | AQ876019 V20F6 mTn |
| C 38 | 409.4 | 5.1 | 748 | 8 | AQ501530 | AQ501530 mgxb0008M |
| C 39 | 408 | 5.1 | 635 | 8 | AQ447643 | AQ447643 mgxb00005I |
| C 40 | 408 | 5.1 | 656 | 8 | AQ447140 | AQ447140 V130H8 mt |
| C 41 | 404 | 5.1 | 790 | 8 | AQ875912 | AQ875912 V152E2 mt |
| C 42 | 404 | 5.1 | 791 | 8 | AQ876201 | AQ876201 V120F2 mt |
| C 43 | 402.6 | 5.0 | 856 | 8 | AQ875050 | AQ875050 EST750653 |
| C 44 | 401.8 | 5.0 | 760 | 7 | CK287931 | CK287931 AGENCOURT |
| C 45 | 398.8 | 5.0 | 722 | 6 | CD641598 | CD641598 AGENCOURT |

ALIGNMENTS

RESULT 1
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DEFINITION
EST747508 Nicotiana benthamiana mixed tissue cDNA library, 935 bp mRNA linear EST 02-AUG-2004
normalized, full-length Nicotiana benthamiana cDNA clone NBMAQ41 5',
end, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CK284786
CK284786.1 GI:39858698
EST.
Nicotiana benthamiana
Nicotiana benthamiana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE
AUTHORS
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskiewicz, B., Jin, H. and Baker, B.

TITLE
JOURNAL
COMMENT
Generation of EST sequences from Nicotiana benthamiana
Other ESTs: EST747509
Contact: Robin Buell

The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org

Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers
1..935

/organism="Nicotiana benthamiana"

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/db_xref="taxon:4100"

/clone="NBMAQ41"

/tissue_type="abiotic and biotic stress-treated leaves,"

callus tissue and root tissue"

/lab_host="DH10B-TonA"

/clone_lib="Nicotiana benthamiana mixed tissue cDNA

library, normalized, full-length"

/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;

tissues that include callus, roots from Nicotiana benthamiana

grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),

cold-stressed leaves (5 C 3 hr, 6hr), and pathogen

challenged leaves (Pseudomonas syringae pv tomato 12 hr;

Xanthomonas campestris pv campestris 12 hr, 18hr;

Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas

campestris pv vesicatoria 18hr). RNA was isolated from

QY 809 CGACGACGACTACTCGGATGGAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGA 868
 Db 422 CGACGACGACGACTACTCGGATGGAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGA 481
 QY 869 GCATCAGGGGCTCGCGCAGCCGAACTGTTGCGCAGGCTCAAGCGCGCATGCCGCGCGG 928
 Db 482 GCATCAGGGGCTCGCGCAGCCGAACTGTTGCGCAGGCTCAAGCGCGCATGCCGCGCGG 541
 QY 929 CGAGGATCTCGTGTGACCATGGCGATGCTGTTGCCGAATATCATGTGGAAATGG 988
 Db 542 CGAGGATCTCGTGTGACCATGGCGATGCTGTTGCCGAATATCATGTGGAAATGG 601
 QY 989 CCGCTTTCTGGATTATCATGACACTGTGGCCGGCTGGGTGTGGCGAAGCGCTATCAGGACAT 1048
 Db 602 CCGCTTTCTGGATTATCATGACACTGTGGCCGGCTGGGTGTGGCGAAGCGCTATCAGGACAT 661
 QY 1049 AGCGTTGGCTACCGCTGATATCTCAAGAGCTTGGCGGATGGGTGTGGCGAAGCGCTATCAGGACAT 1108
 Db 662 AGCGTTGGCTACCGCTGATATCTCAAGAGCTTGGCGGATGGGTGTGGCGAAGCGCTATCAGGACAT 721
 QY 1109 CGTGTCTTACGGTATCGCGCTCCGATTCGAGCGCATCGCTTCTATCGCTTCTTGA 1168
 Db 722 CGTGTCTTACGGTATCGCGCTCCGATTCGAGCGCATCGCTTCTATCGCTTCTTGA 781
 QY 1169 CGAGTTCTCTGAG 1182
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RESULT 3 CK287297 LOCUS

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 normalized, full-length Nicotiana benthamiana cDNA clone NEMB815 5'
 end, mRNA sequence.
 CK287297

ACCESSION VERSION KEYWORDS SOURCE

CK287297.1 GI:39863696
 EST
 Nicotiana benthamiana

ORGANISM

Nicotiana benthamiana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
 Staskawicz, B., Jin, H. and Baker, B.

TITLE

Generation of EST sequences from Nicotiana benthamiana
 Unpublished (2003)

JOURNAL

COMMENT

Other ESTs: ES750020
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 Clones can be requested from the University of Arizona Genomics
 Institute via <http://genome.arizona.edu/orders/>.
 Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source

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 /lab_host="DH10B-Tona"
 /clone_lib="Nicotiana benthamiana mixed tissue cDNA
 library, normalized, full-length"
 /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
 supplier: RNA was isolated from Nicotiana benthamiana
 tissues that include callus, roots from liquid culture
 grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
 cold-stressed leaves (5 C 3 hr, 6hr), and pathogen

ORIGIN

Query Match 9.9%; Score 794; DB 7; Length 856;
 Best Local Similarity 100.0%; Pred. No. 3 8e-174;
 Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 449 CTATGACTGGGCACAAACAGACATCGCTGCTGTATGCGCGCTTCCGGTGGAGGCTATTTCGG 508
 Db 74 CTATGACTGGGCACAAACAGACATCGCTGCTGTATGCGCGCTTCCGGTGGAGGCTATTTCGG 133
 509 GCAGGGGCGCCGGTTCTTTTGTCAAGACCGACCTGTCGGGTGCCGTGCTTCCGGTGGAGGCTATTTCGG 568
 Db 134 GCAGGGGCGCCGGTTCTTTTGTCAAGACCGACCTGTCGGGTGCCGTGCTTCCGGTGGAGGCTATTTCGG 193
 569 GCAGGGGCGCCGGTTCTTTTGTCAAGACCGACCTGTCGGGTGCCGTGCTTCCGGTGGAGGCTATTTCGG 628
 Db 194 GCAGGGGCGCCGGTTCTTTTGTCAAGACCGACCTGTCGGGTGCCGTGCTTCCGGTGGAGGCTATTTCGG 253
 629 CGACCTTGTCACTGAAGCGGGAAGGAGTGGCTGCTATTGGCGAAGTCCGGGCGAGGA 688
 Db 254 CGACCTTGTCACTGAAGCGGGAAGGAGTGGCTGCTATTGGCGAAGTCCGGGCGAGGA 313
 689 TCTCTGTTCATCTACCTTGTCTCTCCGAGAAAGTATCCATCATGGCTGATGCAATCGG 748
 Db 314 TCTCTGTTCATCTACCTTGTCTCTCCGAGAAAGTATCCATCATGGCTGATGCAATCGG 373
 749 GCGCTGCATACGCTTGTATCGGCTACTGCCCATTCGACCCCAAGCAAGCAACATCGCAT 808
 Db 374 GCGCTGCATACGCTTGTATCGGCTACTGCCCATTCGACCCCAAGCAAGCAACATCGCAT 433
 809 CGACGAGCAGTACTCGGATGGAAGCGGCTTCTGTGATCAGGATGATCTGGACGAAGA 868
 Db 434 CGACGAGCAGTACTCGGATGGAAGCGGCTTCTGTGATCAGGATGATCTGGACGAAGA 493
 869 GCATCAGGGGCTCGCGCAGCCGAACTGTTCCGAGAGCTCAAGCGCGCATGCCCGCAGG 928
 Db 494 GCATCAGGGGCTCGCGCAGCCGAACTGTTCCGAGAGCTCAAGCGCGCATGCCCGCAGG 553
 929 CGAGGATCTCGTGTGACCCATGCGGATGCTGTTCCGAAATATCATGTTGGAAATGG 988
 Db 554 CGAGGATCTCGTGTGACCCATGCGGATGCTGTTCCGAAATATCATGTTGGAAATGG 613
 989 CCGCTTTCTGGATTTCATCGACTGTCGGCTGGGTGGGTGGCGGACCGCTATCAGGACAT 1048
 Db 614 CCGCTTTCTGGATTTCATCGACTGTCGGCTGGGTGGGTGGCGGACCGCTATCAGGACAT 673
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 Db 674 AGCGTTGGCTACCGCTGATATTGCTCAAGAGCTTGGCGGAATGGCTCACCGCTTCCT 733
 1109 CGTGTCTTACGGTATCGCGCTCCCGATTGCGAGCGCATCGCTTCTATCGCTTCTTGA 1168
 Db 734 CGTGTCTTACGGTATCGCGCTCCCGATTGCGAGCGCATCGCTTCTATCGCTTCTTGA 793
 1169 CGAGTTCTTCTGAG 1182
 Db 794 CGAGTTCTTCTGAG 807

RESULT 4 CK287930 LOCUS

DEFINITION ES750652 Nicotiana benthamiana mixed tissue cDNA library,
 linear EST 02-AUG-2004
 CK287930
 910 bp mRNA

challenged leaves (*Pseudomonas syringae* pv tomato 12 hr;
Xanthomonas campestris pv *campestris* 12 hr, 18hr;
Pseudomonas syringae pv *phaseolicola* 18hr, and *Xanthomonas*
campestris pv *vesicatoria* 18hr). RNA was isolated from
 these tissues and pooled in approximately equal molar
 amounts."

normalized, full-length Nicotiana benthamiana cDNA clone NBMC75 5',
end, mRNA sequence.
CK287930
CK287930.1 GI:39864940
EST.
Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 910)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST750653
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
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/db_xref="taxon:4100"
/clone="NBMC75"
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callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

Query Match 9.9%; Score 794; DB 7; Length 910;
Best Local Similarity 100.0%; Pred. No. 3.8e-174;
Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

389 GATTGAACAGATGATGACGAGTTCCTCGGCCCGCTTGGTGGAGAGGCTATTCGG 448
|||||
4 GATTGAACAGATGATGACGAGTTCCTCGGCCCGCTTGGTGGAGAGGCTATTCGG 63
|||||

449 CTATGACTGGCAGACAGCAATCGGCTGCTCTGATCGCGCGCTTCGGCTGTACG 508
|||||

64 CTATGACTGGCAGACAGCAATCGGCTGCTCTGATGCGCGCGCTTCGGCTGTACG 123
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509 GCAGGCGCGCGGCTTCCTTTGTCAAGACCGACCTGCTCGGTGCGCTGAATGAATGCA 568
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124 GCAGGCGCGCGGCTTCCTTTGTCAAGACCGACCTGCTCGGTGCGCTGAATGAATGCA 183
|||||

569 GGACGAGGCGCGGCTATCGTGGTGGCAGCGGCGTTCCTGGCGAGCTGTGCT 628
|||||

184 GGACGAGGCGCGGCTATCGTGGTGGCAGCGGCGTTCCTGGCGAGCTGTGCT 243
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629 CGACGTTCTACTGAACGCGGAGGAGTGGCTGCTATTGGGCGAAGTGC CGGGGAGGA 688
|||||

244 CGACGTTGTCTACTGAACGCGGAGGAGTGGCTGCTATTGGGCGAAGTGC CGGGGAGGA 303
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689 TCTCTGTCTATCTCACCTTCTCTCGCGAGAAAGTATCCATCATGGCTGATCGCATGCG 748
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Db TCTCTGTCTATCTCACCTTCTCTCGCGAGAAAGTATCCATCATGGCTGATGCAATCGG 363
Qy GCGGCTGATACGCTTTCGATCGGCTTACCTCGCCATTTCGACCAACGAGCAATCGCAT 808
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Db CGAGGAGCAGTACTCGGATGGAAGCCGGTCTTTGTCGATCAGGATGATCTGGACGAAGA 483
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Db AGCGTTGGCTACCGCTGATTCGTAAGAGCTTGGCGGCGAATGGCGCTTCCT 723
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Qy CGAGTTCCTCTGAG 1182
Db CGAGTTCCTCTGAG 797

RESULT 5
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LOCUS EST754513 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NBMC477 5',
end, mRNA sequence.
CK291799
CK291799.1 GI:39872608
EST.
Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 933)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST754514
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
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/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMC477"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"

FEATURES
source

/note="vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv phaseolicola 18hr, and Xanthomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN

Query Match 9.9%; Score 794; DB 7; Length 933;
Best Local Similarity 100.0%; Pred. No. 3.9e-174;
Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

389 GATTGAACAGATGGATTGACGACGATTTCTCCGCGCGCTTGGTGGAGAGGCTATTCGG 448
Db |||

46 GATTGAACAGATGGATTGACGACGATTTCTCCGCGCGCTTGGTGGAGAGGCTATTCGG 105
Db |||

449 CTATGACTGGGACAAACAGACAATCGGCTGCTCTGATGCGCGCTTCCGCGTGTGACG 508
Db |||

106 CTATGACTGGGACAAACAGACAATCGGCTGCTCTGATGCGCGCTTCCGCGTGTGACG 165
Db |||

509 GCAGGGGCGCCGGTCTTTTGTCAAGACCGACCTGTCGCGTGCCTGAATGAATGCA 568
Db |||

166 GCAGGGGCGCCGGTCTTTTGTCAAGACCGACCTGTCGCGTGCCTGAATGAATGCA 225
Db |||

569 GAGCAGGACGCGCGCTATCGTGTGCGCACGACGCGGCTTCTTGGCGAGCTGTGCT 628
Db |||

226 GAGCAGGACGCGCGCTATCGTGTGCGCACGACGCGGCTTCTTGGCGAGCTGTGCT 285
Db |||

629 CGAGTTGTCTCTGAAGCGGGAAGGACTGGCTGCTATTGGCGAAGTCCGCGGCGAGGA 688
Db |||

286 CGAGTTGTCTCTGAAGCGGGAAGGACTGGCTGCTATTGGCGAAGTCCGCGGCGAGGA 345
Db |||

689 TCTCTGTCTCTACCTTCTCTGCGGAGAAATGATTCATCATGCTGATGAATGCG 748
Db |||

346 TCTCTGTCTCTACCTTCTCTGCGGAGAAATGATTCATCATGCTGATGAATGCG 405
Db |||

749 GCGGCTGCATACGCTTCTGATCGGCTTCTGATCGGCTTCTGATCGGCTTCTGATCGG 808
Db |||

406 GCGGCTGCATACGCTTCTGATCGGCTTCTGATCGGCTTCTGATCGGCTTCTGATCGG 465
Db |||

809 CGAGCGAGCAGCTACTCGGATGGAAGCGGCTTCTGATCGGCTTCTGATCGGCTTCTGAT 868
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466 CGAGCGAGCAGCTACTCGGATGGAAGCGGCTTCTGATCGGCTTCTGATCGGCTTCTGAT 525
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869 GCATCAGGGGCTCGCGCAGCGAATGTTGCGCAGGCTCAAGCGCGCATGCCGACGG 928
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526 GCATCAGGGGCTCGCGCAGCGAATGTTGCGCAGGCTCAAGCGCGCATGCCGACGG 585
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929 CGAGGATCTGCTGACCCATCGGATGCTTCTGCGAATATCATGTTGAAATG 988
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586 CGAGGATCTGCTGACCCATCGGATGCTTCTGCGAATATCATGTTGAAATG 645
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989 CGGCTTTCTGATTCATCGACTGTGCGCGGCTGGGTGTGGCGACCGCTATCAGACAT 1048
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646 CGGCTTTCTGATTCATCGACTGTGCGCGGCTGGGTGTGGCGACCGCTATCAGACAT 705
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1049 AGCGTTGGCTACCGGTGATTTGCTGAAGAGCTTGGCGGCAATGGGCTTCCCT 1108
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706 AGCGTTGGCTACCGGTGATTTGCTGAAGAGCTTGGCGGCAATGGGCTTCCCT 765
Db |||

1109 CGTGTCTTACGGTATCGCGCTCCGATTCGACGCGATCGGCTTCTATCGCTTCTTGA 1168
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766 CGTGTCTTACGGTATCGCGCTCCGATTCGACGCGATCGGCTTCTATCGCTTCTTGA 825
Db |||

1169 CGAGTTCTTCTGAG 1182
Db |||

826 CGAGTTCTTCTGAG 839
Db |||

RESULT 6

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..936

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/cultivar="Kennebec"

/db_xref="taxon:4113"

/clone="POCD170"

/tissue_type="callus"

/lab_host="DH10B-TonR"

/clone_lib="potato callus cDNA library, normalized and full-length"

/note="vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."

ORIGIN

Query Match

Best Local

Similarity

Matches

794; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

389

GATTGAACAGATGGATTGACGACGATTTCTCCGCGCGCTTGGTGGAGAGGCTATTCGG

448

14

GATTGAACAGATGGATTGACGACGATTTCTCCGCGCGCTTGGTGGAGAGGCTATTCGG

73

449

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508

74

CTATGACTGGGACAAACAGACAATCGGCTGCTCTGATGCGCGCTTGGTGGAGAGGCTATTCGG

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568

134

GCAGGGGCGCCGGTCTTTTGTCAAGACCGACCTGTCCGCTGCCCTGAATGAATGCA

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569

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628

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629

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688

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689

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749

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808

374

GCGGCTGCATACGCTTGTATCGGCTTCTGCGGCTTCTGCGGCTTCTGCGGCTTCTGCGGCT

433

Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN

Query Match 9.9%; Score 794; DB 7; Length 947;
Best Local Similarity 100.0%; Pred. No. 3.9e-174; Indels 0; Gaps 0;
Matches 794; Conservative 0; Mismatches 0;

QY 389 GATTGAACAAGATGATTTGACGACGAGGTTCTCCGCGCGCTTTGGGTGGAGAGCTATTTCGG 448
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DB 137 GCAGGGGCGCGCGGTTCTTTTGTCAAGACGACCTGTCCGCTGCCCTGAATGAATGCA 196
QY 569 GCAGGAGGCGCGCGCTATCGTGTGGCCACGACGCGGCTTCCTTGGCGAGCTGTGCT 628
DB 197 GCAGGAGGCGCGCGCTATCGTGTGGCCACGACGCGGCTTCCTTGGCGAGCTGTGCT 256
QY 629 CGACGTTGTCACTGAAGCGGGAAGGACTGGCTGTCTATTGGGCGAGTCCCGGGCAGGA 688
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QY 869 GCATCAGGGGCTCGCGCAGCCGACCTGTCGCGAGGCTCAAGCGCGGCTGCGCGCAGG 928
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QY 929 CGAGGATCTCGTGTGACCCATGGCGATGCTGCTTCCGAATATCATGTTGGAAATGG 988
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QY 1049 AGCGTTGGCTACCGCTGATATTGCTGAAGAGCTTGGCGGCGAAATGGGCTGACCGTTCT 1108
DB 677 AGCGTTGGCTACCGCTGATATTGCTGAAGAGCTTGGCGGCGAAATGGGCTGACCGTTCT 736
QY 1109 CGTGTCTTACGTTATCGCGCTCCCGATTTCGAGCGCATCGCTTCTATCGCTTCTTGA 1168
DB 737 CGTGTCTTACGTTATCGCGCTCCCGATTTCGAGCGCATCGCTTCTATCGCTTCTTGA 796
QY 1169 CGAGTTCTTCTGAG 1182
DB 797 CGAGTTCTTCTGAG 810

RESULT 8

CK283361

LOCUS

DEFINITION

CK283361 954 bp mRNA linear EST 02-AUG-2004
EST746083 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMAG50 5'

QY 809 CGAGCGAGCAGTACTCGGATGGAAGCGGCTTGTGATCAGGATGATCTGGACGAAGA 868
DB 434 CGAGCGAGCAGTACTCGGATGGAAGCGGCTTGTGATCAGGATGATCTGGACGAAGA 493
QY 869 GCATCAGGGGCTCGCGCAGCCGAACTGTCGCGAGGCTCAAGCGCGGCTATCGCGCAGG 928
DB 494 GCATCAGGGGCTCGCGCAGCCGAACTGTCGCGAGGCTCAAGCGCGGCTATCGCGCAGG 553
QY 929 CGAGGATCTCGTGTGACCCATGGCGATGCTGCTTGGCGAATATCATGTTGGAAATGG 988
DB 554 CGAGGATCTCGTGTGACCCATGGCGATGCTGCTTGGCGAATATCATGTTGGAAATGG 613
QY 989 CCGCTTTTCTGATTCATCGACTGTGGCGGCTGGGTGGCGGACCGCTATCAGGACAT 1048
DB 614 CCGCTTTTCTGATTCATCGACTGTGGCGGCTGGGTGGCGGACCGCTATCAGGACAT 673
QY 1049 AGCGTTGGCTACCGCTGATATTGCTGAAGAGCTTGGCGGCGAAATGGGCTGACCGTTCT 1108
DB 674 AGCGTTGGCTACCGCTGATATTGCTGAAGAGCTTGGCGGCGAAATGGGCTGACCGTTCT 733
QY 1109 CGTGTCTTACGTTATCGCGCTCCCGATTTCGAGCGCATCGCTTCTATCGCTTCTTGA 1168
DB 734 CGTGTCTTACGTTATCGCGCTCCCGATTTCGAGCGCATCGCTTCTATCGCTTCTTGA 793
QY 1169 CGAGTTCTTCTGAG 1182
DB 794 CGAGTTCTTCTGAG 807

RESULT 7

CK298208

LOCUS

DEFINITION

CK298208 947 bp mRNA linear EST 02-AUG-2004
EST760922 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMDE30 5',
end, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.

REFERENCE

AUTHORS

1 (bases 1 to 947)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.

TITLE

JOURNAL

COMMENT

Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST760923
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/

FEATURES

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/organism="Nicotiana benthamiana"
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/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;

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end, mRNA sequence.
CK283361
VERSION CK283361.1 GI:39855898
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE asterids; lamids; Solanales; Solanaceae; Nicotiana.
JOURNAL 1 (bases 1 to 954)
COMMENT Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST746084
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
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                supplier: RNA was isolated from Nicotiana benthamiana
                tissues that include callus, roots from liquid culture
                grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
                cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
                challenged leaves (Pseudomonas syringae pv tomato 12 hr;
                Xanthomonas campestris pv campestris 12 hr, 18hr;
                Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
                campestris pv vesicatoria 18hr). RNA was isolated from
                these tissues and pooled in approximately equal molar
                amounts."
ORIGIN
    Query Match
    Best Local Similarity 9.9%; Score 794; DB 7; Length 954;
    Matches 794; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 389 GATTGAACAGATGGATTGCGACGAGTTCTCCGCGCTGGTGGAGGCTATTTCG 448
DB 14 GATTGAACAGATGGATTGCGACGAGTTCTCCGCGCTGGTGGAGGCTATTTCG 73
QY 449 CTATGACTGGGCACACAGACATCGGCTCTGATGCGCGCTTCGGCTGTCAGC 508
DB 74 CTATGACTGGGCACACAGACATCGGCTCTGATGCGCGCTTCGGCTGTCAGC 133
QY 509 GCAGGGGCGCGGTTCTTTTGTCAAGACCGACCTGTCCGGTCCCTGAATGAATGCA 568
DB 134 GCAGGGGCGCGGTTCTTTTGTCAAGACCGACCTGTCCGGTCCCTGAATGAATGCA 193
QY 569 GGACGAGGCGCGGCTATCGTGGCTGGCCACGAGCGGCTTCCTTGGCAGCTGTGCT 628
DB 194 GGACGAGGCGCGGCTATCGTGGCTGGCCACGAGCGGCTTCCTTGGCAGCTGTGCT 253
QY 629 CGACGTTGTCACTGAAGCGGGAAGGACTGGCTGCTATTGGCGAAGTCCGGGCA 688
DB 254 CGACGTTGTCACTGAAGCGGGAAGGACTGGCTGCTATTGGCGAAGTCCGGGCA 313
QY 689 TCTCTGTCTATCTACCTTGTCTTCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGG 748
DB 314 TCTCTGTCTATCTACCTTGTCTTCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGG 373

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QY 749 GCGGCTGCATACGCTTGATCCGCTACTGCGCCATTCGACCAACGCGAAACATCGCAT 808
DB 374 GCGGCTGCATACGCTTGATCCGCTACTGCGCCATTCGACCAACGCGAAACATCGCAT 433
QY 809 CGAGCGAGCACGCTACTCGGATCGGATGGAAGCCGCTCTTGTGATCAGGATGATCTGACGAAGA 868
DB 434 CGAGCGAGCACGCTACTCGGATCGGATGGAAGCCGCTCTTGTGATCAGGATGATCTGACGAAGA 493
QY 869 GCATCAGGGGCTCGCGCCAGCCGAACTGTTGCGCAGGCTCAAGCGCGCATGCCGACGG 928
DB 494 GCATCAGGGGCTCGCGCCAGCCGAACTGTTGCGCAGGCTCAAGCGCGCATGCCGACGG 553
QY 929 CGAGGATCTCGTCTGTCGACCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCAT 988
DB 554 CGAGGATCTCGTCTGTCGACCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCATGCCAT 613
QY 989 CCGCTTTTCTGATTCATCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1048
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DB 674 AGCGTTGGCTACCCGCTGATTTGCTGAAGAGCTTGGCGCGGCTGGTGGCGGACCGCTATCAGGACAT 1108
QY 1109 CGTCTTTTACGGTATCGCGCTCGCGCTCGCGATTCGCGAGCATCGCTTCTATCGCTTCTTTGA 1168
DB 734 CGTCTTTTACGGTATCGCGCTCGCGCTCGCGATTCGCGAGCATCGCTTCTATCGCTTCTTTGA 793
QY 1169 CGAGTTCTTCTGAG 1182
DB 794 CGAGTTCTTCTGAG 807

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RESULT 9
CK288185
LOCUS
DEFINITION EST750907 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMBE61 5',
end, mRNA sequence.
CK288185
VERSION CK288185.1 GI:39865462
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE asterids; lamids; Solanales; Solanaceae; Nicotiana.
JOURNAL 1 (bases 1 to 811)
COMMENT Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
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                callus tissue and root tissue"
                /lab_host="DH10B-Tona"
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                library, normalized, full-length"
                /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
                supplier: RNA was isolated from Nicotiana benthamiana

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tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."

ORIGIN

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|-----------------------|------|--|---------------------|-----------|-------------|
| Query Match | | 9.7%; | Score 778.8; | DB 7; | Length 811; |
| Best Local Similarity | | 99.7%; | Pred. No. 1.3e-170; | | |
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| QY | 386 | CATGATTGAAACAAGATGATTGACACGACGAGTTCTCCGGCCGCTTGGGTGGAGAGGCTATT | 445 | | |
| DB | 30 | CATGATTGAAACAAGATGATTGACACGACGAGTTCTCCGGCCGCTTGGGTGGAGAGGCTATT | 89 | | |
| QY | 446 | CGGCTATGACTGGGCAACAACAGCAATCGGCTGCTCTGATGCGCGCTTCTTCGGCTGTC | 505 | | |
| DB | 90 | CGGCTATGACTGGGCAACAACAGCAATCGGCTGCTCTGATGCGCGCTTCTTCGGCTGTC | 149 | | |
| QY | 506 | AGCGACGGGCGCCGGTCTTTTGTCAAGACCGACCTGTCCGGTGCCTCGAATGAAC | 565 | | |
| DB | 150 | AGCGACGGGCGCCGGTCTTTTGTCAAGACCGACCTGTCCGGTGCCTCGAATGAAC | 209 | | |
| QY | 566 | GCAGGACGAGGACGCGGCTATCGTGGTGGCCACGACGGGCGTTCCTTCGCGAGCTGT | 625 | | |
| DB | 210 | GCAGGACGAGGACGCGGCTATCGTGGTGGCCACGACGGGCGTTCCTTCGCGAGCTGT | 269 | | |
| QY | 626 | GCTCGACGTTGTCACTGAAGCGGGAAGGACCTGGCTGCTATTGGGCGAAGTCCGGGCA | 685 | | |
| DB | 270 | GCTCGACGTTGTCACTGAAGCGGGAAGGACCTGGCTGCTATTGGGCGAAGTCCGGGCA | 329 | | |
| QY | 686 | GGATCTCTGTATCTACCTTGTCTTCGCGAGAAAGTATCCATCATGCTCTGATGCAAT | 745 | | |
| DB | 330 | GGATCTCTGTATCTACCTTGTCTTCGCGAGAAAGTATCCATCATGCTCTGATGCAAT | 389 | | |
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| QY | 806 | CATCGACGAGCAGCTACTCGGATGGAAGCGGCTTGTGATCAGGATGATCTGGACGA | 865 | | |
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| QY | 866 | AGAGCATCAGGGGCTCGCGCAGCCGAACTGTTTCGCGCAGGCTCAAGCGCGCATGCCGA | 925 | | |
| DB | 510 | AGAGCATCAGGGGCTCGCGCAGCCGAACTGTTTCGCGCAGGCTCAAGCGCGCATGCCGA | 569 | | |
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| QY | 986 | TGGCGGCTTTTCTGGAAATTCATGACTGTGGCGGCTGGGTGTGGCGACCGCTATCAGGA | 1045 | | |
| DB | 630 | TGGCGGCTTTTCTGGAAATTCATGACTGTGGCGGCTGGGTGTGGCGACCGCTATCAGGA | 689 | | |
| QY | 1046 | CATAGCGTTGGCTACCCGCTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTT | 1105 | | |
| DB | 690 | CATAGCGTTGGCTACCCGCTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTT | 749 | | |
| QY | 1106 | CCTCGTGTCTTACGGTATCGCGCTCCGATTTCGACGCGCATCGGCTTCTATCGGCTTCT | 1165 | | |
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CK288711
LOCUS
DEFINITION

ACCSSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

CK288711 878 bp mRNA linear EST 02-AUG-2004
EST751433 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMBI49 5'
end, mRNA sequence.
CK288711 GI:39866496
EST.
Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 878)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers
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/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN

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|-----------------------|-----|---|---------------------|-----------|-------------|
| Query Match | | 7.3%; | Score 587; | DB 7; | Length 878; |
| Best Local Similarity | | 100.0%; | Pred. No. 9.3e-126; | | |
| Matches 587; | | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
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| QY | 656 | CTGGCTGTATTTGGCGAAGTGGCGGCGAGATCTCTGTCTCTCTACCTTGTCTCTGC | 715 | | |
| DB | 61 | CTGGCTGTATTTGGCGAAGTGGCGGCGAGATCTCTGTCTCTCTACCTTGTCTCTGC | 120 | | |
| QY | 716 | CGAAGAGTATCCATCATGGCTGTGATGCAATGGCGGCTGCATACGCTTGTATCGGCTAC | 775 | | |
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| QY | 776 | CTGCCCATTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCAGTACTCGATGGAAGC | 835 | | |
| DB | 181 | CTGCCCATTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCAGTACTCGATGGAAGC | 240 | | |
| QY | 836 | CGGTCTTGTGATCGAGGATGATCTGGACGAAGAGCATCAGGGGCTCGGCCAGCGCAACT | 895 | | |
| DB | 241 | CGGTCTTGTGATCGAGGATGATCTGGACGAAGAGCATCAGGGGCTCGGCCAGCGCAACT | 300 | | |

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 QY 1136 TTGCGAGCGCATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAG 1182
 Db 541 TTGCGAGCGCATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAG 587

RESULT 11

AQ361914

LOCUS

DEFINITION 789 bp DNA linear GSS 03-FEB-1999
 clone mgxb0005K01f CUGI Rice Blast BAC Library Magnaporthe grisea genomic

ACCESSION

AQ361914

VERSION

AQ361914.1

KEYWORDS

GSS.

SOURCE

ORGANISM

Magnaporthe grisea (anamorph: Pyricularia grisea)

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

1 (bases 1 to 789)

Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,

Phillips, K., Sasinsowski, M., Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea

Genome

Unpublished (1998)

Contact: Dean RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson University, Clemson, SC 29634

Tel: 864 656 5737

Fax: 864 656 4293

Email: rdean@clemson.edu

Seq primer: TAATACGACTCATATAGGG

Class: BAC ends

High quality sequence start: 41

High quality sequence stop: 392.

Location/Qualifiers

1..789

/organism="Magnaporthe grisea"

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/strain="70-15"

/db_xref="taxon:148305"

/clone="mgxb0005K01f"

/tissue_type="protoplasts"

/lab_host="E. coli DH10B"

/clone_lib="CUGI Rice Blast BAC Library"

/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;

Rice blast is one of the most devastating fungal diseases

of rice world wide. It is a filamentous ascomycete with

a haploid genome (n=7) of approximately 40 Mbp. Rice

blast is an important model fungal pathogen for studying

numerous aspects of the fungal-host interaction. In

order to facilitate genome wide analysis, a BAC library

containing 9216 clones with an average insert size of 130

kbp was constructed. This library represents greater

than 25X genome coverage. High density colony filters

are available upon request."

ORIGIN

Query Match

Best Local Similarity 7.2%; Score 577.4; DB 8; Length 789;

Matches 584; Conservative 97.8%; Pred. No. 1.6e-123;

Mismatches 0; Indels 0; Gaps 0;

QY 581 GCGCTATCTGCTGGTGGCGGACCGCTATCAGCATAGCGTTGGCTACCGGTGATATGCTGA 640
 Db 39 GCGCTATCTGCTGGTGGCGGACCGCTATCAGCATAGCGTTGGCTACCGGTGATATGCTGA 98
 QY 641 TGAAGCGGGAAGGAGTATGCTGCTATTTGGGCGAAGTCCCGGGGACGATCTCTCTGTCATC 700
 Db 99 TGAAGCGGGAAGGAGTATGCTGCTATTTGGGCGAAGTCCCGGGGACGATCTCTCTGTCATC 158
 QY 701 TCACCTTGTCTTGGCGGAGGAGTATCCTATTCATTCATTCATTCATTCATTCATTCATTCAT 760
 Db 159 TCACCTTGTCTTGGCGGAGGAGTATCCTATTCATTCATTCATTCATTCATTCATTCATTCAT 218
 QY 761 GCTTGATCGGCTACCTGCGGACCGCTATTCAGCATAGCGTTGGCTACCGGTGATATGCTGA 820
 Db 219 GCTTGATCGGCTACCTGCGGACCGCTATTCAGCATAGCGTTGGCTACCGGTGATATGCTGA 278
 QY 821 TACTCGGATGGAAGCGGCTCTTGTGATCAGGATGATCTGGACGAGAGATCAGGGGCT 880
 Db 279 TACTCGGATGGAAGCGGCTCTTGTGATCAGGATGATCTGGACGAGAGATCAGGGGCT 338
 QY 881 CCGCGCAGCGCACTGTTGCGCAGGCTCAAGCGGCGCATGCCCGGACGCGGAGGATCTCGT 940
 Db 339 CCGCGCAGCGCACTGTTGCGCAGGCTCAAGCGGCGCATGCCCGGACGCGGAGGATCTCGT 398
 QY 941 CGTGACCCATGCGGATGCTGCTTCCGGAATATCATGTGGAATGCGCGCTTTCTG 1000
 Db 399 CGTGACCCATGCGGATGCTGCTTCCGGAATATCATGTGGAATGCGCGCTTTCTG 458
 QY 1001 ATTCATCGACTGTGCGCGCTGGGTGTGGCGGACCGCTATCAGGACATAGGTTGGCTAC 1060
 Db 459 ATTCATCGACTGTGCGCGCTGGGTGTGGCGGACCGCTATCAGGACATAGGTTGGCTAC 518
 QY 1061 CCGTGATATTCCTGAAGAGCTTGGCGGCAATGGGCTGACCGCTTCTCTGCTTTACGG 1120
 Db 519 CCGTGATATTCCTGAAGAGCTTGGCGGCAATGGGCTGACCGCTTCTCTGCTTTACGG 578
 QY 1121 TATCGCGCTCCCGATTTCGCGGACGATCGCTTCTATCGCTTCTTACCGAGTCTT 1177
 Db 579 TATCGCGCTCCCGATTTCGCGGACGATCGCTTCTATCGCTTCTTACCGAGGNTTT 635

RESULT 12

AQ398387

LOCUS

DEFINITION

620 bp DNA linear GSS 06-MAR-1999

clone mgxb0009J05f CUGI Rice Blast BAC Library Magnaporthe grisea genomic

clone mgxb0009J05f, genomic survey sequence.

ACCESSION

AQ398387

VERSION

AQ398387.1

KEYWORDS

GSS.

SOURCE

ORGANISM

Magnaporthe grisea (anamorph: Pyricularia grisea)

Magnaporthe grisea

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

1 (bases 1 to 620)

Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,

Phillips, K., Sasinsowski, M., Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea

Genome

Unpublished (1998)

Contact: Dean RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson University, Clemson, SC 29634

Tel: 864 656 5737

Fax: 864 656 4293

Email: rdean@clemson.edu

Seq primer: TAATACGACTCATATAGGG

Class: BAC ends

High quality sequence stop: 187.

FEATURES

source

FEATURES

source

Location/Qualifiers

1..620
/organism="Magnaporthe grisea"
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/strain="70-15"
/db_xref="taxon:148305"
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/tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC Library"
/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII; Rice blast is one of the most devastating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."

ORIGIN

Query Match 7.0%; Score 559.8; DB 8; Length 620;
Best Local Similarity 98.8%; Pred. No. 2e-119; 7; Indels 0; Gaps 0;
Matches 564; Conservative 0; Mismatches 0

609 GTTCTTGGCGAGCTGTGTCACGTGTGTCACGTGAGCGGAGGAGGACTGGTGTATTG 668
1 GTTCTTGGCGAGCTGTGTCACGTGTGTCACGTGAGCGGAGGAGGACTGGTGTATTG 60

669 GCGGAAGTGGCGGAGGAGTCTCTGTATCTATCTACCTGCTCTCGGAGAACTATCC 728
61 GCGGAAGTGGCGGAGGAGTCTCTGTATCTATCTACCTGCTCTCGGAGAACTATCC 120

729 ATCATGCTGATGCAATGCGGGCTGTCATACCTGATCGGTACTCTCCCATTCGAC 788
121 ATCATGCTGATGCAATGCGGGCTGTCATACCTGATCGGTACTCTCCCATTCGAC 180

789 CACCAAGCAACATCGCATCGAGCAGCAGTACTCGGATGGAAGCGGTCTTGTGAT 848
181 CACCAAGCAACATCGCATCGAGCAGCAGTACTCGGATGGAAGCGGTCTTGTGAT 240

849 CAGGATGATCTGGAAGAGCAATCAGGGCTCGCGCAGCGCACTGTTGCCAGCTC 908
241 CAGGATGATCTGGAAGAGCAATCAGGGCTCGCGCAGCGCACTGTTGCCAGCTC 300

909 AAGCGCGCATGCGCGAGGATCTCTGCTGACCCATGCGATGCTGTTGCCG 968
301 AAGCGCGCATGCGCGAGGATCTCTGCTGACCCATGCGATGCTGTTGCCG 360

969 AATATCATGGTGAATATGGCGCTTTCTGATTCATCGACTGTGCGCGCTGGTGTG 1028
361 AATATCATGGTGAATATGGCGCTTTCTGATTCATCGACTGTGCGCGCTGGTGTG 420

1029 GCGGACCCCTATCAGGACATAGCTTGGTACCCGTGATATGCTGAAGAGTTGGCGC 1088
421 GCGGACCCCTATCAGGACATAGCTTGGTACCCGTGATATGCTGAAGAGTTGGCGC 480

1089 GAATGGGCTGACCGCTTCTCTGCTGCTTACGGTATCGCGCTCCGATTCGAGCGCATC 1148
481 GAATGGGCTGACCGCTTCTCTGCTGCTTACCGGATCGCGCTCCGATTCGAGCGCATC 540

1149 GCCTTCTATCGCTTCTTACGAGTCTTCT 1179
541 GCCTTCTATCGCTTCTTACGAGTCTTCT 571

RESULT 13

CK801630

LOCUS

DEFINITION

CK801630 549 bp mRNA linear EST 26-FEB-2004
NF32C08f44.r1 Tall Rescue P1283316 44 deg C Heat Stress SSH cDNA
Schedonorus arundinaceus cDNA clone NF32C08f44 5', mRNA sequence.

FEATURES

source

CK801630

GI:43400943

EST.

Schedonorus arundinaceus (Festuca arundinacea)

Schedonorus arundinaceus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooidae; Poaceae; Schedonorus.

1 (bases 1 to 549)

Zhang Y., Zwonitzer, J.C., Chekhovskiy, K., May, G.D. and Mian, M.A.R.

A functional genomics approach for identification of heat tolerance

genes in tall fescue

(in) Hopkins, A., Wang, Z.Y., Mian, R., Sledge, M. and Barker, R.E.

(eds.), MOLECULAR BREEDING OF FORAGE AND TURF, Kluwer Acad. Pub. 0,

87-96 (2003)

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

Department of Chemistry and Biochemistry

Advanced Center for Genome Technology, University of Oklahoma

620 Parrington Oval, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

Contact Dr. Rouf Mian (rmian@ou.edu) regarding clone availability

Seq primer: M13 reverse primer

High quality sequence stop: 470.

Location/Qualifiers

1..549

/organism="Schedonorus arundinaceus"

/mol_type="mRNA"

/cultivar="P1283316"

/db_xref="taxon:4606"

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/tissue_type="shoot"

/lab_host="E.coli"

/clone_lib="Tall Rescue P1283316 44 deg C Heat Stress SSH

cDNA"

/note="Vector: PCR 2.1-TOPO; Site 1: EcoR I; Site 2: EcoR

I; BD/Clontech PCR-select cDNA subtraction library"

Query Match 6.8%; Score 542.4; DB 7; Length 549;

Best Local Similarity 99.8%; Pred. No. 2.2e-115;

Matches 543; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

556 TGAATGAATCGAGCAGCGAGCGGCTATCGTGGTGGCCACGCGGCGTCTCT 615

6 TGAATGAATCGAGCAGCGAGCGGCTATCGTGGTGGCCACGCGGCGTCTCT 65

616 GCGCAGCTGTCTCGAGCTTGTCTCACTGAAGCGGAGGAGTGGTGTCTATTGGCGAAG 675

66 GCGCAGCTGTCTCGAGCTTGTCTCACTGAAGCGGAGGAGTGGTGTCTATTGGCGAAG 125

676 TGCGGGGCGAGGATCTCTGTCTATCTCACCTTGTCTTCCGAGAGAAATTCATCATGG 735

126 TGCGGGGCGAGGATCTCTGTCTATCTCCACCTTGTCTTCCGAGAGAAATTCATCATGG 185

736 CTGATGCAATCGCGGCTGTGATAGCTTGTATCGGCTACCTGCCATTCGACCAACCAAG 795

186 CTGATGCAATCGCGGCTGTGATAGCTTGTATCGGCTACCTGCCATTCGACCAACCAAG 245

796 CGAAACATCGCATCGAGCGAGCAGCTATCTCGATGGAAGCGGCTTGTTCGATCAGGATG 855

246 CGAAACATCGCATCGAGCGAGCAGCTATCTCGATGGAAGCGGCTTGTTCGATCAGGATG 305

856 ATCTGGACGAAGAGCATCAGGGGCTCGCGCAGCGAACTGTTCGAGGCTCAGGCGC 915

306 ATCTGGACGAAGAGCATCAGGGGCTCGCGCAGCGAACTGTTCGAGGCTCAGGCGC 365

916 GATGCGCGCAGCGGAGGATCTCGTCTGACCCATCGCGATGCTCTTGGCCGAATATCA 975

366 GATGCGCGCAGCGGAGGATCTCGTCTGACCCATCGCGATGCTCTTGGCCGAATATCA 425

976 TGGTGGAATATGCGCCCTTTCTTCTGATTCATCGACTGTGCGCGCTGGGTGTGGCGACC 1035

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Db      426  TGGTGGAAATGCGCGCTTTCTGGATTCATCGACTGTGCCGCGCTGGGTGTGGCGAACC 485
QY      1036  GCTATCAGGACATAGCGTTGGCTACCGTTCATGATTTGCTGAAGAGCTTGGCGGCGAATGGG 1095
Db      486  GCTATCAGGACATAGCGTTGGCTACCGTTCATGATTTGCTGAAGAGCTTGGCGGCGAATGGG 545
QY      1096  CTGA 1099
Db      546  CTGA 549

RESULT 14
AQ447874
LOCUS   561 bp      DNA      linear      GSS 08-APR-1999
DEFINITION  clone mgxb0012101f, genomic survey sequence.
ACCESSION  AQ447874
VERSION    AQ447874.1 GI:4577011
KEYWORDS   GSS.
SOURCE     Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM   Magnaporthe grisea
REFERENCE  1 (bases 1 to 561)
AUTHORS    Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
            Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
TITLE      A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
            Genome
JOURNAL    Unpublished (1998)
COMMENT    Contact: Dean RA
            Clemson University Genomics Institute
            100 Jordan Hall, Clemson University, Clemson, SC 29634
            Tel: 864 656 5737
            Fax: 864 656 4293
            Email: rdean@clemson.edu
            Seq primer: TAATACGACTCCTATAGGG
            Class: BAC ends
            High quality sequence start: 42
            High quality sequence stop: 326.
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            1..561
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                /lab_host="E. coli DH10B"
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                /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
                Rice blast is one of the most devastating fungal diseases
                of rice world wide. It is a filamentous ascomycete with
                a haploid genome (n=7) of approximately 40 Mbp. Rice
                blast is an important model fungal pathogen for studying
                numerous aspects of the fungal-host interaction. In
                order to facilitate genome wide analysis, a BAC library
                containing 9216 clones with an average insert size of 130
                kbp was constructed. This library represents greater
                than 25X genome coverage. High density colony filters
                are available upon request."

ORIGIN
Query Match 6.4%; Score 514.8; DB 8; Length 561;
Best Local Similarity 99.6%; Pred. No. 6.4e-109;
Matches 516; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      510  CAGGGGCGCGCGTCTTTTGTCAAGACCGACCTGTCGGGTGCCCTGAATCAATGCGAG 569
Db      44   CAGGGGCGCGCGTCTTTTGTCAAGACCGACCTGTCGGGTGCCCTGTTGAATGCGAG 103
QY      570  GACGAGGACGCGCGGTATCTGGTGGTGGCCACGACGGCGGTTCCTTGGCGAGCTGTGCTC 629

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Db      104  GACGAGCAGCGGGGTATCGTGGCTGGCCACGACGGGCGTTCCTTCGCAGCTGTGCTC 163
QY      630  GACGTTGTCACTGAAGCGGGAAGGCACTGCTGCTATTGGGCGAAGTGCCTGGGCGCAGAT 689
Db      164  GACGTTGTCACTGAAGCGGGAAGGCACTGCTGCTATTGGGCGAAGTGCCTGGGCGCAGAT 223
QY      690  CTCCTGTCACTCACTTCTGCTCTGCGGAGAAAGTATCCATCATGCTGATGAATGCGG 749
Db      224  CTCCTGTCACTCACTTCTGCTCTGCGGAGAAAGTATCCATCATGCTGATGAATGCGG 283
QY      750  CGGCTGCATACCGTTTCATCGGCTACTGCTCCCATTCGACCAACGCAAAACATCGCATC 809
Db      284  CGGCTGCATACCGTTTCATCGGCTACTGCTCCCATTCGACCAACGCAAAACATCGCATC 343
QY      810  GAGCGAGCAGCTACTCGGATGAAGCCGGTCTTGTGATCAGATGATCTGACGGAAGAG 869
Db      344  GAGCGAGCAGCTACTCGGATGAAGCCGGTCTTGTGATCAGATGATCTGACGGAAGAG 403
QY      870  CATCAGGGGCTCGCGCCAGCCGAACCTGTTGCGCAGGCTCAAGGCGCGCATGCCGACGCG 929
Db      404  CATCAGGGGCTCGCGCCAGCCGAACCTGTTGCGCAGGCTCAAGGCGCGCATGCCGACGCG 463
QY      930  GAGGATCTCGTCTGACCCATGCGCATGCTGCTTGGCGAATATCATGTTGGAATATGCG 989
Db      464  GAGGATCTCGTCTGACCCATGCGCATGCTGCTTGGCGAATATCATGTTGGAATATGCG 523
QY      990  CGCTTTCTGGAATTCATCGACTGTGCGCGCTGGGTGT 1027
Db      524  CGCTTTCTGGAATTCATCGACTGTGCGCGCTGGGTGT 561

RESULT 15
AQ447775
LOCUS   509 bp      DNA      linear      GSS 08-APR-1999
DEFINITION  clone mgxb0011E13f, genomic survey sequence.
ACCESSION  AQ447775
VERSION    AQ447775.1 GI:4576912
KEYWORDS   GSS.
SOURCE     Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM   Magnaporthe grisea
REFERENCE  1 (bases 1 to 509)
AUTHORS    Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
            Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
TITLE      A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
            Genome
JOURNAL    Unpublished (1998)
COMMENT    Contact: Dean RA
            Clemson University Genomics Institute
            100 Jordan Hall, Clemson University, Clemson, SC 29634
            Tel: 864 656 5737
            Fax: 864 656 4293
            Email: rdean@clemson.edu
            Seq primer: TAATACGACTCCTATAGGG
            Class: BAC ends
            High quality sequence stop: 342.
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                /clone_lib="CUGI Rice Blast BAC Library"
                /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;
                Rice blast is one of the most devastating fungal diseases
                of rice world wide. It is a filamentous ascomycete with

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Wed Nov 10 09:31:03 2004

a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."

ORIGIN

| | | | | |
|-----------------------|-----------------|---------------------|-----------|-------------|
| Query Match | 6.4% | Score 508; | DB 8; | Length 509; |
| Best Local Similarity | 100.0%; | Pred. No. 2.4e-107; | | |
| Matches 508; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

| | | | |
|----|------|---|------|
| QY | 629 | CGACGTTGTCACTGAAGCGGGAAGGACCTGGCTGCTATTGGCGGAAGTCCCGGGCAGGA | 688 |
| Db | 1 | CGACGTTGTCACTGAAGCGGGAAGGACCTGGCTGCTATTGGCGGAAGTCCCGGGCAGGA | 60 |
| QY | 689 | TCTCCTGTCACTCACTTGTCTCTCCGCGAAGATATCCATCATGGCTGATGCAATGCG | 748 |
| Db | 61 | TCTCCTGTCACTCACTTGTCTCTCCGCGAAGATATCCATCATGGCTGATGCAATGCG | 120 |
| QY | 749 | GCGGCTGCATACGCTTGATCCGGCTACCTGCCATTCGACCCAGCGGGAACATCGCAT | 808 |
| Db | 121 | GCGGCTGCATACGCTTGATCCGGCTACCTGCCATTCGACCCAGCGGGAACATCGCAT | 180 |
| QY | 809 | CGAGCGAGCAGTACTCGGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGA | 868 |
| Db | 181 | CGAGCGAGCAGTACTCGGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGA | 240 |
| QY | 869 | GCATCAGGGGCTCGCGCCAGCGAACTGTTCCGAGGCTCAAGCGCGCATGCCGACGG | 928 |
| Db | 241 | GCATCAGGGGCTCGCGCCAGCGAACTGTTCCGAGGCTCAAGCGCGCATGCCGACGG | 300 |
| QY | 929 | CGAGGATCTCGTGTGACCCATGCGGATGCGCTTGGCCGAATATATGTGGAATGG | 988 |
| Db | 301 | CGAGGATCTCGTGTGACCCATGCGGATGCGCTTGGCCGAATATATGTGGAATGG | 360 |
| QY | 989 | CCGCTTTTCTGGATTATCGACTGTGCGCGGCTGGGTGCGGACCGCTATCAGGACAT | 1048 |
| Db | 361 | CCGCTTTTCTGGATTATCGACTGTGCGCGGCTGGGTGCGGACCGCTATCAGGACAT | 420 |
| QY | 1049 | AGCGTTGGCTACCGTGCATATTGCTGAAGAGCTTGGCGGGAATGGGCTGACCGCTTCCT | 1108 |
| Db | 421 | AGCGTTGGCTACCGTGCATATTGCTGAAGAGCTTGGCGGGAATGGGCTGACCGCTTCCT | 480 |
| QY | 1109 | CGTGTCTTACGGTATCGCGCTCCCGAT | 1136 |
| Db | 481 | CGTGTCTTACGGTATCGCGCTCCCGAT | 508 |

Search completed: November 9, 2004, 10:49:37
Job time : 14590 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 23:39:08 ; Search time 399 Seconds
(without alignments)
14237.155 Million cell updates/sec

Title: US-10-005-469-1

Perfect score: 7992

Sequence: 1 gccagcccccgttggggc.....ctctctgcagatcaagtact 7992

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCRUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 7989 | 100.0 | 7989 | 4 | US-09-539-601-10 |
| 2 | 7967 | 99.7 | 8001 | 4 | US-09-539-601-7 |
| 3 | 7949.4 | 99.5 | 8001 | 4 | US-09-539-601-22 |
| 4 | 7947.8 | 99.4 | 8001 | 4 | US-09-539-601-16 |
| 5 | 7941.4 | 99.4 | 8001 | 4 | US-09-539-601-28 |
| 6 | 7331 | 91.7 | 8637 | 4 | US-09-539-601-4 |
| 7 | 7309 | 91.5 | 8639 | 4 | US-09-539-601-13 |
| 8 | 7273.8 | 91.0 | 8638 | 4 | US-10-029-907-1 |
| 9 | 7272.8 | 91.0 | 8638 | 4 | US-10-029-907-24 |
| 10 | 7249.8 | 90.7 | 8638 | 4 | US-10-029-907-7 |
| 11 | 7248.8 | 90.7 | 8638 | 4 | US-10-029-907-25 |
| 12 | 7246.8 | 90.7 | 8642 | 4 | US-10-029-907-2 |
| 13 | 7245.6 | 90.7 | 8638 | 4 | US-10-029-907-6 |
| 14 | 7229.8 | 90.5 | 8648 | 4 | US-10-029-907-5 |
| 15 | 7222.6 | 90.4 | 8643 | 4 | US-10-029-907-4 |
| 16 | 6186.8 | 77.4 | 11076 | 4 | US-09-539-601-1 |
| 17 | 6169.2 | 77.2 | 11076 | 4 | US-09-539-601-25 |
| 18 | 6167.5 | 77.2 | 11076 | 4 | US-09-539-601-19 |
| 19 | 6161.2 | 77.1 | 11076 | 4 | US-09-539-601-31 |
| 20 | 5318.4 | 66.5 | 9595 | 3 | US-09-014-416-4 |
| 21 | 5218 | 65.3 | 7917 | 1 | US-08-324-977-31 |
| 22 | 5218 | 65.3 | 7917 | 2 | US-08-384-616-31 |
| 23 | 5218 | 65.3 | 7917 | 2 | US-08-904-686A-31 |
| 24 | 5218 | 65.3 | 7917 | 3 | US-09-315-850-31 |
| 25 | 5218 | 65.3 | 9416 | 1 | US-08-324-977-1 |
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| | | | | | | |
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| 28 | 5218 | 65.3 | 9416 | 3 | US-09-315-850-1 | Sequence 1, Appl |
| 29 | 5218 | 65.3 | 9416 | 4 | US-08-823-895A-27 | Sequence 27, Appl |
| 30 | 5211.8 | 65.2 | 9472 | 4 | US-08-150-204E-96 | Sequence 96, Appl |
| 31 | 5175.2 | 64.8 | 7863 | 1 | US-08-324-977-35 | Sequence 35, Appl |
| 32 | 5175.2 | 64.8 | 7863 | 2 | US-08-384-616-35 | Sequence 35, Appl |
| 33 | 5175.2 | 64.8 | 7863 | 2 | US-08-904-686A-35 | Sequence 35, Appl |
| 34 | 5175.2 | 64.8 | 7863 | 3 | US-09-315-850-35 | Sequence 35, Appl |
| 35 | 5175.2 | 64.8 | 9030 | 1 | US-08-324-977-13 | Sequence 13, Appl |
| 36 | 5175.2 | 64.8 | 9030 | 2 | US-08-384-616-13 | Sequence 13, Appl |
| 37 | 5175.2 | 64.8 | 9030 | 2 | US-08-904-686A-13 | Sequence 13, Appl |
| 38 | 5175.2 | 64.8 | 9030 | 3 | US-09-315-850-13 | Sequence 13, Appl |
| 39 | 4103.8 | 51.3 | 9599 | 3 | US-09-014-416-2 | Sequence 2, Appl |
| 40 | 4102.2 | 51.3 | 9599 | 3 | US-09-014-416-6 | Sequence 6, Appl |
| 41 | 4097.8 | 51.3 | 9646 | 3 | US-08-811-566-1 | Sequence 1, Appl |
| 42 | 4097.8 | 51.3 | 9646 | 3 | US-09-034-756-1 | Sequence 1, Appl |
| 43 | 4094.2 | 51.2 | 12980 | 3 | US-08-811-566-5 | Sequence 5, Appl |
| 44 | 4094.2 | 51.2 | 12980 | 3 | US-09-034-756-5 | Sequence 5, Appl |
| 45 | 4021.4 | 50.3 | 9379 | 3 | US-09-388-874-1 | Sequence 1, Appl |

ALIGNMENTS

RESULT 1
US-09-539-601-10
; Sequence 10, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I377/NS3-3'/wt
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1181)
; OTHER INFORMATION: hepatitis C virus core-neomycin phosphotransferase
; OTHER INFORMATION: fusion protein
; FEATURE:
; NAME/KEY: RBS
; LOCATION: (1190)..(1800)
; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1801)..(7759)
; OTHER INFORMATION: hepatitis C virus NS3 - 5B
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (7759)..(7989)
; PUBLICATION INFORMATION:
; AUTHORS: Lohmann, Volker
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; AUTHORS: Bartenschlager, Ralf
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 7989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| QY | 4261 | AAGTGTCTTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGCGCTCGTGGCC | 4320 | Db | 5341 | CTGTCTGGCGCTTCTTTGAAGGCAACATGCACTACCGCTCATGATCCCCGGAACGCTGAC | 5400 |
| Db | 4261 | AAGTGTCTTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGCGCTCGTGGCC | 4320 | QY | 5401 | CTCATCGAGGCAACCTCCTGTGCGCAGAGATGGCGGGAAACATCACCCGGTGGAG | 5460 |
| QY | 4321 | TTTAAGGTCATGAGCGGAGATGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCT | 4380 | Db | 5401 | CTCATCGAGGCAACCTCCTGTGCGGCGAGAGATGGCGGGAAACATCACCCGGTGGAG | 5460 |
| Db | 4321 | TTTAAGGTCATGAGCGGAGATGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCT | 4380 | QY | 5461 | TCAGAAATAAGGTAGTAATTTTGGACTCTTTTCGAGCGCTCCAAAGCGAGGAGATGAG | 5520 |
| QY | 4381 | ATCCTCTCCCTGGCGCCCTAGTCTGGGGTCTGTCGCGAGCGATATGCTCGGCAC | 4440 | Db | 5461 | TCAGAAATAAGGTAGTAATTTTGGACTCTTTTCGAGCGCTCCAAAGCGAGGAGATGAG | 5520 |
| Db | 4381 | ATCCTCTCCCTGGCGCCCTAGTCTGGGGTCTGTCGCGAGCGATATGCTCGGCAC | 4440 | QY | 5521 | AGGGAAGTATCGTTCCGCGGAGATCTCGGAGGTCCAGGAATTCCTCCGACGATG | 5580 |
| QY | 4441 | GTGGGCCACAGGGAGGGGGCTGTGAGTGGATGAACCGGCTGATAGCGTTGCTTCGCGG | 4500 | Db | 5521 | AGGGAAGTATCGTTCCGCGGAGATCTCGGAGGTCCAGGAATTCCTCCGACGATG | 5580 |
| Db | 4441 | GTGGGCCACAGGGAGGGGGCTGTGAGTGGATGAACCGGCTGATAGCGTTGCTTCGCGG | 4500 | QY | 5581 | CCCATATGGGCACGCCCGGATTTACAAACCTCCACCTGTTAGAGTCCCTGGAAGGACCCGGAC | 5640 |
| QY | 4501 | GGTAACCAAGTCTCCCCACGCACTATGTGCTGAGAGCGAGCTGACGATGCTCACT | 4560 | Db | 5581 | CCCATATGGGCACGCCCGGATTTACAAACCTCCACCTGTTAGAGTCCCTGGAAGGACCCGGAC | 5640 |
| Db | 4501 | GGTAACCAAGTCTCCCCACGCACTATGTGCTGAGAGCGAGCTGACGATGCTCACT | 4560 | QY | 5641 | TACGTCCCTCCAGTGGTACACGGGTGTCATTTGCCGCTGCAAGGCCCTCCCGATACA | 5700 |
| QY | 4561 | CAGATCCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTCAACAGTGAATCAAC | 4620 | Db | 5641 | TACGTCCCTCCAGTGGTACACGGGTGTCATTTGCCGCTGCAAGGCCCTCCCGATACA | 5700 |
| Db | 4561 | CAGATCCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTCAACAGTGAATCAAC | 4620 | QY | 5701 | CCTCCACGGAGAGAGAACGGTTGTCTGTTCAGATCTACCGTCTCTCTGCTTGGG | 5760 |
| QY | 4621 | GAGGACTGCTCCACGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGATTGGATATGC | 4680 | Db | 5701 | CCTCCACGGAGAGAGAACGGTTGTCTGTTCAGATCTACCGTCTCTCTGCTTGGG | 5760 |
| Db | 4621 | GAGGACTGCTCCACGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGATTGGATATGC | 4680 | QY | 5761 | GAGTCTCGCAACAAGACCTTCGGAGCTCCGAATCGTGGCGCTCGACAGCGCACCGCA | 5820 |
| QY | 4681 | ACGGTGTGACTGATTTCAAGACCTGGCTCAGTCCAGCTCCTCGCGGATTCGGGGA | 4740 | Db | 5761 | GAGTCTCGCAACAAGACCTTCGGAGCTCCGAATCGTGGCGCTCGACAGCGCACCGCA | 5820 |
| Db | 4681 | ACGGTGTGACTGATTTCAAGACCTGGCTCAGTCCAGCTCCTCGCGGATTCGGGGA | 4740 | QY | 5821 | ACGGCTCTCCTGACACAGCCCTCCGACGACGCGGATCCGATCTCAGCGACGGGTCTG | 5880 |
| QY | 4741 | GTCCCTTCTCTCATGTCAAGTGGGTACAGGAGGTCTGGCGGGGCAAGGATCATG | 4800 | Db | 5821 | ACGGCTCTCCTGACACAGCCCTCCGACGACGCGGATCCGATCTCAGCGACGGGTCTG | 5880 |
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| QY | 4801 | CAAAACCACTGCCATGTGGAGCAGATCACCGGACATGTGAAACCGTTCCATGAGG | 4860 | Db | 5881 | TCCTCATGCCCCCTTTCAGGGGAGCGGGGATCCGATCTCAGCGACGGGTCTGG | 5940 |
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| Db | 4921 | ACCAGGGCCCTGACAGCCCTCCCGGCGCAATTTATTCAGGCGCTGTGGGGGTG | 4980 | QY | 6061 | AGCAACTCTTGTCTCCGTCAACCAACTTGGTCTATGCTACCAATCTCGCAGCGCAAGC | 6120 |
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| QY | 5101 | GATGGGTGCGGTGTCACAGGTACGCTCCAGCGTGCAAAACCCCTCCTACGGAGAGGTC | 5160 | Db | 6181 | GTGCTCAAGAGATGAAGCGGATGCTCAAGTTAAGGTAAACTCTCTATCCGTGGAG | 6240 |
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| QY | 5161 | ACATTCTGGTGGGCTCAATCAATCTGGTGGGTACAGTCCCATGCGAGCGGAGCG | 5220 | Db | 6241 | GAAGCTGTAGTGAAGCGGAGGCGGATTCGAGGCTTAAACCATCTCGGTGGAAGGACTTG | 6300 |
| Db | 5161 | ACATTCTGGTGGGCTCAATCAATCTGGTGGGTACAGTCCCATGCGAGCGGAGCG | 5220 | QY | 6301 | GACGTCCGGAACCTATCCAGCAAGCGCGTTAACCAACATCTCGGTGGAAGGACTTG | 6360 |
| QY | 5221 | CCGAGGTAGAGTGTCACTTCCATGCTCACGACCCCTCCCAATTAACGGGAGCG | 5280 | Db | 6301 | GACGTCCGGAACCTATCCAGCAAGCGCGTTAACCAACATCTCGGTGGAAGGACTTG | 6360 |
| Db | 5221 | CCGAGGTAGAGTGTCACTTCCATGCTCACGACCCCTCCCAATTAACGGGAGCG | 5280 | QY | 6361 | CTGGAAGACACTGAGACCAATTAACCACTCATGCGCAAAATAGGTTTTCTGC | 6420 |
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| Db | 5281 | GCTAAGCGTAGGCTGACAGGAGGATCTCCCGCTCCTTGGCCAGGTCTATGAGTCCAG | 5340 | QY | 6421 | GTCCAAACAGAGAGGCGGCGCAGCGAGCTTATCGTATTTCCAGATTTGGGG | 6480 |
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Qy 6481 GTTCGTGTGCGAGAGAAATGCCCCCTTTAGCATGTGTTCTCCACCTCCCTCAGGCCGTG 6540
Db 6481 GTTCGTGTGCGAGAGAAATGCCCCCTTTAGCATGTGTTCTCCACCTCCCTCAGGCCGTG 6540
Qy 6541 ATGGGCTCTTTCATPACGGATTCCAAATACTCTCCTGGACAGCGGGTCCAGTTCCTGGTGAAT 6600
Db 6541 ATGGGCTCTTTCATPACGGATTCCAAATACTCTCCTGGACAGCGGGTCCAGTTCCTGGTGAAT 6600
Qy 6601 GCTGGAAGCGAAGAAATGCCCCCTTTAGCATGTGTTCTCCACCTCCCTCAGGCCGTG 6660
Db 6601 GCTGGAAGCGAAGAAATGCCCCCTTTAGCATGTGTTCTCCACCTCCCTCAGGCCGTG 6660
Qy 6661 ACGGTCACTGAGATGACATCGGTGTTGAGGAGTCAATCTACCAATGTTGTGACTGGCC 6720
Db 6661 ACGGTCACTGAGATGACATCGGTGTTGAGGAGTCAATCTACCAATGTTGTGACTGGCC 6720
Qy 6721 CCCGAAGCCAGACAGGCCCATAGGTGCGCTCACAGAGCGGCTTTACATCGGGGGCCCCCTG 6780
Db 6721 CCCGAAGCCAGACAGGCCCATAGGTGCGCTCACAGAGCGGCTTTACATCGGGGGCCCCCTG 6780
Qy 6781 ACTAATTTAAAGGCGAGAACTGCGGCTATCGCGGTGCGCGGAGCGGTGTACTGACG 6840
Db 6781 ACTAATTTAAAGGCGAGAACTGCGGCTATCGCGGTGCGCGGAGCGGTGTACTGACG 6840
Qy 6841 ACCAGCTGGGTAAATACCTTCATCTTACTTTGAAGCGCGCTGCGGCCCTGTGAGCTGG 6900
Db 6841 ACCAGCTGGGTAAATACCTTCATCTTACTTTGAAGCGCGCTGCGGCCCTGTGAGCTGG 6900
Qy 6901 AAGCTCCAGGACTGCAAGATGCTGCTATGCGGAGACGACCTTGTCTGTTATCTGTGAAGC 6960
Db 6901 AAGCTCCAGGACTGCAAGATGCTGCTATGCGGAGACGACCTTGTCTGTTATCTGTGAAGC 6960
Qy 6961 GCGGGACCCAGAGAGACAGGCGGACCTTACGGGCTTCACGAGGCTATGACTAGATAC 7020
Db 6961 GCGGGACCCAGAGAGACAGGCGGACCTTACGGGCTTCACGAGGCTATGACTAGATAC 7020
Qy 7021 TCTGCCCTTGGGACCCGCCCAACAGCAATACGACTTGGAGTTGATACATCATCG 7080
Db 7021 TCTGCCCTTGGGACCCGCCCAACAGCAATACGACTTGGAGTTGATACATCATCG 7080
Qy 7081 TCTCCATGTTGCTAGTTCGCGACGATGCTGCGCAAAAGGCTGTACTATCTCACCCGT 7140
Db 7081 TCTCCATGTTGCTAGTTCGCGACGATGCTGCGCAAAAGGCTGTACTATCTCACCCGT 7140
Qy 7141 GACCCACACCCCTTGGCGGGCTGCTGGGAGACAGCTAGACACTCCAGTCAAT 7200
Db 7141 GACCCACACCCCTTGGCGGGCTGCTGGGAGACAGCTAGACACTCCAGTCAAT 7200
Qy 7201 TCTGGCTAGGCAACATCATGATGATGCGCCACCTTGGGCAAGGATGATCCTGATG 7260
Db 7201 TCTGGCTAGGCAACATCATGATGATGCGCCACCTTGGGCAAGGATGATCCTGATG 7260
Qy 7261 ACTCAATTTCTTCCATCTTCTAGCTCAGGAACAACTTTGAAAGCCCTAGATGTCAG 7320
Db 7261 ACTCAATTTCTTCCATCTTCTAGCTCAGGAACAACTTTGAAAGCCCTAGATGTCAG 7320
Qy 7321 ATCTAGGGGCTGTTACTTCCATGAGGACCTTACCTCCTCAGATCATCAACGACTC 7380
Db 7321 ATCTAGGGGCTGTTACTTCCATGAGGACCTTACCTCCTCAGATCATCAACGACTC 7380
Qy 7381 CATGGCTTAGGCAATTTTCACTCCATGTTACTCTCCAGGTGAGATCAATAGGGGGCT 7440
Db 7381 CATGGCTTAGGCAATTTTCACTCCATGTTACTCTCCAGGTGAGATCAATAGGGGGCT 7440
Qy 7441 TCATGCTCAGGAAATCTGGGTACCGCCCTTTCGAGTCTGGAGACATCGGCCAGAAAT 7500
Db 7441 TCATGCTCAGGAAATCTGGGTACCGCCCTTTCGAGTCTGGAGACATCGGCCAGAAAT 7500
Qy 7501 GTCCGGCTAGGCTACTGTTCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTC 7560
Db 7501 GTCCGGCTAGGCTACTGTTCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTC 7560

Qy 7561 AACTGGCAGTAAAGCAAGCTCAAACTCACTCCAAATCCCGCTCGTCCAGTTGGAT 7620
Db 7561 AACTGGCAGTAAAGCAAGCTCAAACTCACTCCAAATCCCGCTCGTCCAGTTGGAT 7620
Qy 7621 TTATCCAGCTGTTGCTGCTGTTACAGCGGGGAGACATATATCACAGCCTGTCTCGT 7680
Db 7621 TTATCCAGCTGTTGCTGCTGTTACAGCGGGGAGACATATATCACAGCCTGTCTCGT 7680
Qy 7681 GCGGACCCCGCTGGTTCATGTGTCCTACTTCCTTCTGTAGGGGTAGGCATCTAT 7740
Db 7681 GCGGACCCCGCTGGTTCATGTGTCCTACTTCCTTCTGTAGGGGTAGGCATCTAT 7740
Qy 7741 CTACTCCCCAACCGATGAACGGGAGCTAAACACATCCAGGCCAATAGGCCATCTCTTT 7800
Db 7741 CTACTCCCCAACCGATGAACGGGAGCTAAACACATCCAGGCCAATAGGCCATCTCTTT 7800
Qy 7801 TTTCCTT 7860
Db 7801 TTTCCTT 7860
Qy 7861 TTTTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
Db 7861 TTTTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
Qy 7921 TAGCTGTGAAAGTCCGTGAGCGCTTCTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 7980
Db 7921 TAGCTGTGAAAGTCCGTGAGCGCTTCTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT 7980
Qy 7981 AGATCAAGT 7989
Db 7981 AGATCAAGT 7989

RESULT 2

US-09-539-601-7
; Sequence 7, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartschlag, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8001
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I389/NS3-3'/wt
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1193)
; OTHER INFORMATION: hepatitis C virus core-neomycin
; OTHER INFORMATION: phosphotransferase fusion protein
; FEATURE:
; NAME/KEY: RBS
; LOCATION: (1202)..(1812)
; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1813)..(7770)
; OTHER INFORMATION: hepatitis C virus nonstructural proteins NS3-5B
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (7771)..(8001)

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Best Local Similarity 99.9%; Pred. No. 0;

Matches 7989; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

| | | | |
|----|-----|--|-----|
| Qy | 1 | GCCAGCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGAACTACTG | 60 |
| Db | 1 | GCGAGCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGAACTACTG | 60 |
| Qy | 61 | TCCTCAGCAGAAAGCGTCTAGCCATGCGCTGTATGATGAGTGTCTGTCAGCCTCCAGGAC | 120 |
| Db | 61 | TCCTCAGCAGAAAGCGTCTAGCCATGCGCTGTATGATGAGTGTCTGTCAGCCTCCAGGAC | 120 |
| Qy | 121 | CCCCCTCCCGGAGACCATAGTGGTCTGCGGACCGGTGAGTACACCGGAATGGCAG | 180 |
| Db | 121 | CCCCCTCCCGGAGACCATAGTGGTCTGCGGACCGGTGAGTACACCGGAATGGCAG | 180 |
| Qy | 181 | GACGACCGGTCCTTTCTTGATCAACCCGCTCAATGCTCGAGATTTGGCGTGGCCCC | 240 |
| Db | 181 | GACGACCGGTCCTTTCTTGATCAACCCGCTCAATGCTCGAGATTTGGCGTGGCCCC | 240 |
| Qy | 241 | GCGAGACTGTAGCGAGTAGTGTGGTTCGCGAAGCGCTTGTGTAAGTCTGCTGATAGG | 300 |
| Db | 241 | GCGAGACTGTAGCGAGTAGTGTGGTTCGCGAAGCGCTTGTGTAAGTCTGCTGATAGG | 300 |
| Qy | 301 | GTGCTTGGAGTGTCCCGGAGGTCTGTAGACCGTGCACCATGAGCAGCAATCTTAAC | 360 |
| Db | 301 | GTGCTTGGAGTGTCCCGGAGGTCTGTAGACCGTGCACCATGAGCAGCAATCTTAAC | 360 |
| Qy | 361 | CTCAAGAAAAACAAA-----GGGCGCGCCATGATTGAAACAAGATGATTC | 408 |
| Db | 361 | CTCAAGAAAAACAAA-----GGGCGCGCCATGATTGAAACAAGATGATTC | 420 |
| Qy | 409 | ACGAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGCTATGACTGGGCAACAAGA | 468 |
| Db | 421 | ACGAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGCTATGACTGGGCAACAAGA | 480 |
| Qy | 469 | CAATCGGTCTGTATGCCCGCTGTTCGGCTGTACGCGAGCGGCGCGGTTCTTT | 528 |
| Db | 481 | CAATCGGTCTGTATGCCCGCTGTTCGGCTGTACGCGAGCGGCGCGGTTCTTT | 540 |
| Qy | 529 | TTGTCAAGACCGACTGTCCGGTGCCTGATGAACTCAGGACGAGGCGAGCGGCTAT | 588 |
| Db | 541 | TTGTCAAGACCGACTGTCCGGTGCCTGATGAACTCAGGACGAGGCGAGCGGCTAT | 600 |
| Qy | 589 | CGTGGTGGCCACGACGGCGTCTTCCGAGCTGTGCTCGAAGTGTCTACTGAGCGG | 648 |
| Db | 601 | CGTGGTGGCCACGACGGCGTCTTCCGAGCTGTGCTCGAAGTGTCTACTGAGCGG | 660 |
| Qy | 649 | GAAGGACTGTGCTATTGGCGAAGTCCGGGCGAGGATCTCTCTGCTACTACCTTG | 708 |
| Db | 661 | GAAGGACTGTGCTATTGGCGAAGTCCGGGCGAGGATCTCTCTGCTACTACCTTG | 720 |
| Qy | 709 | CTCTCCGAGAAAGTATCCATCATGCTGATGCAATCGCGGCTGATACGCTGATC | 768 |
| Db | 721 | CTCTCCGAGAAAGTATCCATCATGCTGATGCAATCGCGGCTGATACGCTGATC | 780 |
| Qy | 769 | CGGCTACCTGCCATTCCACCAACGAGCAACATCGCATCGAGGACGCTACTCGGA | 828 |
| Db | | | |

| | | | |
|----|------|---|------|
| Db | 781 | CGGCTACCTGCCATTCCAGCCACCAAGCGAAACATCGCATCGAGCGACACGTACTCGGA | 840 |
| Qy | 829 | TGGAGCGCGTCTTGTGATCAGATGATCTGGACGAAGACATCAGGGCTCGCGCAG | 888 |
| Db | 841 | TGGAGCGCGTCTTGTGATCAGATGATCTGGACGAAGACATCAGGGCTCGCGCAG | 900 |
| Qy | 889 | CCGAACTGTTGCGCAGGCTCAAGGCGGCGATCCCGGAGGAGATCTCTGCTGACCC | 948 |
| Db | 901 | CCGAACTGTTGCGCAGGCTCAAGGCGGCGATCCCGGAGGAGATCTCTGCTGACCC | 960 |
| Qy | 949 | ATGCGGATGCTGCTTCCGGAATATCATGTTGGAATATGGCGGCTTTCTGATTCATCG | 1008 |
| Db | 961 | ATGCGGATGCTGCTTCCGGAATATCATGTTGGAATATGGCGGCTTTCTGATTCATCG | 1020 |
| Qy | 1009 | ACTGTGCCCGGCTGGGTGTCGCGACCGCTATCAGGACATAGCTTGGCTACCGGTGATA | 1068 |
| Db | 1021 | ACTGTGCCCGGCTGGGTGTCGCGACCGCTATCAGGACATAGCTTGGCTACCGGTGATA | 1080 |
| Qy | 1069 | TTGCTGAAGAGCTTTGGCGGGAATGGGCTGACCGCTTCTCTGCTTTACGGTATCGCG | 1128 |
| Db | 1081 | TTGCTGAAGAGCTTTGGCGGGAATGGGCTGACCGCTTCTCTGCTTTACGGTATCGCG | 1140 |
| Qy | 1129 | CTCCGATTCGACGCGATCGCTTCTATGCGCTTCTTGAGGAGTCTTCTGAGTTAAA | 1188 |
| Db | 1141 | CTCCGATTCGACGCGATCGCTTCTATGCGCTTCTTGAGGAGTCTTCTGAGTTAAA | 1200 |
| Qy | 1189 | CAGACCAACGCTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTCT | 1248 |
| Db | 1201 | CAGACCAACGCTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTCT | 1260 |
| Qy | 1249 | AACGTTACTGGCGAAGCGCTTGGAAATAGGCGGCTGTGGTTGCTATATGTTATT | 1308 |
| Db | 1261 | AACGTTACTGGCGAAGCGCTTGGAAATAGGCGGCTGTGGTTGCTATATGTTATT | 1320 |
| Qy | 1309 | TCCACCATATTGCGCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGCTCTTG | 1368 |
| Db | 1321 | TCCACCATATTGCGCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGCTCTTG | 1380 |
| Qy | 1369 | ACGAGCATTCCTAGGGTCTTTCCCTCTCGCCAAAGAAATGCAAGTCTGTGTAATGTC | 1428 |
| Db | 1381 | ACGAGCATTCCTAGGGTCTTTCCCTCTCGCCAAAGAAATGCAAGTCTGTGTAATGTC | 1440 |
| Qy | 1429 | GTGAAGGAAGCAGTTCCTCTGGAAGCTTTTGAAGACAAAACAAGTCTGTAGCACCTT | 1488 |
| Db | 1441 | GTGAAGGAAGCAGTTCCTCTGGAAGCTTTTGAAGACAAAACAAGTCTGTAGCACCTT | 1500 |
| Qy | 1489 | TGCGAGGACGGAACCCCGACCTGCGACAGGTCCTCTGCGGCAAAAGCCAGCTGA | 1548 |
| Db | 1501 | TGCGAGGACGGAACCCCGACCTGCGACAGGTCCTCTGCGGCAAAAGCCAGCTGA | 1560 |
| Qy | 1549 | TAAGATACCTGCAAAAGCGGCAACCCCGAGTCCACGTTGTGAGTTGGATAGTTGTG | 1608 |
| Db | 1561 | TAAGATACCTGCAAAAGCGGCAACCCCGAGTCCACGTTGTGAGTTGGATAGTTGTG | 1620 |
| Qy | 1609 | GAAGAGTCAAAATGGCTCTCCTCAAGCGTATTCAAGGGGCTGAAGGATGCCAGAG | 1668 |
| Db | 1621 | GAAGAGTCAAAATGGCTCTCCTCAAGCGTATTCAAGGGGCTGAAGGATGCCAGAG | 1680 |
| Qy | 1669 | GTACCCCATTTGATGGGATCTGATCTGGGCTCGGTGCAATGCTTTACATGTTTGTAG | 1728 |
| Db | 1681 | GTACCCCATTTGATGGGATCTGATCTGGGCTCGGTGCAATGCTTTACATGTTTGTAG | 1740 |
| Qy | 1729 | TCGAGGTTAAAAACGCTTAGGCCCCCGAACCCAGCGGAGCTGGTTCCTTTGAAAAA | 1788 |
| Db | 1741 | TCGAGGTTAAAAACGCTTAGGCCCCCGAACCCAGCGGAGCTGGTTCCTTTGAAAAA | 1800 |
| Qy | 1789 | CACGATTAATACCATGGGCTTATTAGGCTTACTTCCCAACAGACGCGAGGCTTCTTGC | 1848 |
| Db | 1801 | CACGATTAATACCATGGGCTTATTAGGCTTACTTCCCAACAGACGCGAGGCTTCTTGC | 1860 |
| Qy | 1849 | TGCATCATCTAGCTTCAAGCGCGGACAGGAAACAGGTCGAGGGGAGGTCCTCAAGTG | 1908 |
| Db | 1861 | TGCATCATCTAGCTTCAAGCGCGGACAGGAAACAGGTCGAGGGGAGGTCCTCAAGTG | 1920 |

QY 1909 GTCTCACCGGAACAATCTTTCTGGCGACCTCGTCAATGGCGTGTGTGGACTGTC 1968
Db 1921 GTCTCACCGGAACAATCTTTCTGGCGACCTCGTCAATGGCGTGTGTGGACTGTC 1980
QY 1969 TATCATGTGTCGGGTCAAAGACCTTGGCGGCCCAAGGGCCCAATCAACCAATGTAC 2028
Db 1981 TATCATGTGTCGGGTCAAAGACCTTGGCGGCCCAAGGGCCCAATCAACCAATGTAC 2040
QY 2029 ACCAATGTGGACAGGACCTCTGGCTGGCAAGCGCCCGGGGCGGTTCCTTGACA 2088
Db 2041 ACCAATGTGGACAGGACCTCTGGCTGGCAAGCGCCCGGGGCGGTTCCTTGACA 2100
QY 2089 CAATGCACTGTGGCAGCTCGACCTTTACTTTGGTCAAGGACATGCCGATCTCATTCG 2148
Db 2101 CAATGCACTGTGGCAGCTCGACCTTTACTTTGGTCAAGGACATGCCGATCTCATTCG 2160
QY 2149 GTGGCCGGCGGGGCGACAGCAGGGGGGACCTACTCTCCGCCAGGCGCGTTCCTACTTG 2208
Db 2161 GTGGCCGGCGGGGCGACAGCAGGGGGGAGCCTACTCTCCGCCAGGCGCGTTCCTACTTG 2220
QY 2209 AAGGGCTCTTGGGGCGGTCCACTGCTCTGCCCTCGGGGCGACGCTGTGGGCATCTTTCCG 2268
Db 2221 AAGGGCTCTTGGGGCGGTCCACTGCTCTGCCCTCGGGGCGACGCTGTGGGCATCTTTCCG 2280
QY 2269 GCTGCGGTGTGACCCGAGGGGTTCGAAAGGGGTGGACTTTGTACCCGTCGAGTCTATG 2328
Db 2281 GCTGCGGTGTGACCCGAGGGGTTCGAAAGGGGTGGACTTTGTACCCGTCGAGTCTATG 2340
QY 2329 GAAACCACTATGCGTCCCGGTCTTACGGACAACTCGTCCCTCGGGCGGTACCGGAG 2388
Db 2341 GAAACCACTATGCGTCCCGGTCTTACGGACAACTCGTCCCTCGGGCGGTACCGGAG 2400
QY 2389 ACATTCCAGTGGGCCATCTACACGCCCTACTGTAGCGGCAAGAGCACTAAAGTGGCG 2448
Db 2401 ACATTCCAGTGGGCCATCTACACGCCCTACTGTAGCGGCAAGAGCACTAAAGTGGCG 2460
QY 2449 GCTGCGTATGAGCCCAAGGATAAAGTGTCTTCTGAAACCGCTCGCTCGCGGCCACC 2508
Db 2461 GCTGCGTATGAGCCCAAGGATAAAGTGTCTTCTGAAACCGCTCGCTCGCGGCCACC 2520
QY 2509 CTAGGTTTCGGGGGTATATGCTTAAGGCAATGATGATCGACCTTAACATCAGAACCGGG 2568
Db 2521 CTAGGTTTCGGGGGTATATGCTTAAGGCAATGATGATCGACCTTAACATCAGAACCGGG 2580
QY 2569 GTAAGGACCACTACACCGGGTGGCCCATCACGTAACCTACCTATGCAAGTTCCTTGGC 2628
Db 2581 GTAAGGACCACTACACCGGGTGGCCCATCACGTAACCTACCTATGCAAGTTCCTTGGC 2640
QY 2629 GACGTTGGTGTCTGGGGGCGCTATGACATCAATATATGATGATGATGATGATGATGAT 2688
Db 2641 GACGTTGGTGTCTGGGGGCGCTATGACATCAATATATGATGATGATGATGATGATGAT 2700
QY 2689 GACTCGACCACTATCTGGGCATCGGCACAGTCTCGACCAAGCGGAGAGCGGTGGAGCG 2748
Db 2701 GACTCGACCACTATCTGGGCATCGGCACAGTCTCGACCAAGCGGAGAGCGGTGGAGCG 2760
QY 2749 CGACTCGTGTGTGGCCACCGCTACGCTTCGGGATCGGTTCGGGATCGGTTCGGGATCGGT 2808
Db 2761 CGACTCGTGTGTGGCCACCGCTACGCTTCGGGATCGGTTCGGGATCGGTTCGGGATCGGT 2820
QY 2809 ATGAGGAGTGGTCTGTCCAGACTGGAGAAATCCCTTTTATGGCAAGGCCATCCCC 2868
Db 2821 ATGAGGAGTGGTCTGTCCAGACTGGAGAAATCCCTTTTATGGCAAGGCCATCCCC 2880
QY 2869 ATGAGGAGTGGTCTGTCCAGACTGGAGAAATCCCTTTTATGGCAAGGCCATCCCC 2928
Db 2881 ATGAGGAGTGGTCTGTCCAGACTGGAGAAATCCCTTTTATGGCAAGGCCATCCCC 2940
QY 2929 GAGCTCGCGGAGCTGTCCGCTCGGACTCAATGCTGTAGCATATTTACCGGGGCTT 2988
Db 2941 GAGCTCGCGGAGCTGTCCGCTCGGACTCAATGCTGTAGCATATTTACCGGGGCTT 3000

QY 2989 GATGTATCGTTCATACCACTAGCGGAGACGTCATTGTCTGTAGCAACGACGCTCTAATG 3048
Db 3001 GATGTATCGTTCATACCACTAGCGGAGACGTCATTGTCTGTAGCAACGACGCTCTAATG 3060
QY 3049 ACGGGCTTTTACCGGGATTTTCGACTCAGTGATCGACTGCAATATCATGTCTACCCAGACA 3108
Db 3061 ACGGGCTTTTACCGGGATTTTCGACTCAGTGATCGACTGCAATATCATGTCTACCCAGACA 3120
QY 3109 GTGCACTTCAGCTCGACCCGACCTTCCACTTGAGACGACGACCGTGCACCAAGCGG 3168
Db 3121 GTGCACTTCAGCTCGACCCGACCTTCCACTTGAGACGACGACCGTGCACCAAGCGG 3180
QY 3169 GTGTCACGCTCGACGCGGAGGACGAGTGTGTAGGGCAGGATGGGCAATTTACAGGTTT 3228
Db 3181 GTGTCACGCTCGACGCGGAGGACGAGTGTGTAGGGCAGGATGGGCAATTTACAGGTTT 3240
QY 3229 GTGACTCCAGGAGAACGGCCCTCGGGCATGTTCGATTCCTCGGTTCTGTGCGAGTGTCTAT 3288
Db 3241 GTGACTCCAGGAGAACGGCCCTCGGGCATGTTCGATTCCTCGGTTCTGTGCGAGTGTCTAT 3300
QY 3289 GACGGGGCTGT 3348
Db 3301 GACGGGGCTGT 3360
QY 3349 TACCTAAACACACACGAGGTTGCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3408
Db 3361 TACCTAAACACACACGAGGTTGCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3420
QY 3409 TTTTACGGCTTCACCCACATAGAGCGCCATTTCTTGTCCAGACTAAGCAGGACGAGAC 3468
Db 3421 TTTTACGGCTTCACCCACATAGAGCGCCATTTCTTGTCCAGACTAAGCAGGACGAGAC 3480
QY 3469 AACTTCCCTTACCTGT 3528
Db 3481 AACTTCCCTTACCTGT 3540
QY 3529 CCATCTGGGACCAAAATGTGAAGTGTCTATAGCTTAAGCTTAAGCTTAAGCTTAAGCTTA 3588
Db 3541 CCATCTGGGACCAAAATGTGAAGTGTCTATAGCTTAAGCTTAAGCTTAAGCTTAAGCTTA 3600
QY 3589 ACGCCCTCTGTATAGGCTGGGAGCGCTTCAAAACGAGGTACTTACACACACCCCATTA 3648
Db 3601 ACGCCCTCTGTATAGGCTGGGAGCGCTTCAAAACGAGGTACTTACACACACCCCATTA 3660
QY 3649 ACCAAATACATCATGT 3708
Db 3661 ACCAAATACATCATGT 3720
QY 3709 CTGCTAGCGGAGTCTGTAGCAGCTCTGGCGCGTATTTGCTGTGACAAACGAGGAGTGTGT 3768
Db 3721 CTGCTAGCGGAGTCTGTAGCAGCTCTGGCGCGTATTTGCTGTGACAAACGAGGAGTGTGT 3780
QY 3769 ATTGTGGGACGAGTATCTTTTGTCCGAAAGCGCGCCATCATTTCCGACAGGAGTCTTCT 3828
Db 3781 ATTGTGGGACGAGTATCTTTTGTCCGAAAGCGCGCCATCATTTCCGACAGGAGTCTTCT 3840
QY 3829 TACCGGAGTTCATGAGATGGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3888
Db 3841 TACCGGAGTTCATGAGATGGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3900
QY 3889 ATCAGCTCGCCGAAACAAATTCAAACAGAGGCAATCGGTTGTGTGTGTGTGTGTGTGTGT 3948
Db 3901 ATCAGCTCGCCGAAACAAATTCAAACAGAGGCAATCGGTTGTGTGTGTGTGTGTGTGTGT 3960
QY 3949 CAAAGCGAGGCTCTGCTCGCTCGGTTGGTGAATCAAAGTGGCGGACCCCTCGAAGCCTTCTG 4008
Db 3961 CAAAGCGAGGCTCTGCTCGCTCGGTTGGTGAATCAAAGTGGCGGACCCCTCGAAGCCTTCTG 4020
QY 4009 GCGAAGCATATGTGGAAATTTTCAATCAGCGGATACAAATATTTAGCAGGCTTGTCCACTCTG 4068
Db 4021 GCGAAGCATATGTGGAAATTTTCAATCAGCGGATACAAATATTTAGCAGGCTTGTCCACTCTG 4080
QY 4069 CCTGGGCAACCCCGCATAGCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4128

| | | | |
|----|------|---|------|
| QY | 6289 | TATGGGGAAAAGCAGTCCGGAAACCTATTCACGAGGCGCGTTAAACCACATCGCTCCGTG | 6348 |
| DB | 6301 | TATGGGGCAAAGCAGTCCGNAACCTATTCAGAGAGCGGTAAACCACATCCGCTCCGTG | 6360 |
| QY | 6349 | TGGAAGGACTTGCTGGAAAGACACTGAGACACCAATTGACACCAACCATATGCGCAAAAAT | 6408 |
| DB | 6361 | TGGAAGGACTTGCTGGAAAGACACTGAGACACCAATTGACACCAACCATATGCGCAAAAAT | 6420 |
| QY | 6409 | GAGGTTTTCTCGCTCCACACAGAGAGAGGGGGCGCAAGCAGCTCGCTTATCGTATTC | 6468 |
| DB | 6421 | GAGGTTTTCTCGCTCCACACAGAGAGAGGGGGCGCAAGCAGCTCGCTTATCGTATTC | 6480 |
| QY | 6469 | CCAGATTTGGGGGTTCTGTGTGGAGAAAATGGCCCTTTACGATGTGGTCTCCACCCCTC | 6528 |
| DB | 6481 | CCAGATTTGGGGGTTCTGTGTGGAGAAAATGGCCCTTTACGATGTGGTCTCCACCCCTC | 6540 |
| QY | 6529 | CCTCAGGCGGTGATGGGCTCTTCTACGGAATTCOAATCTCTCTGGACAGCGGTCGAG | 6588 |
| DB | 6541 | CCTCAGGCGGTGATGGGCTCTTCTACGGAATTCOAATCTCTCTGGACAGCGGTCGAG | 6600 |
| QY | 6589 | TTCTGTGTGAATGCTGGAAAGCGAAGAAATGCCCTATGGCTTCGATATGACACCCGC | 6648 |
| DB | 6601 | TTCTGTGTGAATGCTGGAAAGCGAAGAAATGCCCTATGGCTTCGATATGACACCCGC | 6660 |
| QY | 6649 | TGTTTTGACTCAACGGTCACTGGAATGACATCCGTGTGAGGAGTCAATCTACCAATGT | 6708 |
| DB | 6661 | TGTTTTGACTCAACGGTCACTGGAATGACATCCGTGTGAGGAGTCAATCTACCAATGT | 6720 |
| QY | 6709 | TGTGACTTGGCCCCGGAAGCCAGACAGGCCATAAGTTCGTCTCAGAGCGGCTTTACATC | 6768 |
| DB | 6721 | TGTGACTTGGCCCCGGAAGCCAGACAGGCCATAAGTTCGTCTCAGAGCGGCTTTACATC | 6780 |
| QY | 6769 | GGGGCCCCCTGACTAATTCTTAAAGGCGAAGCTGCGGCTATCGCCGTCGCGCGGAGC | 6828 |
| DB | 6781 | GGGGCCCCCTGACTAATTCTTAAAGGCGAAGCTGCGGCTATCGCCGTCGCGCGGAGC | 6840 |
| QY | 6829 | GGTGTACTGACGACAGCTGCGGTAAATACCCTCACATGTTCATTGAAGGCGCTCGCGCC | 6888 |
| DB | 6841 | GGTGTACTGACGACAGCTGCGGTAAATACCCTCACATGTTCATTGAAGGCGCTCGCGCC | 6900 |
| QY | 6889 | TGTCGAGCTGGAAAGTTCAGGACTGCAAGATGCTGATTCGCGAGACGACCTTGTCTGT | 6948 |
| DB | 6901 | TGTCGAGCTGCGAAGCTCCAGGACTGCACGATGCTGATTCGCGAGACGACCTTGTCTGT | 6960 |
| QY | 6949 | ATCTGTCAAAGCGGGGACCCAGAGAGCGAGGCGAGCCTACGGGCTTTCAGGAGGCT | 7008 |
| DB | 6961 | ATCTGTCAAAGCGGGGACCCAGAGAGCGAGGCGAGCCTACGGGCTTTCAGGAGGCT | 7020 |
| QY | 7009 | ATGACTAGATACCTCTGCCCCCTTGGGGACCCGCCCAAACCAATACGACTTGGAGTTG | 7068 |
| DB | 7021 | ATGACTAGATACCTCTGCCCCCTTGGGGACCCGCCCAAACCAATACGACTTGGAGTTG | 7080 |
| QY | 7069 | ATAACATCATGCTCCTCCAATGTGTAGTCGCGCAGATGCACTCTGGCAAAAAGGCTAC | 7128 |
| DB | 7081 | ATAACATCATGCTCCTCCAATGTGTAGTCGCGCAGATGCACTCTGGCAAAAAGGCTAC | 7140 |
| QY | 7129 | TATCTCACCCGCTGACCCCAACCCCTTTCGCGGGCTGCGTGGAGACAGCTACACAC | 7188 |
| DB | 7141 | TATCTCACCCGCTGACCCCAACCCCTTTCGCGGGCTGCGTGGAGACAGCTACACAC | 7200 |
| QY | 7189 | ACTCCAGTCAATTCCTGGCTAGGCAACATCATATGATGCGCCCACTTGTGGGCAAG | 7248 |
| DB | 7201 | ACTCCAGTCAATTCCTGGCTAGGCAACATCATATGATGCGCCCACTTGTGGGCAAG | 7260 |
| QY | 7249 | ATGATCCTGATGACTCATTTCTTCTCATCTTCTAGCTCAGGAACAACCTGAAAAGCC | 7308 |
| DB | 7261 | ATGATCCTGATGACTCATTTCTTCTCATCTTCTAGCTCAGGAACAACCTGAAAAGCC | 7320 |
| QY | 7309 | CTAGATTGTGAGATCTACGGGGCTGTACTCCATTGAGCCTTGCACCTCAGATC | 7368 |
| DB | 7321 | CTAGATTGTGAGATCTACGGGGCTGTACTCCATTGAGCCTTGCACCTCAGATC | 7380 |

| | | | |
|---|------|---|------|
| QY | 7369 | ATTCAACGACTCCATGGCGCTTAGCGCAATTTTCATCCTCATAGTACTCTCCAGGTGAGATC | 7429 |
| Db | 7381 | ATTCAACGACTCCATGGCGCTTAGCGCAATTTTCATCCTCATAGTACTCTCCAGGTGAGATC | 7440 |
| QY | 7429 | AATAGGGTGCTTCATCGCTCAGGAACAATTGGGGTACCGGCCCTTGCAGTCTGGAGACAT | 7488 |
| Db | 7441 | AATAGGGTGCTTCATCGCTCAGGAACAATTGGGGTACCGGCCCTTGCAGTCTGGAGACAT | 7500 |
| QY | 7489 | CGGGCCAGAAGTGTCCGCGCTAGGCTACTGTCCCAGGGGGGAGGGCTGCCACTTGTGGC | 7548 |
| Db | 7501 | CGGGCCAGAAGTGTCCGCGCTAGGCTACTGTCCCAGGGGGGAGGGCTGCCACTTGTGGC | 7560 |
| QY | 7549 | AAGTACCCTCTTCAACTGGCGAGTAAGGACCAAAGCTCAAACTCCAATCCCAGGCTGG | 7608 |
| Db | 7561 | AAGTACCCTCTTCAACTGGCGAGTAAGGACCAAAGCTCAAACTCCAATCCCAGGCTGG | 7620 |
| QY | 7609 | TCCCAGTTGGATTTATCCAGCTGGTTGCTGCTTACAGCGGGGAGACATATATCAC | 7668 |
| Db | 7621 | TCCCAGTTGGATTTATCCAGCTGGTTGCTGCTTACAGCGGGGAGACATATATCAC | 7680 |
| QY | 7669 | AGCCTGTCTCGTGGCCGACCCGCTGGTTTCATGTGGTGGCTACTCCTACTTTCGTAGGG | 7728 |
| Db | 7681 | AGCCTGTCTCGTGGCCGACCCGCTGGTTTCATGTGGTGGCTACTCCTACTTTCGTAGGG | 7740 |
| QY | 7729 | GTAGGCATCTACTPACTCCCCAACCGGATGAACGGGGAGCTAAACACTCCAGGCCAATAGG | 7788 |
| Db | 7741 | GTAGGCATCTACTPACTCCCCAACCGGATGAACGGGGAGCTAAACACTCCAGGCCAATAGG | 7800 |
| QY | 7789 | CCATCCCTGTTTTTTTCCCTTT | 7848 |
| Db | 7801 | CCATCCCTGTTTTTTTCCCTTT | 7860 |
| QY | 7849 | TTTTTCTCCITTTTTTTTTTCCCTTTTTTTTTTCCCTTTTTTCCCTTTGGTGCGCTCCATCTT | 7908 |
| Db | 7861 | TTTTTCTCCITTTTTTTTTTCCCTTTTTTTTTTCCCTTTTTTCCCTTTGGTGCGCTCCATCTT | 7920 |
| QY | 7909 | CCTAGTCAACGGCTAGCTGTGAAGGTCGGTGAGCCGCTTGACTGCAGAGAGTGCTGATAC | 7968 |
| Db | 7921 | CCTAGTCAACGGCTAGCTGTGAAGGTCGGTGAGCCGCTTGACTGCAGAGAGTGCTGATAC | 7980 |
| QY | 7969 | TGGCCTCTCTGCAGATCAAGT | 7989 |
| Db | 7981 | TGGCCTCTCTGCAGATCAAGT | 8001 |
| RESULT 3 | | | |
| US-09-539-601-22 | | | |
| ; Sequence 22, Application US/09539601C | | | |
| ; Patent No. 6630343 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Bartenschlager, Ralf FW | | | |
| ; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System | | | |
| ; FILE REFERENCE: all sequences | | | |
| ; CURRENT APPLICATION NUMBER: US/09/539,601C | | | |
| ; CURRENT FILING DATE: 2001-08-30 | | | |
| ; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY | | | |
| ; EARLIER FILING DATE: 1999-04-03 | | | |
| ; NUMBER OF SEQ ID NOS: 51 | | | |
| ; SOFTWARE: PatentIn Ver. 2.1 | | | |
| ; SEQ ID NO 22 | | | |
| ; LENGTH: 8001 | | | |
| ; TYPE: DNA | | | |
| ; ORGANISM: Hepatitis C virus | | | |
| ; FEATURE: | | | |
| ; NAME/KEY: 5'UTR | | | |
| ; LOCATION: (1)..(341) | | | |
| ; OTHER INFORMATION: construct I389/NS3-3'/5.1 | | | |
| ; FEATURE: | | | |
| ; NAME/KEY: CDS | | | |
| ; LOCATION: (342)..(1193) | | | |
| ; OTHER INFORMATION: hepatitis C virus core - neomycin | | | |
| ; OTHER INFORMATION: phosphotransferase fusion protein | | | |
| ; FEATURE: | | | |

; NAME/KEY: RBS
; LOCATION: (1202)..(1812)
; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1813)..(7770)
; OTHER INFORMATION: hepatitis C virus nonstructural proteins NS3 - 5B
; OTHER INFORMATION: of cell culture-adapted clone no. 5.1
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (7771)..(8001)
US-09-539-601-22

Query Match 99.5%; Score 7949.4; DB 4; Length 8001;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7978; Conservative 0; Mismatches 11; Indels 12; Gaps 1;

QY 1 GCCAGCCCCGATTGGGGCGACACTCCACATAGATCACTCCCTCTGTGAGGAATCTG 60
Db 1 GCCAGCCCCGATTGGGGCGACACTCCACATAGATCACTCCCTCTGTGAGGAATCTG 60

QY 61 TCTTCAAGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTGTCGAGCCTCCAGGAC 120
Db 61 TCTTCAAGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTGTCGAGCCTCCAGGAC 120

QY 121 CCCCCCTCCGGGAGAGCCATAGTGTCTCGGAAACGGGTGAGTACACCGGAATTCGCGAG 180
Db 121 CCCCCCTCCGGGAGAGCCATAGTGTCTCGGAAACGGGTGAGTACACCGGAATTCGCGAG 180

QY 181 GAGCAGCGGTCCTTTCTGGATCAACCCCTCAATGCCCTGGAGATTGGGCGTGGCCCC 240
Db 181 GAGCAGCGGTCCTTTCTGGATCAACCCCTCAATGCCCTGGAGATTGGGCGTGGCCCC 240

QY 241 GCAGAGCTGCTAGCCGAGTGTGTTGGTTCGGAAGGCTTGTGTGCTGCTGATGAGG 300
Db 241 GCAGAGCTGCTAGCCGAGTGTGTTGGTTCGGAAGGCTTGTGTGCTGCTGATGAGG 300

QY 301 GTCTTTCGAGTGCCTGGGAGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAAC 360
Db 301 GTCTTTCGAGTGCCTGGGAGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAAC 360

QY 361 CTCAGAGAAAACCAAA-----GGGCGCGCCATGATTGAACAAGATGGATTGC 408
Db 361 CTCAGAGAAAACCAAAAGCTAAACACAAAGGCGCGCATGATTGAACAAGATGGATTGC 420

QY 409 ACGCAGGTTCTCCGGCGCTGTGGGTGAGAGGCTATTCCGCTATGACTGGGCAACAGA 468
Db 409 ACGCAGGTTCTCCGGCGCTGTGGGTGAGAGGCTATTCCGCTATGACTGGGCAACAGA 468

QY 421 ACGCAGGTTCTCCGGCGCTGTGGGTGAGAGGCTATTCCGCTATGACTGGGCAACAGA 480
Db 421 ACGCAGGTTCTCCGGCGCTGTGGGTGAGAGGCTATTCCGCTATGACTGGGCAACAGA 480

QY 469 CAATCGGCTCTCTGATGCGCGCTGTTCGGCTGTGAGCGCAGGCGCGCGGTTCTTT 528
Db 469 CAATCGGCTCTCTGATGCGCGCTGTTCGGCTGTGAGCGCAGGCGCGCGGTTCTTT 528

QY 481 CAATCGGCTCTCTGATGCGCGCTGTTCGGCTGTGAGCGCAGGCGCGCGGTTCTTT 540
Db 481 CAATCGGCTCTCTGATGCGCGCTGTTCGGCTGTGAGCGCAGGCGCGCGGTTCTTT 540

QY 529 TTGTCAAGACGACCTGTCCGGTCCCTGTAATGAATGAACTGCAGGACGAGCGCGGCTAT 588
Db 529 TTGTCAAGACGACCTGTCCGGTCCCTGTAATGAATGAACTGCAGGACGAGCGCGGCTAT 588

QY 541 TTGTCAAGACGACCTGTCCGGTCCCTGTAATGAATGAACTGCAGGACGAGCGCGGCTAT 600
Db 541 TTGTCAAGACGACCTGTCCGGTCCCTGTAATGAATGAACTGCAGGACGAGCGCGGCTAT 600

QY 589 GTCGGTGGCCACGAGCGGCTGCTTTCGGAGCTGTGCTGAGCTGTGCTGAGCTGAGCGG 648
Db 589 GTCGGTGGCCACGAGCGGCTGCTTTCGGAGCTGTGCTGAGCTGTGCTGAGCTGAGCGG 648

QY 601 GTCGGTGGCCACGAGCGGCTGCTTTCGGAGCTGTGCTGAGCTGTGCTGAGCTGAGCGG 660
Db 601 GTCGGTGGCCACGAGCGGCTGCTTTCGGAGCTGTGCTGAGCTGTGCTGAGCTGAGCGG 660

QY 649 GAAGGAGTGTGCTATTGGGCGAAGTCCGGGCGAGGATCTCTCTGTCATCTCACCTTG 708
Db 649 GAAGGAGTGTGCTATTGGGCGAAGTCCGGGCGAGGATCTCTCTGTCATCTCACCTTG 708

QY 661 GAAGGAGTGTGCTATTGGGCGAAGTCCGGGCGAGGATCTCTCTGTCATCTCACCTTG 720
Db 661 GAAGGAGTGTGCTATTGGGCGAAGTCCGGGCGAGGATCTCTCTGTCATCTCACCTTG 720

QY 709 CTCCTCGCAGAAAGTATCCATCATGCTGATGCAATGCGCGGCTGATACGCTTGATC 768
Db 709 CTCCTCGCAGAAAGTATCCATCATGCTGATGCAATGCGCGGCTGATACGCTTGATC 768

QY 721 CTCCTCGCAGAAAGTATCCATCATGCTGATGCAATGCGCGGCTGATACGCTTGATC 780
Db 721 CTCCTCGCAGAAAGTATCCATCATGCTGATGCAATGCGCGGCTGATACGCTTGATC 780

QY 769 CGGCTACCTGCCATTCAGACCAAGCGGAACATCGCATCGAGGAGCAGCTACTCGGA 828
Db 769 CGGCTACCTGCCATTCAGACCAAGCGGAACATCGCATCGAGGAGCAGCTACTCGGA 828

QY 781 CGGCTACCTGCCATTCAGACCAAGCGGAACATCGCATCGAGGAGCAGCTACTCGGA 840
Db 781 CGGCTACCTGCCATTCAGACCAAGCGGAACATCGCATCGAGGAGCAGCTACTCGGA 840

QY 829 TGGAAAGCCGGTCTTCTCGATCAGGATGATCTCGAAGAGAGCATCAGGGGCTCGGCCAG 888
Db 841 TGGAAAGCCGGTCTTCTCGATCAGGATGATCTCGAAGAGAGCATCAGGGGCTCGGCCAG 900

QY 889 CCGAACTGTTCCCAAGGCTCAAGGCGCGCATCCGACGCGGAGGATCTCTGCTGACCC 948
Db 901 CCGAACTGTTCCCAAGGCTCAAGGCGCGCATCCGACGCGGAGGATCTCTGCTGACCC 960

QY 949 ATGGCGATGCTGCTTCCGGAATATCATGTCGAAATGCGCGCTTTCTTGGATTATCG 1008
Db 961 ATGGCGATGCTGCTTCCGGAATATCATGTCGAAATGCGCGCTTTCTTGGATTATCG 1020

QY 1009 ACTGTGCGCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGGTTGGCTACCCGTGATA 1068
Db 1021 ACTGTGCGCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGGTTGGCTACCCGTGATA 1080

QY 1069 TTGCTGAAGAGCTTGGCGGGAATGGCTGACCGCTTCTCGCTTTAGGTTATCGCG 1128
Db 1081 TTGCTGAAGAGCTTGGCGGGAATGGCTGACCGCTTCTCGCTTTAGGTTATCGCG 1140

QY 1129 CTCGCCATTCCGAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGTTAAA 1188
Db 1141 CTCGCCATTCCGAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGTTAAA 1200

QY 1189 CAGACCACAAACGGTTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCT 1248
Db 1201 CAGACCACAAACGGTTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCT 1260

QY 1249 AAGCTTACTGGCGAAGCGCTTGGATAGGCGGCTGCTGCTTGTCTATATGTTATTT 1308
Db 1261 AAGCTTACTGGCGAAGCGCTTGGATAGGCGGCTGCTGCTTGTCTATATGTTATTT 1320

QY 1309 TCACACATATGCGCTTCTTGGCAATGTGAGGCGCGGAAACCTGCGCCCTGCTTCTTG 1368
Db 1321 TCACACATATGCGCTTCTTGGCAATGTGAGGCGCGGAAACCTGCGCCCTGCTTCTTG 1380

QY 1369 ACGAGATTCCTTAGGGTCTTCCCTCTCGCAAGGAATGCAAGTCTGTTGAATGTC 1428
Db 1381 ACGAGATTCCTTAGGGTCTTCCCTCTCGCAAGGAATGCAAGTCTGTTGAATGTC 1440

QY 1429 GTGAAGAGAGCTTCTCTGGAAGCTTCTTGAAGACAAACAGCTCTGAGCGACCTT 1488
Db 1441 GTGAAGAGAGCTTCTCTGGAAGCTTCTTGAAGACAAACAGCTCTGAGCGACCTT 1500

QY 1489 TGCAAGCAGCGGAAACCCCACTTGGCGACAGGTGCTCTCGGCGCAAAAGCCACGTGTA 1548
Db 1501 TGCAAGCAGCGGAAACCCCACTTGGCGACAGGTGCTCTCGGCGCAAAAGCCACGTGTA 1560

QY 1549 TAAGATACCTGCAAGGCGGCAACACCCAGTGCCAGCTGTGAGTTGGATAGTTG 1608
Db 1561 TAAGATACCTGCAAGGCGGCAACACCCAGTGCCAGCTGTGAGTTGGATAGTTG 1620

QY 1609 GAAAGAGTCAATGGCTCTCTCAAGGCTATTCAACAGGCGCTGAAGGATGCCAGAG 1668
Db 1621 GAAAGAGTCAATGGCTCTCTCAAGGCTATTCAACAGGCGCTGAAGGATGCCAGAG 1680

QY 1669 GTACCCCATTTGATGGGATCTGATCTGGGCGCTCGGTGCAATGCTTTAATGTTTATG 1728
Db 1681 GTACCCCATTTGATGGGATCTGATCTGGGCGCTCGGTGCAATGCTTTAATGTTTATG 1740

QY 1729 TCGAGGTTAAAAACGCTTAGGCCCCCGGAAACACGCGGAGCTGTTTCTCTTTGAAAA 1788
Db 1741 TCGAGGTTAAAAACGCTTAGGCCCCCGGAAACACGCGGAGCTGTTTCTCTTTGAAAA 1800

QY 1789 CACCATATACATGGCGCTTATTACGCGCTTACTCCCAACAGACGCGAGGCTACTTGGC 1848
Db 1801 CACCATATACATGGCGCTTATTACGCGCTTACTCCCAACAGACGCGAGGCTACTTGGC 1860

QY 1849 TGCATCATCTAGCTTACAGGCGGGAAGGAAACAGGTCTGAGGGGAGGTCGAAGTG 1908
Db 1861 TGCATCATCTAGCTTACAGGCGGGAAGGAAACAGGTCTGAGGGGAGGTCGAAGTG 1920

| | | | | | | | | | |
|----|------|-------------------------------|-------------------------------------|------|----|------|-------------------------------|--------------------------------------|------|
| QY | 1909 | GTCTCCACCGCAACAATCTTTCCTGGCGA | CTCGGTCAATGGCGTGTGTGAGCTGC | 1968 | Db | 3001 | GATGTATCGTATACCAACTAGCGAGACGT | CATTGTGTAGCAACGCGCTCTAATG | 3060 |
| Db | 1921 | GTCTCCACCGCAACAATCTTTCCTGGCGA | CTCGGTCAATGGCGTGTGTGAGCTGC | 1980 | QY | 3049 | ACGGGCTTTACCGCGAATTCGACTCAGT | GAATCGACTCAATATGTGTACCCAGACA | 3108 |
| QY | 1969 | TATCATGTGTCGGGCTCAAGACCTTTCG | CGGCCCAAGGGCCCAATCACCAATGTAC | 2028 | Db | 3061 | ACGGGCTTTACCGGTGACTTCGACTCAG | TGATCGACTCAANTATGTGTACCCAGACA | 3120 |
| Db | 1981 | TATCATGTGTCGGGCTCAAGACCTTTCG | CGGCCCAAGGGCCCAATCACCAATGTAC | 2040 | QY | 3109 | GTGCACTTCAGCTCGACCCGACCTTTC | ACANTGTAGACCGCTGCCAAGAAGCGG | 3168 |
| QY | 2029 | ACCAATGTGGACAGGACCTTCGTGGCTG | CGCAAGCGCCCGCGGGCGGTTCCTTGACA | 2088 | Db | 3121 | GTGCACTTCAGCTCGACCCGACCTTTC | ACANTGTAGACCGCTGCCAAGAAGCGG | 3180 |
| Db | 2041 | ACCAATGTGGACAGGACCTTCGTGGCTG | CGCAAGCGCCCGCGGGCGGTTCCTTGACA | 2100 | QY | 3169 | GTGTCAAGCTTCGACGCGGAGGAGGAG | CTGTGTAGGGGAGGATGGCAATTCAGGTTT | 3228 |
| QY | 2089 | CCATGCACTTCGCGGAGCTCGACCTTTA | CTTGTGTACAGGAGGATGCCGATGTCAATCCG | 2148 | Db | 3181 | GTGTCAAGCTTCGACGCGGAGGAGGAG | CTGTGTAGGGGAGGATGGCAATTCAGGTTT | 3240 |
| Db | 2101 | CCATGCACTTCGCGGAGCTCGACCTTTA | CTTGTGTGTACAGGAGGATGCCGATGTCAATCCG | 2160 | QY | 3229 | GTGACTCCAGGAGAAACGGCCCTTCGG | GCATGTTCGATTCCTCGGTTCTGTGCGAGTGTCTAT | 3288 |
| QY | 2149 | GTGCGCGCGGCGGCGACAGAGGGGAG | CGGCTTCTCTCCCGGCAAGCTGTGGGCACTTTTGG | 2208 | Db | 3241 | GTGACTCCAGGAGAAACGGCCCTTCGG | GCATGTTCGATTCCTCGGTTCTGTGCGAGTGTCTAT | 3300 |
| Db | 2161 | GTGCGCGCGGCGGCGACAGAGGGGAG | CGGCTTCTCTCCCGGCAAGCTGTGGGCACTTTTGG | 2220 | QY | 3289 | GACGCGGCTGTGCTTGTGTAGAGCTCA | CGCCCGCGGAGACCTCAGTTAGTTGGGGCT | 3348 |
| QY | 2209 | AAGGCTCTTTGGGCGGTCACATGCTCT | CGCCCTTCGGGCGACGCTGTGGGCACTTTTGG | 2268 | Db | 3301 | GACGCGGCTGTGCTTGTGTAGAGCTCA | CGCCCGCGGAGACCTCAGTTAGTTGGGGCT | 3360 |
| Db | 2221 | AAGGCTCTTTGGGCGGTCACATGCTCT | CGCCCTTCGGGCGACGCTGTGGGCACTTTTGG | 2280 | QY | 3349 | TACCTAAACACACACAGGCTTGCCTCT | CGCAGGACCATCTGGAGTTCTGGGAGCGTC | 3408 |
| QY | 2269 | GCTGCGGTGTGCACCGAGGGGTTCGGA | AGGCGGTGGACTTTGTACCCGTGCGAGTCTATG | 2328 | Db | 3361 | TACCTAAACACACACAGGCTTGCCTCT | CGCAGGACCATCTGGAGTTCTGGGAGCGTC | 3420 |
| Db | 2281 | GCTGCGGTGTGCACCGAGGGGTTCGGA | AGGCGGTGGACTTTGTACCCGTGCGAGTCTATG | 2340 | QY | 3409 | TTTACAGGCTCAACCAATAGACGCCCAT | TTCTTTGTCCAGACTAAGCAGGACGAGAC | 3468 |
| QY | 2329 | GAACCACTATGCGGTGCGCCCGCTTTC | ACGGACAACCTGTTCGCGGCACTTTCGCGG | 2388 | Db | 3421 | TTTACAGGCTCAACCAATAGACGCCCAT | TTCTTTGTCCAGACTAAGCAGGACGAGAC | 3480 |
| Db | 2341 | GAACCACTATGCGGTGCGCCCGCTTTC | ACGGACAACCTGTTCGCGGCACTTTCGCGG | 2400 | QY | 3469 | AACTTCCCTTACCTGGTAGCATACAGG | CTACGCTGCGGCGCAGGCTCCACCT | 3528 |
| QY | 2389 | ACATTCAGGTGGCCACTACACGCCCTA | ATGGTAGCGGCAAGAGCACTAAGGTGCGG | 2448 | Db | 3481 | AACTTCCCTTACCTGGTAGCATACAGG | CTACGCTGCGGCGCAGGCTCCACCT | 3540 |
| Db | 2401 | ACATTCAGGTGGCCACTACACGCCCTA | ATGGTAGCGGCAAGAGCACTAAGGTGCGG | 2460 | QY | 3529 | CCATCGTGGGACCAAAATGTGAAGTGT | CTCATAGGCTTAAAGCTTACGCTGACCGGGCA | 3588 |
| QY | 2449 | GCTCGGTATGACGCCAAGGATTAAGGT | GCTTGTTCCTGAAACCGCTCGCGCCACC | 2508 | Db | 3541 | CCATCGTGGGACCAAAATGTGAAGTGT | CTCATAGGCTTAAAGCTTACGCTGACCGGGCA | 3600 |
| Db | 2461 | GCTCGGTATGACGCCAAGGATTAAGGT | GCTTGTTCCTGAAACCGCTCGCGCCACC | 2520 | QY | 3589 | ACGCCCCCTGTGTATAGCTGGGAGCG | GTTCAAAACGAGGTTACTACCAACACCCCA | 3648 |
| QY | 2509 | CTAGGTTTCGGGGGTATATGCTTAAG | GCACATGATCGACCTTAAACATCAGAACCGGG | 2568 | Db | 3601 | ACGCCCCCTGTGTATAGCTGGGAGCG | GTTCAAAACGAGGTTACTACCAACACCCCA | 3660 |
| Db | 2521 | CTAGGTTTCGGGGGTATATGCTTAAG | GCACATGATCGACCTTAAACATCAGAACCGGG | 2580 | QY | 3649 | ACCAATATACATCATGGATGATGCTCG | GCTGACCTGGAGGTCGTCAGAGCACTTGGGTG | 3708 |
| QY | 2569 | GTAAGGACCATCACACGGGTGCCCCAT | CACTGACTCCACTATGGAAGTTTCTTGCC | 2628 | Db | 3661 | ACCAATATACATCATGGATGATGCTCG | GCTGACCTGGAGGTCGTCAGAGCACTTGGGTG | 3720 |
| Db | 2581 | GTAAGGACCATCACACGGGTGCCCCAT | CACTGACTCCACTATGGAAGTTTCTTGCC | 2640 | QY | 3709 | CTGTAGGCGGAGTCTTAGCAGCTCTCG | CCGCTGATTCGCTGACCAAGCAGGCGTGGTC | 3768 |
| QY | 2629 | GACGCTGTTGCTCTGGGGGCGCTATGA | CATCATATATGTATGTAGTGCCTCAACT | 2688 | Db | 3721 | CTGTAGGCGGAGTCTTAGCAGCTCTCG | CCGCTGATTCGCTGACCAAGCAGGCGTGGTC | 3780 |
| Db | 2641 | GACGCTGTTGCTCTGGGGGCGCTATGA | CATCATATATGTATGTAGTGCCTCAACT | 2700 | QY | 3769 | ATTGTGGCGAGGATCATCTTTGTCCG | AAAGCCGSCCATCATTCGCCGACAGGAGTCCCT | 3828 |
| QY | 2689 | GACTCGACCACTATCTTGGGCATCGGC | ATCGCTCCGGGATCGGTCAACGTCACATCCAAAC | 2748 | Db | 3781 | ATTGTGGCGAGGATCATCTTTGTCCG | AAAGCCGSCCATCATTCGCCGACAGGAGTCCCT | 3840 |
| Db | 2701 | GACTCGACCACTATCTTGGGCATCGGC | ATCGCTCCGGGATCGGTCAACGTCACATCCAAAC | 2760 | QY | 3829 | TACCGGAGTTGATGATGAGTGGAGTG | AGTGCCTCACACCTCCCTTACATCGAACAGGGA | 3888 |
| QY | 2749 | CGACTCGTGTGTCACCGCTACCGCTC | CGGGATCGGTCAACGTCACATCCAAAC | 2808 | Db | 3841 | TACCGGAGTTGATGATGAGTGGAGTG | AGTGCCTCACACCTCCCTTACATCGAACAGGGA | 3900 |
| Db | 2761 | CGACTCGTGTGTCACCGCTACCGCTC | CGGGATCGGTCAACGTCACATCCAAAC | 2820 | QY | 3889 | ATGCACTGCCCAACAAATTCAAACAG | AGGCAATCGGGTGTGCAAAACAGCCACCAAG | 3948 |
| QY | 2809 | ATCGAGAGGTGCTCTGTCAGACATCG | GAGAAATCCCTTTTATGCAAGCAATCCCT | 2868 | Db | 3901 | ATGCACTGCCCAACAAATTCAAACAG | AGGCAATCGGGTGTGCAAAACAGCCACCAAG | 3960 |
| Db | 2821 | ATCGAGAGGTGCTCTGTCAGACATCG | GAGAAATCCCTTTTATGCAAGCAATCCCT | 2880 | QY | 3949 | CAAGCGAGGCTGCTCTCCCGTGGTGG | AATCCAAAGTGGCGGACCCCTTCGAAGCCCTTCGG | 4008 |
| QY | 2869 | ATCGAGACCATCAAGGGGGGAGGACCT | CAATTTCTGCGCATTCCAAGAGAAATGTAT | 2928 | Db | 3961 | CAAGCGAGGCTGCTCTCCCGTGGTGG | AATCCAAAGTGGCGGACCCCTTCGAAGCCCTTCGG | 4020 |
| Db | 2881 | ATCGAGACCATCAAGGGGGGAGGACCT | CAATTTCTGCGCATTCCAAGAGAAATGTAT | 2940 | QY | 4009 | GCGAAGCATATGTGAATTTTCATCAG | GGGATCAATATTTAGCAGGCTTGTCCACTCTG | 4068 |
| QY | 2929 | GAGTCTGCCGCGAGTGTCCGCGCTCG | GACTCAATGCTGTAGCATATTTACCGGGGCTT | 2988 | Db | 4021 | GCGAAGCATATGTGAATTTTCATCAG | GGGATCAATATTTAGCAGGCTTGTCCACTCTG | 4080 |
| Db | 2941 | GAGTCTGCCGCGAGTGTGTCCGCGCT | CGGACTCAATGCTGTAGCATATTTACCGGGGCTT | 3000 | QY | 4069 | CCTGGCAACCCCGGATAGCATCAGTGG | CAATTCACAGCTCTATCACCAGCCGCTC | 4128 |
| QY | 2989 | GATGTATCCGTATACCAACTAGGGGAG | CGTCAATTTGTGTAGCAACGCGCTTAATG | 3048 | | | | | |

Db 4081 CCTGCAACCCCGGATAGCATCACTGATGGCAATTCACAGCCCTCTATCACCAGCCGGTCT 4140
Qy 4129 ACCACCCAAATACCTCTCTGTTTAAATCATCTCTGGGGGATGGTGGCCGCCCAACTTCTCT 4188
Db 4141 ACCACCCAAATACCTCTCTGTTTAAATCATCTCTGGGGGATGGTGGCCGCCCAACTTCTCT 4200
Qy 4189 CTTCCAGCGCT 4248
Db 4201 CTTCCAGCGCT 4260
Qy 4249 ATAGGCTTTGGGAAGGTCT 4308
Db 4261 ATAGGCTTTGGGAAGGTCT 4320
Qy 4309 GGGCTCGTGGCTTTAAGGTCT 4368
Db 4321 GGGCTCGTGGCTTTAAGGTCT 4380
Qy 4369 CTACTCCCTGCTATCT 4428
Db 4381 CTACTCCCTGCTATCT 4440
Qy 4429 CTGCGTCGGCACGTGGGCCAGGGAGGGGGCTGTGCAAGTGTGTAACCGGGCTGTATAGCG 4488
Db 4441 CTGCGTCGGCACGTGGGCCAGGGAGGGGGCTGTGCAAGTGTGTAACCGGGCTGTATAGCG 4500
Qy 4489 TTGCGTTGGGGGTAAACAGCTCTCCCCACACCTATGTGCTGAGCGGAGCTGTCA 4548
Db 4501 TTGCGTTGGGGGTAAACAGCTCTCCCCACACCTATGTGCTGAGCGGAGCTGTCA 4560
Qy 4549 GCAAGGTGCTACTCAGATCT 4608
Db 4561 GCAAGGTGCTACTCAGATCT 4620
Qy 4609 CAGTGGATCAACGAGGACTGCTCCACGCCATGCTCGGGCTCGTGGCTTAAGATGTTTGG 4668
Db 4621 CAGTGGATCAACGAGGACTGCTCCACGCCATGCTCGGGCTCGTGGCTTAAGATGTTTGG 4680
Qy 4669 GATTGGATGACGGTGTGACTGATTTCAAGACTGGCTCCAGCTCCAGCTCCAGCTCCAGCTCC 4728
Db 4681 GATTGGATGACGGTGTGACTGATTTCAAGACTGGCTCCAGCTCCAGCTCCAGCTCCAGCTCC 4740
Qy 4729 CGATTGCGGGAGTCCCT 4788
Db 4741 CGATTGCGGGAGTCCCT 4800
Qy 4789 GACGGCATCATGCAAAACCACTGCCATGTGGAGCACAGATCAACCGGACATGTGAAAAAC 4848
Db 4801 GACGGCATCATGCAAAACCACTGCCATGTGGAGCACAGATCAACCGGACATGTGAAAAAC 4860
Qy 4849 GGTTCATGAGGATCGTGGGGCTTAGGACCTGTAGTAACTGATGATGATGATGATGATGATGATG 4908
Db 4861 GGTTCATGAGGATCGTGGGGCTTAGGACCTGTAGTAACTGATGATGATGATGATGATGATGATG 4920
Qy 4909 ATTAACCGGTACACACGGGGCCCTGACGCGCTCTCCCGGGCCCAAAATTAATTTAGGGCG 4968
Db 4921 ATTAACCGGTACACACGGGGCCCTGACGCGCTCTCCCGGGCCCAAAATTAATTTAGGGCG 4980
Qy 4969 CTGTGGGGGTGGTGTGTGAGAGTACCTGAGGTGATGAGGTGATGAGGTGATGAGGTGATGAG 5028
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 Db 7621 TCCAGTTGGATTTATCAGCTGGTTCGTTGCTGTGTACAGCGGGGAGACATATATCAC 7680
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 Db 7981 TGGGCTCTCTGCAGATCAAGT 8001

RESULT 4
 US-09-539-601-16
 ; Sequence 16, Application US/09539601C
 ; Patent No. 6630343
 ; GENERAL INFORMATION:
 ; APPLICANT: Bartschlag, Ralf FW
 ; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
 ; FILE REFERENCE: all sequences
 ; CURRENT APPLICATION NUMBER: US/09/539, 601C
 ; CURRENT FILING DATE: 2001-08-30
 ; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
 ; EARLIER FILING DATE: 1999-04-03
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 16
 ; LENGTH: 8001
 ; TYPE: DNA
 ; ORGANISM: Hepatitis C virus
 ; FEATURE:
 ; NAME/KEY: 5'UTR
 ; LOCATION: (1)..(341)
 ; OTHER INFORMATION: construct I389/NS3-3'/9-13F
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (342)..(1193)
 ; OTHER INFORMATION: hepatitis C virus core-neomycin phosphotransferase
 ; OTHER INFORMATION: fusion protein
 ; FEATURE:
 ; NAME/KEY: RBS

1 LOCATION: (1202)...(1812)
2 OTHER INFORMATION: internal ribosome entry site from
3 OTHER INFORMATION: encephalomyocarditis virus
4 FEATURE:
5 NAME/KEY: CDS
6 LOCATION: (1813)...(7770)
7 OTHER INFORMATION: hepatitis C virus nonstructural protein NS3-5B;
8 OTHER INFORMATION: carries cell culture-adaptive mutations from clone
9 OTHER INFORMATION: 9-13F
10 FEATURE:
11 NAME/KEY: 3' UTR
12 LOCATION: (7771)...(8001)
13 US-09-539-601-16

Query Match 99.4%; Score 7947.8; DB 4; Length 8001;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7977; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

QY 1 GCCAGCCCCCGATTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGGAATCTACTG 60
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QY 121 CCCCCCTCCGGAGAGCCATAGTGTCTGCCGAACCGGTGAGTACACCGGAATTGCCAG 180
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QY 181 GACGACCGGGTCTTCTTTGGATCAACCCGCTCAATGCCCTGGAGATTTGGGGGTGCCCCC 240
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QY 301 GTGCTTGCAGTGCCTGGGCGGAGTCTCGTAGCCGTGACCGTGCACCAAGATTCCTAAAC 360
DB 301 GTGCTTGCAGTGCCTGGGCGGAGTCTCGTAGCCGTGACCGTGCACCAAGATTCCTAAAC 360

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DB 361 CTCAAGAAAAACCAAAAGCTAACCAACCGGCGGCCATGATTTGAACAAGATGATTC 420

QY 409 ACGAGGTTCTCGGCGCGTCTGGGTGAGAGGCTATTCGCTATGACTGGGCAACAGAG 468
DB 409 ACGAGGTTCTCGGCGCGTCTGGGTGAGAGGCTATTCGCTATGACTGGGCAACAGAG 480

QY 469 CAATCGGCTGCTGATGCGCGTCTCCGGTGTGAGCGGCGCGCGGTTCTTT 528
DB 469 CAATCGGCTGCTGATGCGCGTCTCCGGTGTGAGCGGCGCGCGGTTCTTT 540

QY 529 TTGTCGAAGACCGACCTGTCCGGTGCCTGAATGAATGCAAGTGCAGGCGAGCGCGCTAT 588
DB 529 TTGTCGAAGACCGACCTGTCCGGTGCCTGAATGAATGCAAGTGCAGGCGAGCGCGCTAT 600

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QY 1849 TGCATCATCACTAGCCTCAGGCGGAGACAGAAACAGGTTCGAGGGGAGGTCCAAAGTG 1908
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|----|------|---|------|----|------|---|------|
| Db | 4081 | CCTGGCAACCCCGGATAGCATCACTGATGCAATTCACAGCCTCTATCACCAGCCCGCTC | 4140 | Qy | 5209 | TGCGAGCCGAAACCGGACGTAGCTGCTACTTCCATGCTCAACGACCCCTCCACATTT | 5268 |
| Qy | 4129 | ACCAACCAACATACCTCTCTTTAAACATCTGGGGGATGGTGGCGCCCACTTCTCT | 4188 | Db | 5221 | TGCGGCGCGAAACCGGACGTAGCTGCTCACTTCCATGCTCACGACCCCTCCACATTT | 5280 |
| Db | 4141 | ACCAACCAACATACCTCTCTTTAAACATCTGGGGGATGGTGGCGCCCACTTCTCT | 4200 | Qy | 5269 | ACGGCGGAGACGGCTAGCGTAGCTGGCCAGGGGATCTCCCTCTCTTGGCCAGCTCA | 5328 |
| Qy | 4189 | CCTCCAGCGTCTCTCTCTCTTTCTAGGCGCGGCATCGCTGGAGCGGCTGTTGGCAGC | 4248 | Db | 5281 | ACGGCGGAGACGGCTAGCGTAGCTGGCCAGGGGATCTCCCTCTCTTGGCCAGCTCA | 5340 |
| Db | 4201 | CCTCCAGCGTCTCTCTCTCTTTCTAGGCGCGGCATCGCTGGAGCGGCTGTTGGCAGC | 4260 | Qy | 5329 | TCAGTACCCAGCTGCTCTGGCGCTTCTTGAAGGCAACATGCACTTACCCTCATGACTCC | 5388 |
| Qy | 4249 | ATAGCCCTTGGGAAGCTGCTGTGTGATATTTTGGCAGGTATTTAGAGAGAGGGTGGCAGGC | 4308 | Db | 5341 | TCAGTACCCAGCTGCTCTGGCGCTTCTTGAAGGCAACATGCACTTACCCTCATGACTCC | 5400 |
| Db | 4261 | ATAGCCCTTGGGAAGCTGCTGTGTGATATTTTGGCAGGTATTTAGAGAGAGGGTGGCAGGC | 4320 | Qy | 5389 | CCGACGCTGACCTCATCAGAGCCAACTCTCTGTGGCGGAGGAGATGGGCGGGAACATC | 5448 |
| Qy | 4309 | GGCTCTGGGCTTTAAAGTCATGAGCGCGAGATGCCCTCCACAGAGACCTGTTTAACT | 4368 | Db | 5401 | CCGACGCTGACCTCATCAGAGCCAACTCTCTGTGGCGGAGGAGATGGGCGGGAACATC | 5460 |
| Db | 4321 | GGCTCTGGGCTTTAAAGTCATGAGCGCGAGATGCCCTCCACAGAGACCTGTTTAACT | 4380 | Qy | 5449 | ACCGCGTGGAGTCAGAAATAAGTAGTAATTTTGGACTCTTTTCGAGCGCTCCAAGCG | 5508 |
| Qy | 4369 | CTACTCCCTGCTATCTCTCTCCCTGGCGCCCTAGTCTGTGGGGTCTGTGTGCGACGATA | 4428 | Db | 5461 | ACCGCGTGGAGTCAGAAATAAGTAGTAATTTTGGACTCTTTTCGAGCGCTCCAAGCG | 5520 |
| Db | 4381 | CTACTCCCTGCTATCTCTCTCCCTGGCGCCCTAGTCTGTGGGGTCTGTGTGCGACGATA | 4440 | Qy | 5509 | GAGGAGGATGAGAGGAAAGTATCCCTTCCGGCGGAGATCCTTCCGAGGTCAGGAAATTC | 5568 |
| Qy | 4429 | CTGCGTGGCAGCTGGGCCAGGGAGAGGGGCTGTGAGTGAATGAACCGGCTGATAGG | 4488 | Db | 5521 | GAGGAGGATGAGAGGAAAGTATCCCTTCCGGCGGAGATCCTTCCGAGGTCAGGAAATTC | 5580 |
| Db | 4441 | CTGCGTGGCAGCTGGGCCAGGGAGAGGGGCTGTGAGTGAATGAACCGGCTGATAGG | 4500 | Qy | 5569 | CCTCAGCGATGCCCATATGGGCAACCGCGGATTAACACCTTCCACTGTTAGAGTCTCTGG | 5628 |
| Qy | 4489 | TTCCGCTTCGGGGTAAACACGCTCTCCCCACGCACTATGTCCCTGAGAGCGACCTGCA | 4548 | Db | 5581 | CCTCAGCGATGCCCATATGGGCAACCGCGGATTAACACCTTCCACTGTTAGAGTCTCTGG | 5640 |
| Db | 4501 | TTCCGCTTCGGGGTAAACACGCTCTCCCCACGCACTATGTCCCTGAGAGCGAGCTGCA | 4560 | Qy | 5629 | RAGGACCGGACTAGTCCCTCCAGTGTACAGGGTGTCCATTCGCGCTCCCAAGGCG | 5688 |
| Qy | 4549 | GCAGCTGTCACTCAGATCCTCTCTAGTCTTACCATCACTCAGTCTGTGAAGAGGCTTCA | 4608 | Db | 5641 | AAGGACCGGACTAGTCCCTCCAGTGTACAGGGTGTCCATTCGCGCTCCCAAGGCG | 5700 |
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| Qy | 4729 | CGATTCCCGGAGTCCCTTCTCTCATGTCAACGTGGGTCAAGAGGAGTCTGGCGGGC | 4788 | Db | 5821 | ACGGCAGCGCAACCGCTCTCTGACAGCCCTCCGACGCGGCGGAGCCGGATCCGAC | 5880 |
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| Qy | 4969 | CTGTGCGGGTGTCTCTGAGAGTACGTGGAGTTACCGGGTGGGATTTCCACTAC | 5028 | Db | 6061 | GTCAATGCACTGAGCAACTCTTTGCTCCGTTCACCAACTTGGTCTATGCTACAACTCT | 6120 |
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RESULT 5
US-09-539-601-28
; Sequence 28, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenschlager, Ralf FW
; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REFERENCE: all sequences
; CURRENT APPLICATION NUMBER: US/09/539,601C
; CURRENT FILING DATE: 2001-08-30
; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
; EARLIER FILING DATE: 1999-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 8001
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(341)
; OTHER INFORMATION: construct I389/NS3-3'/19
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342)..(1193)
; OTHER INFORMATION: hepatitis C virus core - neomycin
; OTHER INFORMATION: phosphotransferase fusion protein
; FEATURE:
; NAME/KEY: RBS

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; LOCATION: (1202)..(1812)
; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1813)..(7770)
; OTHER INFORMATION: hepatitis C virus nonstructural proteins NS3 - 5B
; OTHER INFORMATION: of cell culture adapted clone no. 19
; FEATURE:
; NAME/KEY: 3' UTR
; LOCATION: (7771)..(8001)
US-09-539-601-28

Query Match      99.4%; Score 7941.4; DB 4; Length 8001;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7973; Conservative 0; Mismatches 16; Indels 12; Gaps 1;

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QY 1549 TGAAGATACCTGCAAGGCGGCAACCCCGACAGTGCCTCTGCGGCAAAAGCAACCTGTA 1608
DB 1561 TGAAGATACCTGCAAGGCGGCAACCCCGACAGTGCCTCTGCGGCAAAAGCAACCTGTA 1620
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DB 1621 GAAGAGTCAAAATGGCTCTCTCAAGCTATTCAACAGGGGCTGAAGGATGCCAGAAG 1680
QY 1669 GTACCCCATTTGATGGGATCTGATCTGGGCGCTCGGTGCACATGCTTTATGTTAG 1728
DB 1681 GTACCCCATTTGATGGGATCTGATCTGGGCGCTCGGTGCACATGCTTTATGTTAG 1740
QY 1729 TCGAGGTTAAAAACGCTTAGGCCCCCGAAACCAAGGAGAGTGTGTTTCTTTGAAAA 1788
DB 1741 TCGAGGTTAAAAACGCTTAGGCCCCCGAAACCAAGGAGAGTGTGTTTCTTTGAAAA 1800
QY 1789 CAGGATTAATACCATGGCGCTATTACGGCTACTCTCCAAACAGACGGGAGCTTACCTGGC 1848
DB 1801 CAGGATTAATACCATGGCGCTATTACGGCTACTCTCCAAACAGACGGGAGCTTACCTGGC 1860
QY 1849 TGCATCATCATAGCTTCAAGCGCGGACAGGAACAGCTCGAGGGGAGGTCCAGTG 1908
DB 1861 TGCATCATCATAGCTTCAAGCGCGGACAGGAACAGCTCGAGGGGAGGTCCAGTG 1920
QY 1909 GTCTCCACGCAACAACTTTCTTCTGGCGACCTGCGTCAATGCGGCTGTGTTGGACTGTC 1968
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Db 1921 GTCTCACGGAACAAATCTTTCTCGGCACTCGCTCAATGGCGTGTGTGGACTGTC 1980
QY 1969 TATCATGTGTGCGGCTCAAAGACCTTTGCGGCCCAAAGGGGCCCAATACCCCAAATGTAC 2028
Db 1981 TATCATGTGTGCGGCTCAAAGACCTTTGCGGCCCAAAGGGGCCCAATACCCCAAATGTAC 2040
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Db 2401 ACATTCAGGTGGCCCATCTACAGCCCTACTGTAGCGGCAAGAGCACTAAGGTGCGG 2460
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Db 2461 GCTGCGGTATGACGCCAAGGTATAAGGTGCTTCTCTGAACCCGTCTCGTCCGCCACCC 2520
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QY 2629 GACGTTGTTGCTCTGCGGGCGCTATGACATCATATATGTGATGAGTGCACCTCAACT 2688
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QY 2929 GAGCTGCGCGGAGCTGTCCGCTCGGACTCAATGCTGTAGCATATTAACCGGGGCTT 2988
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Db 3841 TACCGGAGTTCGATGAGATGGAAGTGGCGCTCACACCTCCCTTACATCGACACGGA 3900
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Db 4081 CTTGGCAACCCCGCGATAGCATCATCTGATGGGATTCACAGCTCTTATCACCGCCGCTC 4140

| | | | | | | | |
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| QY | 4129 | ACCACCAACATACCTCTCTGTTTAAATCTCTGGGGGATGGTGGCGGCCCAACTTGTCT | 4188 | QY | 5209 | TGCGAGCCGGAACCGGACGTAGCTGCTCACTTCCATGCTCACCGACCCCTCCACATT | 5268 |
| Db | 4141 | ACCACCAACATACCTCTCTGTTTAAATCTCTGGGGGATGGTGGCGGCCCAACTTGTCT | 4200 | Db | 5221 | TGCGAGCCGGAACCGGATGTAGCTGCTCACTTCCATGCTCACCGACCCCTCCACATT | 5280 |
| QY | 4189 | CCTCCACAGCGCTCTCTGCTTTCGTAGCGCGGCATCGCTGGAGCGCTGTGGCAGC | 4248 | QY | 5269 | ACGGCGGAGACGGCTAAAGCTAGGCTGGCCAGGGATCTCCGCCCTCTTGGCCAGCTCA | 5328 |
| Db | 4201 | CCTCCACAGCGCTCTCTGCTTTCGTAGCGCGGCATCGCTGGAGCGCTGTGGCAGC | 4260 | Db | 5281 | ACGGCGGAGACGGCTAAAGCTAGGCTGGCCAGGGATCTCCGCCCTCTTGGCCAGCTCA | 5340 |
| QY | 4249 | ATAGCGCTTGGGAAGGTGTCTGGATATTTTGGCAGGTTATGGAGCAGGGTGGCAGGC | 4308 | QY | 5329 | TCAGCTAGCCAGCTCTCTGCGCTTCTTTGAAGGCAACATCACTACCCGTATGACTCC | 5388 |
| Db | 4261 | ATAGCGCTTGGGAAGGTGTCTGGATATTTTGGCAGGTTATGGAGCAGGGTGGCAGGC | 4320 | Db | 5341 | TCAGCTAGCCAGCTCTCTGCGCTTCTTTGAAGGCAACATCACTACCCGTATGACTCC | 5400 |
| QY | 4309 | GGCTCTGTCCTTTAAAGTATGAGCGCGAGATGCCCTCCACCGAGACCTGGTTAAC | 4368 | QY | 5389 | CCGACCGTGAACCTCATCGAGGCCAACCTCTCTGGCGGACAGAGATGGCGGGACATC | 5448 |
| Db | 4321 | GGCTCTGTCCTTTAAAGTATGAGCGCGAGATGGCTCCCTCCACCGAGACCTGGTTAAC | 4380 | Db | 5401 | CCGACCGTGAACCTCATCGAGGCCAACCTCTCTGGCGGACAGAGATGGCGGGACATC | 5460 |
| QY | 4369 | CTACTCCCTGCTATCCCTCTCCCTGGCGCCTTAGTCTCGGGTCTGTGGCAGCGATA | 4428 | QY | 5449 | ACCCCGTGGAGTCAGAAATAAGTAGTAAATTTTGGACTCTTTCCAGCCGGTCCCAAGCG | 5508 |
| Db | 4381 | CTACTCCCTGCTATCCCTCTCCCTGGCGCCTTAGTCTCGGGTCTGTGGCAGCGATA | 4440 | Db | 5461 | ACCCCGTGGAGTCAGAAATAAGTAGTAAATTTTGGACTCTTTCCAGCCGGTCCCAAGCG | 5520 |
| QY | 4429 | CTGCGTTCGCACTGGGGCCACAGGGAGGGGCTGTGCAGTGTATGAACCGGCTGATAGC | 4488 | QY | 5509 | GAGGAGGATGAGAGGGAAGTATCCGTTCCGGCGGAGATCCTGCGGAGGTCAGGAAATTC | 5568 |
| Db | 4441 | CTGCGTTCGCACTGGGGCCACAGGGAGGGGCTGTGCAGTGTATGAACCGGCTGATAGC | 4500 | Db | 5521 | GAGGAGGATGAGAGGGAAGTATCCGTTCCGGCGGAGATCCTGCGGAGGTCAGGAAATTC | 5580 |
| QY | 4489 | TTGCGCTTCGGGGTAAACACGCTCTCCCGACGACTATGTGCTGAGAGCGACGTGCA | 4548 | QY | 5569 | CCTCGAGCGATGCCATATGGGCAACCGCGGATTACACCCCTCCACTGTTAGAGTCTCTG | 5628 |
| Db | 4501 | TTGCGCTTCGGGGTAAACACGCTCTCCCGACGACTATGTGCTGAGAGCGACGTGCA | 4560 | Db | 5581 | CCTCGAGCGATGCCATATGGGCAACCGCGGATTACACCCCTCCACTGTTAGAGTCTCTG | 5640 |
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| Db | 4621 | CAGTGTATCAACAGAGCTCTCCAGCCATGCTCCGGCTCTGGCTGTAGAGATGTTGG | 4680 | Db | 5701 | CCTCCGATACCACTCCACGGAGGAAGAGACGGTTGCTCTGTCAAACTACCGTGTCT | 5760 |
| QY | 4669 | GATTGATATGACAGGTTGTTACTGTATTTCAAGACCTGGCTCCAGTCCCAAGCTCTGCCG | 4728 | QY | 5749 | TCCTGCTTGGGAGCTCCGCAAAAGACTTTCGGCAGCTCCGAAATCGCTGGCCGCTCGAC | 5808 |
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| QY | 4729 | CGATTCCGGGAGTCCCTTCTTCTCATGTCAACGTGGGTACAGGGAGTCTGGCGGGC | 4788 | QY | 5809 | AGCGGACCGCAACCGCTCTCTGACCGACCTCCCGACGACGCGGACGCGGATCCGAC | 5868 |
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| Db | 4801 | GACGGATCATGAAACACCTCTGATGTCAACGTGGGTACAGGGAGTCTGGCGGGC | 4860 | Db | 5881 | GTTGAGTCTGTAATCTCTCCATGCCCCCTTTGAGGGGAGCGGGGATCCGATCTCAGC | 5940 |
| QY | 4849 | GGTTCCATGAGGATCGTGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAAATTCCTCC | 4908 | QY | 5929 | GACGGTCTTGGTCTTACCGTAAGCGAGGAGGTAGTGAGACCTCGTCTCTGCTCGATG | 5988 |
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| Db | 4921 | ATTACCGCTACACACCGGCGCCCTGCAACCGCTTCCCGCGGCGCAATTTCTAGGGCG | 4980 | Db | 6001 | TCCTACACATGGACAGCGCCCTGATCAACCGATGCGCTCGGAGGAAACCAAGTCCCG | 6060 |
| QY | 4969 | CTGTGGCGGTGCTGTAGGAGTACGTGGAGGTTACGGGTTACGGGTTCCCACTAC | 5028 | QY | 6049 | ATCAATGCACTGAGCAACTCTTTGCTCCGTCACAACTTGGTCTATGCTACAACTCT | 6108 |
| Db | 4981 | CTGTGGCGGTGCTGTAGGAGTACGTGGAGGTTACGGGTTACGGGTTCCCACTAC | 5040 | Db | 6061 | ATCAATGCACTGAGCAACTCTTTGCTCCGTCACAACTTGGTCTATGCTACAACTCT | 6120 |
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| QY | 5149 | CGGAGGAGGTCAATTCCTGGTGGCTCAATCAATACCTGGTGGGTACAGCTCCCA | 5208 | QY | 6229 | CTATCCGTGGAGGAGCTGTAGCTGACGCCGCCCACTTCGCGCCAGACTTAAATTTGGC | 6288 |
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 QY TGGCTCTCTGCGAGATCAAGT 7989
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RESULT 6
 US-09-539-601-4
 ; Sequence 4, Application US/09539601C
 ; Patent No. 6630343
 ; GENERAL INFORMATION:
 ; APPLICANT: Bartenschlager, Ralf FW
 ; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
 ; FILE REFERENCE: all sequences
 ; CURRENT APPLICATION NUMBER: US/09/539,601C
 ; EARLIER FILING DATE: 2001-08-30
 ; EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
 ; EARLIER FILING DATE: 1999-04-03
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 8637
 ; TYPE: DNA
 ; ORGANISM: Hepatitis C virus
 ; FEATURE:
 ; NAME/KEY: 5'UTR
 ; LOCATION: (1)..(341)
 ; OTHER INFORMATION: construct I377/NS2-3'/wt
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (342)..(1181)
 ; OTHER INFORMATION: HCV core-neomycin phosphotransferase fusion
 ; OTHER INFORMATION: protein
 ; FEATURE:
 ; NAME/KEY: RBS
 ; LOCATION: (1190)..(1800)

; OTHER INFORMATION: internal ribosome entry site from
; OTHER INFORMATION: encephalomyocarditis virus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1801)..(8406)

; OTHER INFORMATION: hepatitis C virus NS2 - 5B

; FEATURE:

; NAME/KEY: 3'UTR

; LOCATION: (8407)..(8637)

; PUBLICATION INFORMATION:

; AUTHORS: Lohmann, Volker

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; TITLE: hepatoma cell line

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Best Local Similarity 92.5%; Pred. No. 0;

Matches 7989; Conservative 0; Mismatches 0; Indels 648; Gaps 1;

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DB 1 GCCAGCCCCGATGTTGGGCGGACATCCACCATAGATCACTCCCTGTGAGGAAGTACTG 60

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QY 241 GCGAGACTGTAGCCAGTAGTGTGTCGCGAAAGGCGCTGTGTACTGCTGATAGG 300

DB 241 GCGAGACTGTAGCCAGTAGTGTGTCGCGAAAGGCGCTGTGTACTGCTGATAGG 300

QY 301 GTGCTTTCGAGTGCCTCCGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCCTAAC 360

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Dd 7561 TGCAGGATGTCGTATGCGGAGACGACTTGTGCTTATCTGTGAAAGCGCGGGACCCAA 7620
Qy 6973 GAGGACGAGGCGGAGCTACGGGCTTACGGAGGCTATGATAGTACTCTGCCGCCCT 7032
Dd 7621 GAGGACGAGGCGGAGCTACGGGCTTACGGAGGCTATGATAGTACTCTGCCGCCCT 7680
Qy 7033 GGGACCCGCCCAACACAGAACTAGACTTGGAGTTGTAACATCATGCTCTCCAACTG 7092
Dd 7681 GGGACCCGCCCAACACAGAACTAGACTTGGAGTTGTAACATCATGCTCTCCAACTG 7740
Qy 7093 TCAGTCCGCGACGATGATCTGCGAAAGGGTGTACTATCTCACCCGCTGACCCACACC 7152
Dd 7741 TCAGTCCGCGACGATGATCTGCGAAAGGGTGTACTATCTCACCCGCTGACCCACACC 7800
Qy 7153 CCCCTTCGCGGGCTGCGTGGGAGACAGTACACACTCAGTCAATCTCTGGCTAGGC 7212
Dd 7801 CCCCTTCGCGGGCTGCGTGGGAGACAGTACACACTCAGTCAATCTCTGGCTAGGC 7860
Qy 7213 AACATCATGATGATGCGCCACCTTGTGGCAAGGATGATCCCTGATGACTCAATTTCTTC 7272
Dd 7861 AACATCATGATGATGCGCCACCTTGTGGCAAGGATGATCCCTGATGACTCAATTTCTTC 7920
Qy 7273 TCCATCTTCTAGCTCAGGAACAACCTTGAAGGCGCTAGATTGTCTCAGATCTACGGGCGC 7332
Dd 7921 TCCATCTTCTAGCTCAGGAACAACCTTGAAGGCGCTAGATTGTCTCAGATCTACGGGCGC 7980
Qy 7333 TGTACTCCATTCAGCCACTTGACCTTACCTCAGATCAATCAACAGCTCCATGGCTTAGC 7392
Dd 7981 TGTACTCCATTCAGCCACTTGACCTTACCTCAGATCAATCAACAGCTCCATGGCTTAGC 8040
Qy 7393 GCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGTTGGCTTCATGCTCAGG 7452
Dd 8041 GCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGTTGGCTTCATGCTCAGG 8100
Qy 7453 AAATTTGGGTACCGCCCTTTCGAGTCTGAGACATCGGGCCAGAAAGTGTCCGCGCTAGG 7512
Dd 8101 AAATTTGGGTACCGCCCTTTCGAGTCTGAGACATCGGGCCAGAAAGTGTCCGCGCTAGG 8160
Qy 7513 CTACTGTCCAGGGGGAGGCTGCCACTTGTGCAAGTACCTCTTCACTGGGCAAGTA 7572
Dd 8161 CTACTGTCCAGGGGGAGGCTGCCACTTGTGCAAGTACCTCTTCACTGGGCAAGTA 8220
Qy 7573 AGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCGCTCCAGTTGGATTTTATCCAGCTGG 7632
Dd 8221 AGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCGCTCCAGTTGGATTTTATCCAGCTGG 8280
Qy 7633 TTCGTTGCTGTTACAGCGGGGAGACATATATCAAGCCTGTCTCGTCCGCCACCCCGC 7692
Dd 8281 TTCGTTGCTGTTACAGCGGGGAGACATATATCAAGCCTGTCTCGTCCGCCACCCCGC 8340

QY 1009 ACTGTGGCGGTGGGTGGCGGCGCTATCAGGACATAGCTTGGCTACCCGTGATA 1068
Db 1021 ACTGTGGCGGTGGGTGGCGGCGCTATCAGGACATAGCTTGGCTACCCGTGATA 1080
QY 1069 TTGCTGAAGAGCTTGGCGGCGGATGGGTGACCGGTCTCTCGTCTTACGGTATCGCG 1128
Db 1081 TTGCTGAAGAGCTTGGCGGCGGATGGGTGACCGGTCTCTCGTCTTACGGTATCGCG 1140
QY 1129 CTCCGATTCGAGCGCATCGCTTCTATCGCTTCTTGAAGAGTCTTCTGAGTTTAA 1188
Db 1141 CTCCGATTCGAGCGCATCGCTTCTATCGCTTCTTGAAGAGTCTTCTGAGTTTAA 1200
QY 1189 CAGACCAACAGGTTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCT 1248
Db 1201 CAGACCAACAGGTTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCT 1260
QY 1249 AACGTACTGCGGAGCGGCTTGAATTAAGCCGGTGTGGTGTCTATATGTTATT 1308
Db 1261 AACGTACTGCGGAGCGGCTTGAATTAAGCCGGTGTGGTGTCTATATGTTATT 1320
QY 1309 TCCACCATATTCGGGTCTTTTGGCAATGTGAGGCGCGGAACCTGGCCCTGTCTTCTG 1368
Db 1321 TCCACCATATTCGGGTCTTTTGGCAATGTGAGGCGCGGAACCTGGCCCTGTCTTCTG 1380
QY 1369 ACGAGCATTCCTAGGGTCTTTTCCCTCTCGCAAGGAATGCAAGTCTGTGAAATGTC 1428
Db 1381 ACGAGCATTCCTAGGGTCTTTTCCCTCTCGCAAGGAATGCAAGTCTGTGAAATGTC 1440
QY 1429 GTGAAGNAGAGTCTCTCTGAGAGTCTTGAAGACAAACAGTCTGTGAGGACCTT 1488
Db 1441 GTGAAGNAGAGTCTCTCTGAGAGTCTTGAAGACAAACAGTCTGTGAGGACCTT 1500
QY 1489 TGCAGGACGCGAACCCTCGGACAGTGTGCGGCAAGTCTCGGCAAGGCGGCGGTA 1548
Db 1501 TGCAGGACGCGAACCCTCGGACAGTGTGCGGCAAGGCGGCGGCGGTA 1560
QY 1549 TAAGATACACTGCAAGGGGCGCAACCCAGTGCCACGTTGTGATGATAGTTGTG 1608
Db 1561 TAAGATACACTGCAAGGGGCGCAACCCAGTGCCACGTTGTGATGATAGTTGTG 1620
QY 1609 GAAAGATCAATGGTCTCTCTGAGCGTATTAACAGGGGCTGAAGATGCCAGAG 1668
Db 1621 GAAAGATCAATGGTCTCTCTGAGCGTATTAACAGGGGCTGAAGATGCCAGAG 1680
QY 1669 GTACCCCATTTATGGATCTGATCTGGGCTCGTGCCATCTTACATGTGTTAG 1728
Db 1681 GTACCCCATTTATGGATCTGATCTGGGCTCGTGCCATCTTACATGTGTTAG 1740
QY 1729 TCGAGGTTAAAAAGCTTAGGCCCCCGAACCACGGGAGCGTGTCTTCTTTGAAAAA 1788
Db 1741 TCGAGGTTAAAAAGCTTAGGCCCCCGAACCACGGGAGCGTGTCTTCTTTGAAAAA 1800
QY 1789 CACGATTAATACCATG----- 1803
Db 1801 CACGATTAATACCATG----- 1803
QY 1804 ----- 1803
Db 1861 CTGATCTCTTGACCTTGTCACCGCACTATAAGCTGTCTTCGCTAGGCTCATATGTGG 1920
QY 1804 ----- 1803
Db 1921 TTACAATATTTATCACAGGGCGGAGGACACCTTGCAAGTGTGGATCCCGCCCTCAAC 1980
QY 1804 ----- 1803
Db 1981 GTTCGGGGGGCGCGATGCGGTATCTCTCAGTGTGCGATCCACCGAGACTAATC 2040
QY 1804 ----- 1803
Db 2041 TTTACCATCAACAAATCTTGCTCGGCATCTCGGTCCACTCATGTGCTCCAGGTGGT 2100

QY 1804 ----- 1803
Db 2101 ATAACAAAGTGCCTACTTCTGTGCGGCAACAGGGCTCATTTCTGTATGATGCTGTG 2160
QY 1804 ----- 1803
Db 2161 CGAAGGTTGTGGGGGTCAATTATGTCCAAATGGCTCTCATGAAGTTGCGCGCACTGACA 2220
QY 1804 ----- 1803
Db 2221 GGTACGTACGTTTATGACCATCTCACCCACTGCGGAGCTGGGCCACCGCGGCTACGA 2280
QY 1804 ----- 1803
Db 2281 GACCTTGGGTGGAGTTGAGCCGTCTTCTCTGATATGAGACCAAGTTTATCACC 2340
QY 1804 ----- 1803
Db 2341 TGGGGGCGAGACACCGCGCGTGTGGGACATCATCTTGGGCTGCTCCCGCTCTCCGCGC 2400
QY 1804 ----- 1803
Db 2401 AGGGGAGGAGATATCATCTGGGACCGGACAGACCTTGAAGGGCAGGGGTGCGACTC 2460
QY 1804 ----- 1803
Db 2461 CTGGGCTATTTACGGCTACTCCCAACAGACGAGGAGCTTGGCTGATCATCACT 1860
QY 2461 CTGGGCTATTTACGGCTACTCCCAACAGACGAGGAGCTTGGCTGATCATCACT 2520
Db 1861 AGCTCAAGCGCGGACAGGACAGGTGAGGGGAGGTCCAAAGTGGTCTCCACCGCA 1920
QY 2521 AGCTCAAGCGCGGACAGGACAGGTGAGGGGAGGTCCAAAGTGGTCTCCACCGCA 2580
QY 1921 ACACAAATCTTCTCTGGGACCTGGTCAATGGCTGTGTGGACTGTCTATCATGTGCTC 1980
Db 2581 ACACAAATCTTCTCTGGGACCTGGTCAATGGCTGTGTGGACTGTCTATCATGTGCTC 2640
QY 1981 GGCTCAAGAGCTTGTGGGCGGCAAGGGCGGCTTCTTGAACCAATGACCACTGACCTGC 2100
Db 2641 GGCTCAAGAGCTTGTGGGCGGCAAGGGCGGCTTCTTGAACCAATGACCACTGACCTGC 2700
QY 2041 CAGACCTCGTCTGGCTGGCAAGCGCCCGGGGCGGCTTCTTGAACCAATGACCACTGACCTGC 2100
Db 2701 CAGACCTCGTCTGGCTGGCAAGCGCCCGGGGCGGCTTCTTGAACCAATGACCACTGACCTGC 2760
QY 2101 GCGAGCTCGGACCTTACTTGTGTGACAGGATGCGGATGTCAATCGGTGCGCGCGG 2160
Db 2761 GCGAGCTCGGACCTTACTTGTGTGACAGGATGCGGATGTCAATCGGTGCGCGCGG 2820
QY 2161 GCGACAGCAGGGGAGCTACTCTCCCGGCGGCTTCTCTACTTGAAGGGCTCTTTCG 2220
Db 2821 GCGACAGCAGGGGAGCTACTCTCCCGGCGGCTTCTCTACTTGAAGGGCTCTTTCG 2880
QY 2221 GCGGTCATGCTCTGCGGCGGCTTGTGGGCACTTGTGGGCTTCTTTCGCGGCTGCGGTGTC 2280
Db 2881 GCGGTCATGCTCTGCGGCGGCTTGTGGGCACTTGTGGGCTTCTTTCGCGGCTGCGGTGTC 2940
QY 2281 ACCGAGGGTGTGGAGGGGCTGACTTTGTACCGGTGAGTATGGAACCACTATG 2340
Db 2941 ACCGAGGGTGTGGAGGGGCTGACTTTGTACCGGTGAGTATGGAACCACTATG 3000
QY 2341 CGGTCCCGGTCTTACGAGCAACTCGTCCCTCCGCGCGTACCGGAGACTTCCAGGTG 2400
Db 3001 CGGTCCCGGTCTTACGAGCAACTCGTCCCTCCGCGCGTACCGGAGACTTCCAGGTG 3060
QY 2401 GCCCATCTACACCCCTACTTGTAGCGGCAAGGACACTAAGGTGCGGCTGCGTATGCA 2460
Db 3061 GCCCATCTACACCCCTACTTGTAGCGGCAAGGACACTAAGGTGCGGCTGCGTATGCA 3120
QY 2461 GCCCAGGGTATAGGTGTGTTCTGAAACCGGTGCTGCGCGGCACTTAGGTTCGGG 2520
Db 3121 GCCCAGGGTATAGGTGTGTTCTGAAACCGGTGCTGCGCGGCACTTAGGTTCGGG 3180
QY 2521 GGTATATGCTTAAGGCACATGTATCGACCTTAAACATCAGAACCGGGGTAAAGCACTC 2580

| | | | | |
|----|------|-----|---|------|
| Db | 3181 | GC | GTATATGCTTAAGGCACATGGTATTCGACCCCTAAACATCAGAAACCGGGGTAAAGCACCATC | 3240 |
| Qy | 2581 | AC | CACGGGTGCCCCCATCAGTACTCACTATGGCAAGTTTCTTCCGACGGTGTGTC | 2640 |
| Db | 3241 | ACC | ACGGGTGCCCCCATCAGTACTCACTATGGCAAGTTTCTTCCGACGGTGTGTC | 3300 |
| Qy | 2641 | TC | TGGGGCGCTATGACATCATAAATGTGTAGTGAGTGCCACTCAACTGACTCGACCACT | 2700 |
| Db | 3301 | TC | TGGGGCGCTATGACATCATAAATGTGTAGTGAGTGCCACTCAACTGACTCGACCACT | 3360 |
| Qy | 2701 | AT | CTCTGGGCATCGGCACAGTCTCTGGACCAAGCGGAGACGGCTGGAGCGCACTCGTGCTG | 2760 |
| Db | 3361 | AT | CTCTGGGCATCGGCACAGTCTCTGGACCAAGCGGAGACGGCTGGAGCGCACTCGTGCTG | 3420 |
| Qy | 2761 | CT | CGCCACCGGTACGCCCTCGGGATCGGTCAACCGTGCCACATCCAAACATCGAGGAGGTG | 2820 |
| Db | 3421 | CT | CGCCACCGGTACGCCCTCGGGATCGGTCAACCGTGCCACATCCAAACATCGAGGAGGTG | 3480 |
| Qy | 2821 | GCT | CTGTCCAGACTGGAGAATCCCTTTTATGGCAAAGCCATCCCCATCGAGACCATC | 2880 |
| Db | 3481 | GCT | CTGTCCAGACTGGAGAATCCCTTTTATGGCAAAGCCATCCCCATCGAGACCATC | 3540 |
| Qy | 2881 | AAG | GGGGGAGGCACCTCAATTTCTGCCATTTCAAGAAGAAATGTGATGAGCTGCGCGG | 2940 |
| Db | 3541 | AAG | GGGGGAGGCACCTCAATTTCTGCCATTTCAAGAAGAAATGTGATGAGCTGCGCGG | 3600 |
| Qy | 2941 | AAG | CTGTCCGCGCTCGNACTCAATGCTGTAGCATATTTACGGGGCCCTTGATGATCCGTC | 3000 |
| Db | 3601 | AAG | CTGTCCGCGCTCGNACTCAATGCTGTAGCATATTTACGGGGCCCTTGATGATCCGTC | 3660 |
| Qy | 3001 | AT | CCAACTAGCGGAGACGTCATTTGCTAGCAACGACGCTCTAAATGACGGGCTTTTACC | 3060 |
| Db | 3661 | AT | CCAACTAGCGGAGACGTCATTTGCTAGCAACGACGCTCTAAATGACGGGCTTTTACC | 3720 |
| Qy | 3061 | GG | CGATTTTCGACTCGACTGCAATCATGTGTCAACGAGCATGTGTCAACGAGCAGTTCGACG | 3120 |
| Db | 3721 | GG | CGATTTTCGACTCGACTGCAATCATGTGTCAACGAGCATGTGTCAACGAGCAGTTCGACG | 3780 |
| Qy | 3121 | CT | GGACCGACCTTCACCATTTGACGACGACCGTGCCACAGACGGGTGTCAACGCTG | 3180 |
| Db | 3781 | CT | GGACCGACCTTCACCATTTGACGACGACCGTGCCACAGACGGGTGTCAACGCTG | 3840 |
| Qy | 3181 | CAG | CGCGGAGCAGACGCTGTGTAGGGGAGGATGGCATTTACAGGTTGTGACTCCAGGA | 3240 |
| Db | 3841 | CAG | CGCGGAGCAGACGCTGTGTAGGGGAGGATGGCATTTACAGGTTGTGACTCCAGGA | 3900 |
| Qy | 3241 | GA | ACGGCCCTCGGGCATGTTTCGATTTCTCTCGGTTCTGTGCGAGTGCTATGACGGGGTGT | 3300 |
| Db | 3901 | GA | ACGGCCCTCGGGCATGTTTCGATTTCTCTCGGTTCTGTGCGAGTGCTATGACGGGGTGT | 3960 |
| Qy | 3301 | GC | TTGGTACGACTCACGCCCGCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACA | 3360 |
| Db | 3961 | GC | TTGGTACGACTCACGCCCGCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACA | 4020 |
| Qy | 3361 | CA | AGGTTGCGCGTCTGCCAGACCATCTGGAGTTCTCGGAGAGCGTCTTTACAGGCTC | 3420 |
| Db | 4021 | CA | AGGTTGCGCGTCTGCCAGACCATCTGGAGTTCTCGGAGAGCGTCTTTACAGGCTC | 4080 |
| Qy | 3421 | AC | CCACATAGACGCCCATTTCTTTGTCGAGACTAAGCAGGCGAGAGCACTTCCCTTAC | 3480 |
| Db | 4081 | AC | CCACATAGACGCCCATTTCTTTGTCGAGACTAAGCAGGCGAGAGCACTTCCCTTAC | 4140 |
| Qy | 3481 | CT | GTTAGCATACAGGCTACGGTGTGCGCCAGGCTCAGGCTCCACCTCATCTGTGGAC | 3540 |
| Db | 4141 | CT | GTTAGCATACAGGCTACGGTGTGCGCCAGGCTCAGGCTCCACCTCATCTGTGGAC | 4200 |
| Qy | 3541 | CAA | ATGTGAAGTGTCTCATACGGCTAAAGCCTACGCTGCAACGGGCCAACGCCCTGCTG | 3600 |
| Db | 4201 | CAA | ATGTGTGAAGTGTCTCATACGGCTAAAGCCTACGCTGCAACGGGCCAACGCCCTGCTG | 4260 |
| Qy | 3601 | TAT | AGGCTGGGAGCGGTTTCAAACAGAGGTTTACTACACACACCCCATACCAATACATC | 3660 |

| | | | |
|----|------|---|------|
| Db | 4261 | TATAGGCTGGAGCGCGTTCAAAACGAGGTTACTACACACACCCCAATACCAATATACATC | 4322 |
| Qy | 3661 | ATGGCATGCATGTCTGGCTGACCTCGGAGGTGCTCACGAGCACCTGGGTGCTGTAGCGGGA | 3720 |
| Db | 4321 | ATGGCATGCATGTCTGGCTGACCTCGGAGGTGCTCACGAGCACCTGGGTGCTGTAGCGGGA | 4380 |
| Qy | 3721 | GTCCTAGCAGCTCTGGCCGGTATTGCTCTGACAAACGAGCAGCGTGTCTCATTTGTGGCAGG | 3780 |
| Db | 4381 | GTCCTAGCAGCTCTGGCCGGTATTGCTCTGACAAACGAGCAGCGTGTCTCATTTGTGGCAGG | 4440 |
| Qy | 3781 | ATCATCTTGTCCGAAAGCCGGCCATCATTTCCGACAGGGAAGTCTCTTTTACCGGGAGTTTC | 3840 |
| Db | 4441 | ATCATCTTGTCCGAAAGCCGGCCATCATTTCCGACAGGGAAGTCTCTTTTACCGGGAGTTTC | 4500 |
| Qy | 3841 | GATGAGATGGAAGAGTCGGCTCACACCTCCCTTTATATCGAAACAGGGAATGCAAGCTCGCC | 3900 |
| Db | 4501 | GATGAGATGGAAGAGTCGGCTCACACCTCCCTTTATATCGAAACAGGGAATGCAAGCTCGCC | 4560 |
| Qy | 3901 | GAACAATTCAAACAGAAAGGCAATCGGGTTGCTGCAAAACAGCCACCAAGCAGCGGAGGCT | 3960 |
| Db | 4561 | GAACAATTCAAACAGAAAGGCAATCGGGTTGCTGCAAAACAGCCACCAAGCAGCGGAGGCT | 4620 |
| Qy | 3961 | GCTGCTCCGCTGGTGGGAATCCAAAGTGCAGACCTCGAAGCCTTCTGGCGGAAGCATATG | 4020 |
| Db | 4621 | GCTGCTCCGCTGGTGGHAATCAAGTGCAGACCTCGAAGCCTTCTGGCGGAAGCATATG | 4680 |
| Qy | 4021 | TGGAATTTTCATCAGCGGGATACAAATATTTAGCAGGTTGTCCACTCTGCTGCGCAACCCC | 4080 |
| Db | 4681 | TGGAATTTTCATCAGCGGGATACAAATATTTAGCAGGTTGTCCACTCTGCTGCGCAACCCC | 4740 |
| Qy | 4081 | GCGATAGCATCACTGATGGCAATTCACAGCCCTATATCACCAGCCCGCTCACCAACCAACAT | 4140 |
| Db | 4741 | GCGATAGCATCACTGATGGCAATTCACAGCCCTATATCACCAGCCCGCTCACCAACCAACAT | 4800 |
| Qy | 4141 | ACCCTCCGTTTAAACATCCTGGGGGATGGTGGCCGCCCAACTTGCTCTCCACAGCGCT | 4200 |
| Db | 4801 | ACCCTCCGTTTAAACATCCTGGGGGATGGTGGCCGCCCAACTTGCTCTCCACAGCGCT | 4860 |
| Qy | 4201 | GCTTCTGCTTTTCGTAGGCGCCGGCATCGCTGGAGCGGCTGTGGCAGCAGATAGGCTTTGGG | 4260 |
| Db | 4861 | GCTTCTGCTTTTCGTAGGCGCCGGCATCGCTGGAGCGGCTGTGGCAGCAGATAGGCTTTGGG | 4920 |
| Qy | 4261 | AAGGTGCTTTGGATATTTTGGCAGGTTATGAGCAGGGTGGCAGCGGCGCTCGTGGCC | 4320 |
| Db | 4921 | AAGGTGCTTTGGATATTTTGGCAGGTTATGAGCAGGGTGGCAGCGGCGCTCGTGGCC | 4980 |
| Qy | 4321 | TTTAAAGTTCATAGCGGCGAGATGCCCTCCACCCAGGACCTGGTTAACTACTCCCTGCT | 4380 |
| Db | 4981 | TTTAAAGTTCATAGCGGCGAGATGCCCTCCACCCAGGACCTGGTTAACTACTCCCTGCT | 5040 |
| Qy | 4381 | ATCCTCTCCCTGGCGCCCTAGTCTGTGGGGTCTGTTCGCGAGCGATACTCGCTCGGCAC | 4440 |
| Db | 5041 | ATCCTCTCCCTGGCGCCCTAGTCTGTGGGGTCTGTTCGCGAGCGATACTCGCTCGGCAC | 5100 |
| Qy | 4441 | GTGGGCCACAGGGAGGGGGCTGTGCAGTGTGATGAACCGGCTGTAGCGTTCCGTTCCGGG | 4500 |
| Db | 5101 | GTGGGCCACAGGGAGGGGGCTGTGCAGTGTGATGAACCGGCTGTAGCGTTCCGTTCCGGG | 5160 |
| Qy | 4501 | GGTAACACAGTCTCCCCACGCATATGTGTGCTGAGAGCGAGCTGCAGACAGTGTCACT | 4560 |
| Db | 5161 | GGTAACACAGTCTCCCCACGCATATGTGTGCTGAGAGCGAGCTGCAGACAGTGTCACT | 5220 |
| Qy | 4561 | CAGATCTCTCTAGTCTTTACCATCACTCAGCTGTGTGAAGAGGCTTCAACAGTGGATCAAC | 4620 |
| Db | 5221 | CAGATCTCTCTAGTCTTTACCATCACTCAGCTGTGTGAAGAGGCTTCAACAGTGGATCAAC | 5280 |
| Qy | 4621 | GAGGACTGTCTCACGCCATGTCTCGGCTCTGGCTTAAGAGATGTTTGGGATTTGGATATGC | 4680 |
| Db | 5281 | GAGGACTGTCTCACGCCATGTCTCGGCTCTGGCTTAAGAGATGTTTGGGATTTGGATATGC | 5340 |
| Qy | 4681 | ACGGTGTTCATGATTTTCAAGACCTGGCTCCAGTCCAAAGCTTCTGCCCGCGATTGCCGGGA | 4740 |
| Db | 5341 | ACGGTGTTCATGATTTTCAAGACCTGGCTTCCAGTCCAAAGCTTCTGCCCGCGATTGCCGGGA | 5400 |


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Db 7561 AAGCTCCAGGACTGACGATGCTGTATGCGAGAGACCTTGTCTGTATCTGTGAAGC 7620
QY GCGGGGACCCAGAGAGGACGAGCGAGCTTACGGGCTTTCACGGAGGCTATGACTAGATAC 7020
Db 7621 GCGGGGACCCAGAGAGGACGAGCGAGCTTACGGGCTTTCACGGAGGCTATGACTAGATAC 7680
QY TCTGCCCCCTTGGGACCCGACCAACAGATAGCCTTGGAGTGTGATACATCATGC 7080
Db 7681 TCTGCCCCCTTGGGACCCGACCAACAGATAGCCTTGGAGTGTGATACATCATGC 7740
QY TCTTCCAAATGTCTAGTCCGACGATGATCTGCGCAAGGCTGTACTATCTCACCCGT 7140
Db 7741 TCTTCCAAATGTCTAGTCCGACGATGATCTGCGCAAGGCTGTACTATCTCACCCGT 7800
QY GACCCACACACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACATCTCAGTCAAT 7200
Db 7801 GACCCACACACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACATCTCAGTCAAT 7860
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Db 7861 TCTTGGCTAGGCAACATCATGATGATGCGCCACCTTGTGGCAAGGATGATGATCTGTATG 7920
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Db 7921 ACTCATTTCTTCTCCATCTTCTAGCTCAGGAACTTGAAGGCTGTAGATTTCTAG 7980
QY ATCTAGGGGCTGTATCTCATTAGGACCTTGTAGCTACCTACCTCAGATCATCTCAGCTC 7380
Db 7981 ATCTAGGGGCTGTATCTCATTAGGACCTTGTAGCTACCTACCTCAGATCATCTCAGCTC 8040
QY CATGGCTTAGCGCATTTTCACTTCCATAGTACTCTCCAGGCTGAGATCAATAGGCTGGT 7440
Db 8041 CATGGCTTAGCGCATTTTCACTTCCATAGTACTCTCCAGGCTGAGATCAATAGGCTGGT 8100
QY TCATGCTCAGGAACTTGGGCTTACCGCTTGTGGAGTCTGGAGACATCGGGCCAGAAAT 7500
Db 8101 TCATGCTCAGGAACTTGGGCTTACCGCTTGTGGAGTCTGGAGACATCGGGCCAGAAAT 8160
QY GTCCGGCTTAGGCTATGTCCTCAGGGGAGGGCTGCGACTTGTGGCAAGTACTCTTTC 7560
Db 8161 GTCCGGCTTAGGCTATGTCCTCAGGGGAGGGCTGCGACTTGTGGCAAGTACTCTTTC 8220
QY ACTTGGGCTAGGAGGCTCAAACTCACTCCAACTCCGCTGCTGCCAGTTGGAT 7620
Db 8221 ACTTGGGCTAGGAGGCTCAAACTCACTCCAACTCCGCTGCTGCCAGTTGGAT 8280
QY TTATCCAGCTGGTTCTGTTGTCTGTTACAGCGGGGAGACATATACAGCCCTGTCTCGT 7680
Db 8281 TTATCCAGCTGGTTCTGTTGTCTGTTACAGCGGGGAGACATATACAGCCCTGTCTCGT 8340
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Db 8341 GCGGACCCGCTGTTCTGTTGTCTGTTACAGCGGGGAGACATATACAGCCCTGTCTCGT 8400
QY CTACTCCCAACCGATGAAAGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTGTTT 7800
Db 8401 CTACTCCCAACCGATGAAAGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTGTTT 8460
QY TTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
Db 8461 TTTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 8520
QY TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
Db 8521 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 8580
QY TAGCTGTGAAGGCTCGGTGAGCCGCTTGAAGTGAAGAGAGTGTGCTGATCTGCTCTCTGC 7980
Db 8581 TAGCTGTGAAGGCTCGGTGAGCCGCTTGAAGTGAAGAGAGTGTGCTGATCTGCTCTCTGC 8640
QY AGATCAAGT 7989
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Db 8641 AGATCAAGT 8649
RESULT 8
US-10-029-907-1
; Sequence 1, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/029,907
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 8639
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1803)... (8408)
US-10-029-907-1
Query Match 91.0%; Score 7273.8; DB 4; Length 8639;
Best Local Similarity 92.2%; Pred. No. 0;
Matches 7976; Conservative 0; Mismatches 2; Indels 671; Gaps 3;
QY 1 GCAGCCCCCGATTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGGAATCTACTG 60
Db 2 GCAGCCCCCGATTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGGAATCTACTG 61
QY 61 TCTTACGACAGAAAGCTCTAGCCATGCGGTAGTATGATGATGATGATGATGATGATGATGAT 120
Db 62 TCTTACGACAGAAAGCTCTAGCCATGCGGTAGTATGATGATGATGATGATGATGATGATGAT 121
QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTCGCCAG 180
Db 122 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATTCGCCAG 181
QY 181 GACGACCGGGTCTTTCTTTGGATCAACCCGCTCAATGCTGAGATTTGGGCGTGCCTCC 240
Db 182 GACGACCGGGTCTTTCTTTGGATCAACCCGCTCAATGCTGAGATTTGGGCGTGCCTCC 241
QY 241 GCGAGACTCTAGCCGAGTAGTGTGGGTGCGGAAGGCTTGTGCTACTGCTGATAGG 300
Db 242 GCGAGACTCTAGCCGAGTAGTGTGGGTGCGGAAGGCTTGTGCTACTGCTGATAGG 301
QY 301 GTGCTTGGAGTCCCGGGGAGGTCTCGTAGACCGTGCACCATGAGCAGGAATCTTAAAC 360
Db 302 GTGCTTGGAGTCCCGGGGAGGTCTCGTAGACCGTGCACCATGAGCAGGAATCTTAAAC 361
QY 361 CTCAAAGAAAACCAAAAGGCGCGCATGATTTGAAAGATGATGATGATGATGATGATGATGAT 420
Db 362 CTCAAAGAAAACCAAAAGGCGCGCATGATTTGAAAGATGATGATGATGATGATGATGATGAT 421
QY 421 CGGCCGCTTGGGTGGAGAGCTATTCGGCTATGCTGCGGCAACAGACATCGGCTGCT 480
Db 422 CGGCCGCTTGGGTGGAGAGCTATTCGGCTATGCTGCGGCAACAGACATCGGCTGCT 481
QY 481 CTGATGCGCGCTGTTCCGGCTCTCAGCGCAGGGGCGCGGCTTCTTTTGTCAAGACCG 540
Db 482 CTGATGCGCGCTGTTCCGGCTCTCAGCGCAGGGGCGCGGCTTCTTTTGTCAAGACCG 541
QY 541 ACTGTCCGCTGCTGATGAACTGAGCTGAGGAGCGGCTGATCTGCTGCTGCTGCTGCTGCT 600
Db 542 ACTGTCCGCTGCTGATGAACTGAGCTGAGGAGCGGCTGATCTGCTGCTGCTGCTGCTGCT 601
QY 601 CGAGCGGCTTCTTGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
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|------|----|---|------|
| 602 | Db | CGACGGGGCTTCTTGGCCGAGCTGTGCTGCAGCTTTGTCACCTGAAGCGGGAAAGGAGCTGGC | 661 |
| 661 | Qy | TGCTATTGGGCGAAGTGGCGGGCAGGAGTCTCTGTCACTCATCTCACTGTCTCTCCGCCGAGA | 720 |
| 662 | Db | TGCTATTGGGCGAAGTGGCGGGCAGGAGTCTCTGTCACTCATCTGTCTCTCCGCCGAGA | 721 |
| 721 | Qy | AAGTATCCATCATGTGCTGATGCAATGGCGGGCTGTCATAGCGTTGATCCGGCTACCTGCC | 780 |
| 722 | Db | AAGTATCCATCATGTGCTGATGCAATGGCGGGCTGTCATAGCGTTGATCCGGCTACCTGCC | 781 |
| 781 | Qy | CATTGCGACCCAAAGCGAAACATCGCATCGAGCGAGCAGCTACTCGGATGGAAGCCGGTC | 840 |
| 782 | Db | CATTGCGACCCAAAGCGAAACATCGCATCGAGCGAGCAGCTACTCGGATGGAAGCCGGTC | 841 |
| 841 | Qy | TTGTGCGATCAGGATGATCTGAGCAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGC | 900 |
| 842 | Db | TTGTGCGATCAGGATGATCTGAGCAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGC | 901 |
| 901 | Qy | CCAGGCTCAAGCGCGGATGCGCCGAGCGGAGGATCTCTGTCGTGACCCATGGGGATCCCT | 960 |
| 902 | Db | CCAGGCTCAAGCGCGGATGCGCCGAGCGGAGGATCTCTGTCGTGACCCATGGGGATCCCT | 961 |
| 961 | Qy | GCTTGGCGAATATCATGCTGGAAATGCGCGCTTTCTGGAATTCATGCACTGGCCGGC | 1020 |
| 962 | Db | GCTTGGCGAATATCATGCTGGAAATGCGCGCTTTCTGGAATTCATGCACTGGCCGGC | 1021 |
| 1021 | Qy | TGGGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCGGTGATTTGCTGAAGAGC | 1080 |
| 1022 | Db | TGGGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCGGTGATTTGCTGAAGAGC | 1081 |
| 1081 | Qy | TTGGCGGGAATGGGCTGACCGCTTCTGTCGTTTACGGTATCGCGCTCCCGATTCGC | 1140 |
| 1082 | Db | TTGGCGGGAATGGGCTGACCGCTTCTGTCGTTTACGGTATCGCGCTCCCGATTCGC | 1141 |
| 1141 | Qy | AGCGCATCGCTTCTATCGCTTCTTGACAGTCTCTCTGAGTT-----TAAA | 1188 |
| 1142 | Db | AGCGCATCGCTTCTATCGCTTCTTGACAGTCTCTCTGAGTT-----TAAA | 1189 |
| 1189 | Qy | CAGACCAACACGGTTTCCCTTAGCGGGATCAATTCGCGCCCTCTCCCTCCCGCCCGCT | 1248 |
| 1202 | Db | CAGACCAACACGGTTTCCCTTAGCGGGATCAATTCG-----CCCCCCCCCT | 1250 |
| 1249 | Qy | AAGTTACTGGCGAAGCCGCTTGGAAATAAGGCGGTGTGCTGTATATGTTATTT | 1308 |
| 1251 | Db | AAGTTACTGGCGAAGCCGCTTGGAAATAAGGCGGTGTGCTGTATATGTTATTT | 1310 |
| 1309 | Qy | TCCACCATAATGCGCTTTTGGCAATGTAGGGCCCGGAAACCTGCGCTGTCTCTTG | 1368 |
| 1311 | Db | TCCACCATAATGCGCTTTTGGCAATGTAGGGCCCGGAAACCTGCGCTGTCTCTTG | 1370 |
| 1369 | Qy | ACGAGCATTCCTTAGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGTCTGTGTAATGC | 1428 |
| 1371 | Db | ACGAGCATTCCTTAGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGTCTGTGTAATGC | 1430 |
| 1429 | Qy | GTGAAGGAGCAGTTCTCTGGAAGTTCTTGAAGACAAACACGCTGTAGCGACCTT | 1488 |
| 1431 | Db | GTGAAGGAGCAGTTCTCTGGAAGTTCTTGAAGACAAACACGCTGTAGCGACCTT | 1490 |
| 1489 | Qy | TGCAGCAGCGGAACCCCGACCTGCGGACAGTGTCTGCGGCCAAAGCCACGTGTA | 1548 |
| 1491 | Db | TGCAGCAGCGGAACCCCGACCTGCGGACAGTGTCTGCGGCCAAAGCCACGTGTA | 1550 |
| 1549 | Qy | TAAGATACACCTGCAAGGCGGCACAAACCGAGTGCACGTTGTGAGTTGATGTTGTG | 1608 |
| 1551 | Db | TAAGATACACCTGCAAGGCGGCACAAACCGAGTGCACGTTGTGAGTTGATGTTGTG | 1610 |
| 1609 | Qy | GAAAGAGTCAAAATGGCTCTCTCAAGCGTATTCAACAAGGGCTGAAGGATCCCGAAG | 1668 |
| 1611 | Db | GAAAGAGTCAAAATGGCTCTCTCAAGCGTATTCAACAAGGGCTGAAGGATCCCGAAG | 1670 |
| 1669 | Qy | GTACCCCATTTGATGGATCTGATCTGGGGCTCTCGGTGCATGCTTTACATGTTTAG | 1728 |
| 1671 | Db | GTACCCCATTTGATGGATCTGATCTGGGGCTCTCGGTGCATGCTTTACATGTTTAG | 1730 |
| 1729 | Qy | TCCAGGTTTAAAAACGCTTAGGCCCGCCGAAACACACGGGACGTTGGTTTCTTTGAAAAA | 1788 |
| 1731 | Db | TCCAGGTTTAAAAACGCTTAGGCCCGCCGAAACACACGGGACGTTGGTTTCTTTGAAAAA | 1790 |
| 1789 | Qy | CAGGATAATACCATG----- | 1803 |
| 1791 | Db | CAGGATAATACCATG----- | 1803 |
| 1804 | Qy | CTGATACTCTTGACCTTGTACCGCACTATAAGCTGTCTCGCTAGGCTCATATGTTGG | 1910 |
| 1804 | Qy | CTGATACTCTTGACCTTGTACCGCACTATAAGCTGTCTCGCTAGGCTCATATGTTGG | 1910 |
| 1911 | Db | TTACAATATTTTATACCAAGGGCGGAGGCACACTTGTCAAGTGTGGATCCCCCCTCAAC | 1970 |
| 1804 | Qy | TTACAATATTTTATACCAAGGGCGGAGGCACACTTGTCAAGTGTGGATCCCCCCTCAAC | 1970 |
| 1971 | Db | GTTTGGGGGGCGCGATGCGCTCATCTCTCTCACTGTGCGGATCCACCAGAGCTAATC | 2030 |
| 1804 | Qy | GTTTGGGGGGCGCGATGCGCTCATCTCTCTCACTGTGCGGATCCACCAGAGCTAATC | 2030 |
| 2031 | Db | TTTACCATCACAAAATCTTGCTGCGCATACTCGTCCACTCATGCTGTCTCCAGGCTGT | 2090 |
| 1804 | Qy | TTTACCATCACAAAATCTTGCTGCGCATACTCGTCCACTCATGCTGTCTCCAGGCTGT | 2090 |
| 2091 | Db | ATAACAAAGTCCGCTACTTGTGCGCGCACACGGGCTCATTCGTGCATGATGTGTGTG | 2150 |
| 1804 | Qy | ATAACAAAGTCCGCTACTTGTGCGCGCACACGGGCTCATTCGTGCATGATGTGTGTG | 2150 |
| 2151 | Db | CGGAAGTTTGCTGGGGTCAATTATGTCGCAATGGCTCTCATGAAGTTGGCCGACTGACA | 2210 |
| 1804 | Qy | CGGAAGTTTGCTGGGGTCAATTATGTCGCAATGGCTCTCATGAAGTTGGCCGACTGACA | 2210 |
| 2211 | Db | GGTACGTAGCTTTATGACCATCTCACCCACTGCGGGACTGGGCCACCGCGGCTTACGA | 2270 |
| 1804 | Qy | GGTACGTAGCTTTATGACCATCTCACCCACTGCGGGACTGGGCCACCGCGGCTTACGA | 2270 |
| 2271 | Db | GACCTTGGGTGGCAGTTGAGCCGTCGTCTTCTCTGATATGGAGACCAAGTTATCACC | 2330 |
| 1804 | Qy | GACCTTGGGTGGCAGTTGAGCCGTCGTCTTCTCTGATATGGAGACCAAGTTATCACC | 2330 |
| 2331 | Db | TGGGGGCGAGACACCGCGGCTGTGGGACATCATCTTGGGCGCTCCCGCTCTCCGCCGC | 2390 |
| 1804 | Qy | TGGGGGCGAGACACCGCGGCTGTGGGACATCATCTTGGGCGCTCCCGCTCTCCGCCGC | 2390 |
| 2391 | Db | AGGGGAGGGAGATACATCTGGGACCGCGCAGACAGCCCTTGAAGGCGAGGGTGGCGACT | 2450 |
| 1804 | Qy | AGGGGAGGGAGATACATCTGGGACCGCGCAGACAGCCCTTGAAGGCGAGGGTGGCGACT | 2450 |
| 2451 | Db | CGGCTTATTCGGCTTCTCCCAACAGACGCGAGCCTACTTGGCTGATCATCACT | 2510 |
| 1861 | Qy | AGCTTACAGCGCGGACAGGAACACAGGTCCAGGGGGAGGTCGAAGTGTCTCCACCGCA | 1920 |
| 2511 | Db | AGCTTACAGCGCGGACAGGAACACAGGTCCAGGGGGAGGTCGAAGTGTCTCCACCGCA | 2570 |
| 1921 | Qy | ACAAATCTTCTGGGACCTGCGTCAATGGCGCTGTGTGGAGCTGTCTATCATGTTGCC | 1980 |
| 2571 | Db | ACAAATCTTCTGGG | |

2161 GGCACAGCAGGGGAGCTACTCTCCCGCCAGGCGCGTCTCTCTACTTGAAGGGCTCTTCG 2220
2811 GGCACAGCAGGGGAGCTACTCTCCCGCCAGGCGCGTCTCTCTACTTGAAGGGCTCTTCG 2870
2221 GCGGTCCACTGCTCTGCGCCCTCGGGGCAOGCTGTGGGCACTTTTCGGGCTCGCGTGTGC 2280
2871 GCGGTCCACTGCTCTGCGCCCTCGGGGCAOGCTGTGGGCACTTTTCGGGCTCGCGTGTGC 2930
2281 ACCGAGGGGTTCGAAGGGGTGAGCTACTTGTACCGGTGAGTCTATGGAACCACTATG 2340
2931 ACCGAGGGGTTCGAAGGGGTGAGCTTTGTACCGGTGAGTCTATGGAACCACTATG 2990
2341 CGGTCCCGGTCTTCAAGGACAACCTCGTCCCGTCCGGCGGTACCGGACAGACATTCAGGTG 2400
2991 CGGTCCCGGTCTTCAAGGACAACCTCGTCCCGTCCGGCGGTACCGGACAGACATTCAGGTG 3050
2401 GCCCATCTACAGCCCTTACTGGTAGCGGCAAGAGACATAAGGTGCGGGCTCGGTATGCA 2460
3051 GCCCATCTACAGCCCTTACTGGTAGCGGCAAGAGACATAAGGTGCGGGCTCGGTATGCA 3110
2461 GCCAAGGGTATAAGGTGCTTCTGTAACCCGTCGTCGCGCCACCCCTAGGTTTCGGG 2520
3111 GCCAAGGGTATAAGGTGCTTCTGTAACCCGTCGTCGCGCCACCCCTAGGTTTCGGG 3170
2521 GGGTATATGCTAAGGCACATGGTATCGAACCCCTAAATCAGAACCGGGTAAAGCAATC 2580
3171 GGGTATATGCTAAGGCACATGGTATCGAACCCCTAAATCAGAACCGGGTAAAGCAATC 3230
2581 ACCAAGGGTATGAGTGTCTGTAACCCGTCGTCGCGCCACCCCTAGGTTTCGGG 2640
3231 ACCAAGGGTATGAGTGTCTGTAACCCGTCGTCGCGCCACCCCTAGGTTTCGGG 3290
2641 TCTGGGGGCGGTATGAGTGTCTGTAACCCGTCGTCGCGCCACCCCTAGGTTTCGGG 2700
3291 TCTGGGGGCGGTATGAGTGTCTGTAACCCGTCGTCGCGCCACCCCTAGGTTTCGGG 3350
2701 ATCTGGGCGATGGGACAGTCTGTAACCCGTCGTCGCGCCACCCCTAGGTTTCGGG 2760
3351 ATCTGGGCGATGGGACAGTCTGTAACCCGTCGTCGCGCCACCCCTAGGTTTCGGG 3410
2761 CTGCGCACCGCTACGGCTCGGGATCGGTGCAACCGTGCACATCCCAACATCGAGGAGGTG 2820
3411 CTGCGCACCGCTACGGCTCGGGATCGGTGCAACCGTGCACATCCCAACATCGAGGAGGTG 3470
2821 GCTCTGTCAGACTGGAAGTATCCCTTTTATGGCAAGCCATCCCTCGAGAGCCATC 2880
3471 GCTCTGTCAGACTGGAAGTATCCCTTTTATGGCAAGCCATCCCTCGAGAGCCATC 3530
2881 AAGGGGGGAGGACCTCATTTTCTGCCATTCGAAGAAATGTGATGAGCTCGCGCG 2940
3531 AAGGGGGGAGGACCTCATTTTCTGCCATTCGAAGAAATGTGATGAGCTCGCGCG 3590
2941 AAGCTGTCCGGCTCGGACTCAATGTGTAGCATATTAACGGGGCTTGTATGATCGGTC 3000
3591 AAGCTGTCCGGCTCGGACTCAATGTGTAGCATATTAACGGGGCTTGTATGATCGGTC 3650
3001 ATACCAACTAGCGGAGAGCTGATTCGTAGCAACGAGAGCTCTATATGAGCGGCTTACC 3060
3651 ATACCAACTAGCGGAGAGCTGATTCGTAGCAACGAGAGCTCTATATGAGCGGCTTACC 3710
3061 GGGGATTTGACTTCAGTGTGAGTGTGCAATGATGTGTCAACCGAGAGCTGATGAGT 3120
3711 GGGGATTTGACTTCAGTGTGAGTGTGCAATGATGTGTCAACCGAGAGCTGATGAGT 3770
3121 CTGGAACCGGACCTTACCATTTAGACGACACCGTGCACCAAGACGGGTGACCGTCG 3180
3771 CTGGAACCGGACCTTACCATTTAGACGACACCGTGCACCAAGACGGGTGACCGTCG 3830
3181 CAGCGGAGGAGCAGTGTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTTCCAGGA 3240
3831 CAGCGGAGGAGCAGTGTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTTCCAGGA 3890
3241 GAACGGCCCTCGGGCATGTTTCGATTCCTCGGTTCTGTGCGAGTGTCTATGACGGGGCTGT 3300

3891 GAACGGCCCTCGGGCATGTTCCGATTCCTCGGTTCTGTGCGAGTGTCTATGACGGGGCTGT 3950
3301 GCTTGGTAGAGCTCACGCCCGCGAGACCTCAGTTAGTGTTCGGGCTTACTTAACACA 3360
3951 GCTTGGTAGAGCTCACGCCCGCGAGACCTCAGTTAGTGTTCGGGCTTACTTAACACA 4010
3361 CCAGGTTGCCGCTGTCCAGGACCACTGAGGTTCTGGAGAGCTCTTTACAGGCTC 3420
4011 CCAGGTTGCCGCTGTCCAGGACCACTGAGGTTCTGGAGAGCTCTTTACAGGCTC 4070
3421 ACCGATAGAGCCCATTTCTTGTCCAGACTAAGCAGGAGGAGACAACTTCCCTTAC 3480
4071 ACCGATAGAGCCCATTTCTTGTCCAGACTAAGCAGGAGGAGACAACTTCCCTTAC 4130
3481 CTGTGTAGCATACAGGCTACGGTGTGCGCCAGGCTCAGGCTCCACCTCCATCGTGGAC 3540
4131 CTGTGTAGCATACAGGCTACGGTGTGCGCCAGGCTCAGGCTCCACCTCCATCGTGGAC 4190
3541 CAAATGTGGAAGTGTCTCATCGGCTAAAGCTTACGCTGCAAGGGGCAACGCGCCCTGCTG 3600
4191 CAAATGTGGAAGTGTCTCATCGGCTAAAGCTTACGCTGCAAGGGGCAACGCGCCCTGCTG 4250
3601 TATAGGCTGGGAGCGGTTCAAAACGAGGTTACTACACACACCCCATACCAAAATACATC 3660
4251 TATAGGCTGGGAGCGGTTCAAAACGAGGTTACTACACACACCCCATACCAAAATACATC 4310
3661 ATGGGATGATGCTCGGCTGACCTGGAGTGTGTCAGGACACCTGGTGTCTGTTAGGCGGA 3720
4311 ATGGGATGATGCTCGGCTGACCTGGAGTGTGTCAGGACACCTGGTGTCTGTTAGGCGGA 4370
3721 GTCTAGGAGCTCTGCGCGCTATTGCTGTGCAAAAGGAGGCTGTGTTAGGCGGAG 3780
4371 GTCTAGGAGCTCTGCGCGCTATTGCTGTGCAAAAGGAGGCTGTGTTAGGCGGAG 4430
3781 ATCATCTTGTTCGGAAAGCGGCGCATCATTCGCGAGGAGTCTTTCACCGGAGTTTC 3840
4431 ATCATCTTGTTCGGAAAGCGGCGCATCATTCGCGAGGAGTCTTTCACCGGAGTTTC 4490
3841 GATGAGATGGAAGTGTGCGCTCACACCTCCCTTACATCGAACAGGAAATGACGCTCGCC 3900
4491 GATGAGATGGAAGTGTGCGCTCACACCTCCCTTACATCGAACAGGAAATGACGCTCGCC 4550
3901 GAACAAATCAACAGAGGCAATTCGGGTTGCTGCAAAAGCCACCAAGACGGAGGCT 3960
4551 GAACAAATCAACAGAGGCAATTCGGGTTGCTGCAAAAGCCACCAAGACGGAGGCT 4610
3961 GCTGCTCCGCTGGTGAATCCCAAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG 4020
4611 GCTGCTCCGCTGGTGAATCCCAAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG 4670
4021 TGGAAATTCATCAGCGGATACAATATTTAGCAGGCTTGTCCAATCTGCTGCTGGCAACCCC 4080
4671 TGGAAATTCATCAGCGGATACAATATTTAGCAGGCTTGTCCAATCTGCTGCTGGCAACCCC 4730
4081 GCGATAGATCACTGATGGAATTCAGAGCTCTATCAGAGCCCGCTCACCACCGACAT 4140
4731 GCGATAGATCACTGATGGAATTCAGAGCTCTATCAGAGCCCGCTCACCACCGACAT 4790
4141 ACCCTCTCTTTAAACATCTCTGGGGGATGGTGGCGCGCCCAACTTGTCTCTCCAGCGCT 4200
4791 ACCCTCTCTTTAAACATCTCTGGGGGATGGTGGCGCGCCCAACTTGTCTCTCCAGCGCT 4850
4201 GCTTCTGCTTCTAGGCGCGGCACTCGCTGGAGCGGCTGTGGGAGCATAGGCTTGGG 4260
4851 GCTTCTGCTTCTAGGCGCGGCACTCGCTGGAGCGGCTGTGGGAGCATAGGCTTGGG 4910
4261 AAGGTGCTTGTGATATTTTGGCAGGTTATGAGCAGGAGGAGGAGCGGCTGCTGCGCC 4320
4911 AAGGTGCTTGTGATATTTTGGCAGGTTATGAGCAGGAGGAGGAGCGGCTGCTGCGCC 4970
4321 TTTAAGGTGATGAGCGGAGATGCCCTCCACCGAGGACCTGGTTAACTTCTCCTGCT 4380

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|----|------|--|------|
| Dd | 4971 | TTTAAGGTCAAGCGCGGAGATGCCCTCCACCGAGGACCTGTGTTAACTACTCCTCGCT | 5030 |
| Qy | 4381 | ATCCTCTCCCTGGCGCCCTAGTCTCGGGGTCGTGTCGACGATATCTGCTCGGCAC | 4440 |
| Dd | 5031 | ATCCTCTCCCTGGCGCCCTAGTCTCGGGGTCGTGTCGACGATATCTGCTCGGCAC | 5090 |
| Qy | 4441 | GTGGCCACAGGGAGGGGCTGTGCAAGTGGATGAACCGGCTGATAGCTTCGCTCGCG | 4500 |
| Dd | 5091 | GTGGCCACAGGGAGGGGCTGTGCAAGTGGATGAACCGGCTGATAGCTTCGCTCGCG | 5150 |
| Qy | 4501 | GTTAAACACGCTCTCCACGACACTATGCTGAGAGGCGCTGACGACGCTGCTACT | 4560 |
| Dd | 5151 | GTTAAACACGCTCTCCACGACACTATGCTGAGAGGCGCTGACGACGCTGCTACT | 5210 |
| Qy | 4561 | CAGATCCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTACACAGTGGATCAAC | 4620 |
| Dd | 5211 | CAGATCCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTACACAGTGGATCAAC | 5270 |
| Qy | 4621 | GAGACTGCTCCAGCCATGCTCCGGCTCGTGGCTTAAGAGATGTTTGGGATTGGATATGC | 4680 |
| Dd | 5271 | GAGACTGCTCCAGCCATGCTCCGGCTCGTGGCTTAAGAGATGTTTGGGATTGGATATGC | 5330 |
| Qy | 4681 | ACGGTGTGACTGATTTCAAGACCTGCTCCAGTCCCAAGCTCTCGCCGATTCGCGGA | 4740 |
| Dd | 5331 | ACGGTGTGACTGATTTCAAGACCTGCTCCAGTCCCAAGCTCTCGCCGATTCGCGGA | 5390 |
| Qy | 4741 | GTCCCTCTCTCATGTCATGTCAGTGGGTACAGGGAGTCTGGCGGGGACGGCATCATG | 4800 |
| Dd | 5391 | GTCCCTCTCTCATGTCATGTCAGTGGGTACAGGGAGTCTGGCGGGGACGGCATCATG | 5450 |
| Qy | 4801 | CAAAACACCTGCTCCAGTGGAGCAAGATCAACGGGATGTTGAAGATGTTTCCATGAGG | 4860 |
| Dd | 5451 | CAAAACACCTGCTCCAGTGGAGCAAGATCAACGGGATGTTGAAGATGTTTCCATGAGG | 5510 |
| Qy | 4861 | ATCGTGGGCTTAGGACTGATGAACACGCGGATCGAAATTTCCCTTAAACCGGTAC | 4920 |
| Dd | 5511 | ATCGTGGGCTTAGGACTGATGAACACGCGGATCGAAATTTCCCTTAAACCGGTAC | 5570 |
| Qy | 4921 | ACACGGGCCCCCTGACGCCCCCTCCCGCGGCAAAATTTCTAGGGGCTGTGGCGGTG | 4980 |
| Dd | 5571 | ACACGGGCCCCCTGACGCCCCCTCCCGCGGCAAAATTTCTAGGGGCTGTGGCGGTG | 5630 |
| Qy | 4981 | GCTGCTGAGAGTACGTGGAGTTACCGGGTGGGGATTTCCACTACGTGACGGGCATG | 5040 |
| Dd | 5631 | GCTGCTGAGAGTACGTGGAGTTACCGGGTGGGGATTTCCACTACGTGACGGGCATG | 5690 |
| Qy | 5041 | ACCACTGACAACTGAAAGTCCCGTGTACGTTCCCGCCCCCGAAATTTCTCACAAGATG | 5100 |
| Dd | 5691 | ACCACTGACAACTGAAAGTCCCGTGTACGTTCCCGCCCCCGAAATTTCTCACAAGATG | 5750 |
| Qy | 5101 | GATGGGTGCGGTGACAGGTACGCTCCAGCGTGCAAAACCCCTCTACGGGAGGCTC | 5160 |
| Dd | 5751 | GATGGGTGCGGTGACAGGTACGCTCCAGCGTGCAAAACCCCTCTACGGGAGGCTC | 5810 |
| Qy | 5161 | ACATTCTGTCGGGCTCAATCAATACCTGGTGGGTGTCAGCTCCCATCGAGCCCGAA | 5220 |
| Dd | 5811 | ACATTCTGTCGGGCTCAATCAATACCTGGTGGGTGTCAGCTCCCATCGAGCCCGAA | 5870 |
| Qy | 5221 | CCGAGCTAGAGTGCCTCACTTCATGCTCAGCGACCCCTCCACATTAAGCGGAGACG | 5280 |
| Dd | 5871 | CCGAGCTAGAGTGCCTCACTTCATGCTCAGCGACCCCTCCACATTAAGCGGAGACG | 5930 |
| Qy | 5281 | GCTAAGCTAGGCTGGCGAGGGATCTCCCGCTCTCTGGCGAGCTCATCAGCTAGCCAG | 5340 |
| Dd | 5931 | GCTAAGCTAGGCTGGCGAGGGATCTCCCGCTCTCTGGCGAGCTCATCAGCTAGCCAG | 5990 |
| Qy | 5341 | CTGCTGCGCTCTCTTGAAGGCAACATGCACTACCGCTCATGCTCCCGGACGCTGAC | 5400 |
| Dd | 5991 | CTGCTGCGCTCTCTTGAAGGCAACATGCACTACCGCTCATGCTCCCGGACGCTGAC | 6050 |
| Qy | 5401 | CTCATCGAGGCCAACCTCTGCGCGCAGAGATGGCGGGGAAACATCAACCCCGGTGAG | 5460 |
| Dd | 6051 | CTCATCGAGGCCAACCTCTGCGCGCAGAGATGGCGGGGAAACATCAACCCCGGTGAG | 6110 |
| Qy | 5461 | TCAGAAATAAGGTAGTAAATTTTGGACTCTTTCGAGCGCTCTCAAGCGGAGGATGAG | 5520 |
| Dd | 6111 | TCAGAAATAAGGTAGTAAATTTTGGACTCTTTCGAGCGCTCTCAAGCGGAGGATGAG | 6170 |
| Qy | 5521 | AGGAAAGTATCCGTTCCCGCGGAGATCTCGGGAGTCCAGGAAATTCCTCGAGCGATG | 5580 |
| Dd | 6171 | AGGAAAGTATCCGTTCCCGCGGAGATCTCGGGAGTCCAGGAAATTCCTCGAGCGATG | 6230 |
| Qy | 5581 | CCCATATGGGACGCGCCCGGATTAACAACCTCACTGTTAGAGTCTCTGAAAGGACCCGAC | 5640 |
| Dd | 6231 | CCCATATGGGACGCGCCCGGATTAACAACCTCACTGTTAGAGTCTCTGAAAGGACCCGAC | 6290 |
| Qy | 5641 | TACGTCCTCCAGTGGTACAGGGGTGTCATTCGCGCTCCAGGCCCCCTCCGATACCA | 5700 |
| Dd | 6291 | TACGTCCTCCAGTGGTACAGGGGTGTCATTCGCGCTCCAGGCCCCCTCCGATACCA | 5760 |
| Qy | 5701 | CCTCCACGAGGAAAGAGGACGGTTCCTGTCAGAAATCTACCGTGTCTTCTGCCCTTGGC | 6410 |
| Dd | 6351 | CCTCCACGAGGAAAGAGGACGGTTCCTGTCAGAAATCTACCGTGTCTTCTGCCCTTGGC | 6470 |
| Qy | 5761 | GAGCTCGGCAAAAGACCTTCGGCAGCTCCGAATTCGTCGGCCGTGCAAGCGGCAACGCA | 5820 |
| Dd | 6411 | GAGCTCGGCAAAAGACCTTCGGCAGCTCCGAATTCGTCGGCCGTGCAAGCGGCAACGCA | 5880 |
| Qy | 5821 | ACGGCTCTCTGACGACCCCTCCGACGACGCGGAGTCCGAGCTTGGTTCGCTGAGTCTG | 5880 |
| Dd | 6471 | ACGGCTCTCTGACGACCCCTCCGACGACGCGGAGTCCGAGCTTGGTTCGCTGAGTCTG | 6530 |
| Qy | 5881 | TCCTCCATGCCCCCTTTAGGGGGAGCCGGGGATCCCGATCTCAGCGACGGGTCTTGG | 5940 |
| Dd | 6531 | TCCTCCATGCCCCCTTTAGGGGGAGCCGGGGATCCCGATCTCAGCGACGGGTCTTGG | 6590 |
| Qy | 5941 | TCTACCGTAAAGGAGGCTAGTGAAGAGCTGCTGCTGCTCGATGTCCTACACATG | 6000 |
| Dd | 6591 | TCTACCGTAAAGGAGGCTAGTGAAGAGCTGCTGCTGCTCGATGTCCTACACATG | 6650 |
| Qy | 6001 | ACAGGCCCTGATACGCCATGCGCTGCGGAGGAAACCAAGCTGCCCTCAATGCACTG | 6060 |
| Dd | 6651 | ACAGGCCCTGATACGCCATGCGCTGCGGAGGAAACCAAGCTGCCCTCAATGCACTG | 6710 |
| Qy | 6061 | AGCAACTCTTTGCTCCCTACCAACTTGTCTATGCTCAACATCTCGCAGCGCAAGC | 6120 |
| Dd | 6711 | AGCAACTCTTTGCTCCCTACCAACTTGTCTATGCTCAACATCTCGCAGCGCAAGC | 6770 |
| Qy | 6121 | CTCGGCGAGAGAGGTCACTTTTGACAGACTGCAAGTCTCTGACGACCACTACCGGAC | 6180 |
| Dd | 6771 | CTCGGCGAGAGAGGTCACTTTTGACAGACTGCAAGTCTCTGACGACCACTACCGGAC | 6830 |
| Qy | 6181 | GTGCTCAAGGAGATGAAGCGAGGCGTCCACAGTTAAGGCTAACTTCTATCCGTCGAG | 6240 |
| Dd | 6831 | GTGCTCAAGGAGATGAAGCGAGGCGTCCACAGTTAAGGCTAACTTCTATCCGTCGAG | 6890 |
| Qy | 6241 | GAAGCTGTAAAGTGAAGCGCCCACTTCGCGCAGATCTAAATTTGGCTATGGGCAAG | 6300 |
| Dd | 6891 | GAAGCTGTAAAGTGAAGCGCCCACTTCGCGCAGATCTAAATTTGGCTATGGGCAAG | 6950 |
| Qy | 6301 | GAGCTCGGAACTTATCCAGCAAGCGGCTTAAACCATCCGCTCCGCTGCTGGAAGGACTT | 6360 |
| Dd | 6951 | GAGCTCGGAACTTATCCAGCAAGCGGCTTAAACCATCCGCTCCGCTGCTGGAAGGACTT | 7010 |
| Qy | 6361 | CTGGAAGACACTGAGACACCAATTTGACACCACTATGCGCAAAATAAGGTTTCTGCG | 6420 |
| Dd | 7011 | CTGGAAGACACTGAGACACCAATTTGACACCACTATGCGCAAAATAAGGTTTCTGCG | 7070 |
| Qy | 6421 | GTCCAAACAGAGAGGGGGCGCAAGCGAGCTTCCTTATTCGTTATTCAGATTTTGGG | 6480 |
| Dd | 7071 | GTCCAAACAGAGAGGGGGCGCAAGCGAGCTTCCTTATTCGTTATTCAGATTTTGGG | 7130 |
| Qy | 6481 | GTTCTGTGTGCGAGAAATGCGCTTTTACGATGTGCTTCCACCCCTCCCTCAGGCGGT | 6540 |
| Dd | 7131 | GTTCTGTGTGCGAGAAATGCGCTTTTACGATGTGCTTCCACCCCTCCCTCAGGCGGT | 7190 |

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|----|------|---|------|
| Db | 242 | CGAGACTGCTAGCCGAGTAGTGTGGTTCGCAAAAGGCCTTGTGTA | 301 |
| QY | 302 | TGCTTTGCGAGTGC | 361 |
| Db | 302 | TGCTTTGCGAGTGC | 361 |
| QY | 362 | TCAAAGAAAACCA | 421 |
| Db | 362 | TCAAAGAAAACCA | 421 |
| QY | 422 | GSCCGCTTGGGTGGAGAGGCTA | 481 |
| Db | 422 | GSCCGCTTGGGTGGAGAGGCTA | 481 |
| QY | 482 | TGATCCGCGCGTGTCCGCTGT | 541 |
| Db | 482 | TGATCCGCGCGTGTCCGCTGT | 541 |
| QY | 542 | CCTGTCCCGTGCCTTGAATGA | 601 |
| Db | 542 | CCTGTCCCGTGCCTTGAATGA | 601 |
| QY | 602 | GACGGGCGTTCCTTCGCGAGCT | 661 |
| Db | 602 | GACGGGCGTTCCTTCGCGAGCT | 661 |
| QY | 662 | GCTATTGGGCGAAGTGC | 721 |
| Db | 662 | GCTATTGGGCGAAGTGC | 721 |
| QY | 722 | AGTATCCATCATGCTGATG | 781 |
| Db | 722 | AGTATCCATCATGCTGATG | 781 |
| QY | 782 | ATTTCGACCAACCAAGCGAA | 841 |
| Db | 782 | ATTTCGACCAACCAAGCGAA | 841 |
| QY | 842 | TGTCGATCAGGATGATCTG | 901 |
| Db | 842 | TGTCGATCAGGATGATCTG | 901 |
| QY | 902 | CAGGCTC | 961 |
| Db | 902 | CAGGCTC | 961 |
| QY | 962 | CTTGCCGAATCATGTTGG | 1021 |
| Db | 962 | CTTGCCGAATCATGTTGG | 1021 |
| QY | 1022 | GGGTGTGGCGGACCGCTAT | 1081 |
| Db | 1022 | GGGTGTGGCGGACCGCTAT | 1081 |
| QY | 1082 | TGGCGGCGAATGGGCTG | 1141 |
| Db | 1082 | TGGCGGCGAATGGGCTG | 1141 |
| QY | 1142 | GCGCATCGCCTTCTATCG | 1189 |
| Db | 1142 | GCGCATCGCCTTCTATCG | 1189 |
| QY | 1190 | AGACCAACACGGTTTCC | 1249 |
| Db | 1202 | AGACCAACACGGTTTCC | 1250 |
| QY | 1250 | ACGTTACTGCGCGAAGCG | 1309 |
| Db | 1251 | ACGTTACTGCGCGAAGCG | 1310 |
| QY | 1310 | CCACCATATTGCGCTCT | 1369 |

| | | | |
|----|------|---|------|
| Db | 1311 | CCACCATATGTCGCGCTTTTGGCAATGTGAGGGCCGCAAACTGGGCCCTGCTCTCTTGA | 1370 |
| QY | 1370 | CGAGCATTTCTTAGGGTCTTTCCCTCTCGCAAAAGGAATGCAAGTCTGTGTAATCTCG | 1429 |
| Db | 1371 | CGAGCATTTCTTAGGGTCTTTCCCTCTCGCAAAAGGAATGCAAGTCTGTGTAATCTCG | 1430 |
| QY | 1430 | TGAAGGAAGCTGTTCTCTGGAAGCTTTTGAAGACAAACAGTCTGTAGCGACCCCTTT | 1489 |
| Db | 1431 | TGAAGGAAGCTGTTCTCTGGAAGCTTTTGAAGACAAACAGTCTGTAGCGACCCCTTT | 1490 |
| QY | 1490 | GCAGCAGCGGAACCCCCACTCGGCACAGGTGCTCTGGGCCAAAGACGACGTGTAT | 1549 |
| Db | 1491 | GCAGCAGCGGAACCCCCACTCGGCACAGGTGCTCTGGGCCAAAGACGACGTGTAT | 1550 |
| QY | 1550 | AAGATACACCTTGCAAGGCGGCAAAACCCAGTGCACAGTTGTGAGTTGCATAGTTGTGG | 1609 |
| Db | 1551 | AAGATACACCTTGCAAGGCGGCAAAACCCAGTGCACAGTTGTGAGTTGCATAGTTGTGG | 1610 |
| QY | 1610 | AAAGAGTCAATGGCTCTCTCAAGCGTATTCAACAAGGGGCTGAAGATGCCCGAAGG | 1669 |
| Db | 1611 | AAAGAGTCAATGGCTCTCTCAAGCGTATTCAACAAGGGGCTGAAGATGCCCGAAGG | 1670 |
| QY | 1670 | TACCCCATTTATGGATCTGATCTGGGCGCTCGTGCAATGCTTTACATGTTTGTAGT | 1729 |
| Db | 1671 | TACCCCATTTATGGATCTGATCTGGGCGCTCGTGCAATGCTTTACATGTTTGTAGT | 1730 |
| QY | 1730 | CGAGGTTAAAAAAGCTGTAGGCCCGCCGAAACCAACGGGACGTGGTTTCTTTGAAAAAC | 1789 |
| Db | 1731 | CGAGGTTAAAAAAGCTGTAGGCCCGCCGAAACCAACGGGACGTGGTTTCTTTGAAAAAC | 1790 |
| QY | 1790 | ACGATATACCATG----- | 1803 |
| Db | 1791 | ACGATATACCATGACCGGAGATGGACATCGTGGGAGCGGGTTTTCTGTAGGTC | 1850 |
| QY | 1804 | ----- | 1803 |
| Db | 1851 | TGATACTCTTGACCTTGCTGACCGACATTAAGGTGTTCTCGCTAGGCTCATATGGTGT | 1910 |
| QY | 1804 | ----- | 1803 |
| Db | 1911 | TACAATATTTATCACAGGGCCGAGGCACATTGCAAGTGTGGATCCCCCCTCAACG | 1970 |
| QY | 1804 | ----- | 1803 |
| Db | 1971 | TTCCGGGGGCGCGATGCGGTCACTCTCTCACGTGCGGATCCACCCAGAGCTAATCT | 2030 |
| QY | 1804 | ----- | 1803 |
| Db | 2031 | TTACCATCACCAAAATCTTGCTCGCCATACTCGTCCACTCATGTTGCTCCAGGCTGTA | 2090 |
| QY | 1804 | ----- | 1803 |
| Db | 2091 | TAACCAAGTCCGTACTTGTCGGCGCACACGGGCTCATTCGTGCATGTCATGCTGTGC | 2150 |
| QY | 1804 | ----- | 1803 |
| Db | 2151 | GGAAGTTGCTGGGGTTCATTATGTCCAAATGGCTCTCATGAAGTTGGCCGCACTGACAG | 2210 |
| QY | 1804 | ----- | 1803 |
| Db | 2211 | GTAGTACGTTTATGACCATCTCACCCACTCGGGAATGGGCCCAACGGGCTTACAG | 2270 |
| QY | 1804 | ----- | 1803 |
| Db | 2271 | ACCTTGGGTGGAGTTGACCGGTGCTTCTCTGATATGAGACCAAGGTTATCACT | 2330 |
| QY | 1804 | ----- | 1803 |
| Db | 2331 | GGGGGCGACACCGCGGTGTGGGACATCATCTTGGGCTGCCCGTCTCCGCCCGCA | 2390 |
| QY | 1804 | ----- | 1803 |
| Db | 2391 | GGGGGAGGAGATACATCTGGGACCGGCAGACAGCTTTGAAGGCGAGGGTGGGACTCC | 2450 |

| | | | | | | | |
|----|------|--|------|----|------|---|------|
| QY | 1804 | --GCGCCTATTACGGCCTACTCCACACAGCGGCGCCTACTTGGCTGCATCATCACTA | 1861 | QY | 2882 | AGGGGGGAGGAGCACTCTATTTCTGCCATTCACAGAAATGTGATGAGCTCGCGCGA | 2941 |
| Db | 2451 | TCGCGCCTATTACGGCCTACTCCACACAGCGGCGCCTACTTGGCTGCATCATCACTA | 2510 | Db | 3531 | AGGGGGGAGGAGCACTCTATTTCTGCCATTCACAGAAATGTGATGAGCTCGCGCGA | 3590 |
| QY | 1862 | GCTCACAGCGCGGACAGAAACAGGTCCAGGGGAGGTCCAAAGTGGTCTCCACCGCAA | 1921 | QY | 2942 | AGCTGTCCGGCTTCGGACTCAATGCTGTAGCATATATACCGGGCCTTGATGTATCGTCA | 3001 |
| Db | 2511 | GCTCACAGCGCGGACAGAAACAGGTCCAGGGGAGGTCCAAAGTGGTCTCCACCGCAA | 2570 | Db | 3591 | AGCTGTCCGGCTTCGGACTCAATGCTGTAGCATATATACCGGGCCTTGATGTATCGTCA | 3650 |
| QY | 1922 | CACAAATCTTTCCTGGCGACCTCGGTCAATGGCGGTGTGTGGACTGTCTATCATGTGGCG | 1981 | QY | 3002 | TACCAACTAGCGGAGAGCTATTGTGTAGCAACGAGCCTCTAATGACGGGCTTTTACCG | 3061 |
| Db | 2571 | CACAAATCTTTCCTGGCGACCTCGGTCAATGGCGGTGTGTGGACTGTCTATCATGTGGCG | 2630 | Db | 3651 | TACCAACTAGCGGAGAGCTATTGTGTAGCAACGAGCCTCTAATGACGGGCTTTTACCG | 3710 |
| QY | 1982 | GCTCAAGACCTTTCGCGCCCAAGAGGCCAATCACCAATGTACCAATGTGGAC | 2041 | QY | 3062 | GGCATTTCCACTCAGTGATCGATGCAATACATGTGTACCCAGACAGTGCATTCAGCC | 3121 |
| Db | 2631 | GCTCAAGACCTTTCGCGCCCAAGAGGCCAATCACCAATGTACCAATGTGGAC | 2690 | Db | 3711 | GGCATTTCCACTCAGTGATCGATGCAATACATGTGTACCCAGACAGTGCATTCAGCC | 3770 |
| QY | 2042 | AGGACCTCGTTCGGCTCGGCAAGCGCCCGCGGGCGGTTCCTTGACACCATGCACCTGGC | 2101 | QY | 3122 | TGGAACCGGACCTTCACTTGGAGACGACCGTGCACAAAGACGGGTGTACGCTCGC | 3181 |
| Db | 2691 | AGGACCTCGTTCGGCTCGGCAAGCGCCCGCGGGCGGTTCCTTGACACCATGCACCTGGC | 2750 | Db | 3771 | TGGAACCGGACCTTCACTTGGAGACGACCGTGCACAAAGACGGGTGTACGCTCGC | 3830 |
| QY | 2102 | GGAGCTCGACCTTTTCTTGGTCAAGAGCATGCCGATGTCAATCCGGTTCGCGCGCGGG | 2161 | QY | 3182 | AGCGGCGAGGAGGACTGGTAGGGCAGGATGGGCAATTTACAGGTTTGTGACTCCAGGAG | 3241 |
| Db | 2751 | GGAGCTCGACCTTTTCTTGGTCAAGAGCATGCCGATGTCAATCCGGTTCGCGCGCGGG | 2810 | Db | 3831 | AGCGGCGAGGAGGACTGGTAGGGCAGGATGGGCAATTTACAGGTTTGTGACTCCAGGAG | 3890 |
| QY | 2162 | GGACAGGAGGGGAGGACTCTCCCGCAGGCGCGTCTCTACTTTGAAGGGCTCTTCGG | 2221 | QY | 3242 | AACGGCCCTCGGCGATTTCTCGTTCGTGTGAGTGTCTATGACGCGGGCTGTG | 3301 |
| Db | 2811 | GGACAGGAGGGGAGGACTCTCTCCCGCAGGCGCGTCTCTACTTTGAAGGGCTCTTCGG | 2870 | Db | 3891 | AACGGCCCTCGGCGATTTCTCGTTCGTGTGAGTGTCTATGACGCGGGCTGTG | 3950 |
| QY | 2222 | GCGGTCCACTGCTCTGCGGCGGCGACGCTGTGGGCACTTTTCGGGCTGCGGTGTGCA | 2281 | QY | 3302 | CTTGGTACGAGCTCAGCGCGGAGACCTCAGTTAGTTGGGGCTTACTTAAACACAC | 3361 |
| Db | 2871 | GCGGTCCACTGCTCTGCGGCGGCGACGCTGTGGGCACTTTTCGGGCTGCGGTGTGCA | 2930 | Db | 3951 | CTTGGTACGAGCTCAGCGCGGAGACCTCAGTTAGTTGGGGCTTACTTAAACACAC | 4010 |
| QY | 2282 | CCGAGGGGTTCGAAAGCGGTGGACTTTGTACCCGTGAGTCTATGGAAACCACTATGC | 2341 | QY | 3362 | CAGGGTTCCCGCTCTCCAGGACCATCTGGAGTTCTGGGAGAGCGTCTTTTACAGGCTCA | 3421 |
| Db | 2931 | CCGAGGGGTTCGAAAGCGGTGGACTTTGTACCCGTGAGTCTATGGAAACCACTATGC | 2990 | Db | 4011 | CAGGGTTCCCGCTCTCCAGGACCATCTGGAGTTCTGGGAGAGCGTCTTTTACAGGCTCA | 4070 |
| QY | 2342 | GGTCCCGGCTTCAGGACCACTCCGTCCTCGGCGGTACCGGACATTTCCAGGTGG | 2401 | QY | 3422 | CCACATAGACGCCCATTTCTTCCAGACTAAGCAGGAGGAGAGCACTTCCCTTACC | 3481 |
| Db | 2991 | GGTCCCGGCTTCAGGACCACTCCGTCCTCGGCGGTACCGGACATTTCCAGGTGG | 3050 | Db | 4071 | CCACATAGACGCCCATTTCTTCCAGACTAAGCAGGAGGAGAGCACTTCCCTTACC | 4130 |
| QY | 2402 | CCCATCTACAGCGCCCTACTGTAGCGGCAAGAGCACTAAGGTGCCGGCTGCGTATGCG | 2461 | QY | 3482 | TGCTAGCATACAGGCTACGGTGTGCGCCAGGCTCAGGCTCCACCTCCATCGTGGAGC | 3541 |
| Db | 3051 | CCCATCTACAGCGCCCTACTGTAGCGGCAAGAGCACTAAGGTGCCGGCTGCGTATGCG | 3110 | Db | 4131 | TGCTAGCATACAGGCTACGGTGTGCGCCAGGCTCAGGCTCCACCTCCATCGTGGAGC | 4190 |
| QY | 2462 | CCCAAGGGTATAAGGTGCTTGTCTGAAACCGTCCGTCGCGCACCCCTAGGTTTCGGG | 2521 | QY | 3542 | AAATGTGGAAGTGTCTCATACGGCTAAAGCCTACGCTGCAACGGGCCCAACCCCTCTGT | 3601 |
| Db | 3111 | CCCAAGGGTATAAGGTGCTTGTCTGAAACCGTCCGTCGCGCACCCCTAGGTTTCGGG | 3170 | Db | 4191 | AAATGTGGAAGTGTCTCATACGGCTAAAGCCTACGCTGCAACGGGCCCAACCCCTCTGT | 4250 |
| QY | 2522 | CGTATATGCTAAGGCACATGGTATCGACCTTAACATCAGAACCGGGTAAAGACCATCA | 2581 | QY | 3602 | ATAGGCTGGGAGCGGCTTCAAAACGAGGTTACTACCAACAGGGAATGAGCTCGCGG | 3661 |
| Db | 3171 | CGTATATGCTAAGGCACATGGTATCGACCTTAACATCAGAACCGGGTAAAGACCATCA | 3230 | Db | 4251 | ATAGGCTGGGAGCGGCTTCAAAACGAGGTTACTACCAACAGGGAATGAGCTCGCGG | 4310 |
| QY | 2582 | CCACGGGTGCCCATCAGCTACTCCACCTATGSCAAAGTTCTTTCGCGAGCGGTGGTGTCT | 2641 | QY | 3662 | TGCGATGCTAGTCCGGCTGACCTGAGGTCTGACGAGCCTGGGTCTGTTAGGCGGAG | 3721 |
| Db | 3231 | CCACGGGTGCCCATCAGCTACTCCACCTATGSCAAAGTTCTTTCGCGAGCGGTGGTGTCT | 3290 | Db | 4311 | TGCGATGCTAGTCCGGCTGACCTGAGGTCTGACGAGCCTGGGTCTGTTAGGCGGAG | 4370 |
| QY | 2642 | CTGGGGCGGCTATGACATCATATATGTGATGAGTCCCACTCAACTGACTCGACCATTA | 2701 | QY | 3722 | TCCTAGCAGCTCTGGCGCGCTATTGCTGACAAAGGAGGAGGCTGCTTGTGGGAGGA | 3781 |
| Db | 3291 | CTGGGGCGGCTATGACATCATATATGTGATGAGTCCCACTCAACTGACTCGACCATTA | 3350 | Db | 4371 | TCCTAGCAGCTCTGGCGCGCTATTGCTGACAAAGGAGGAGGCTGCTTGTGGGAGGA | 4430 |
| QY | 2702 | TCCTGGGCATCGGCACAGTCTTGACCAAGCGGAGCGGTGGAGCGGACTCGTCTGTC | 2761 | QY | 3782 | TCATCTTGTTCGGAAGCGCGCATCTCCCGACAGGGAATGAGCTCGCGG | 3841 |
| Db | 3351 | TCCTGGGCATCGGCACAGTCTTGACCAAGCGGAGCGGTGGAGCGGACTCGTCTGTC | 3410 | Db | 4431 | TCATCTTGTTCGGAAGCGCGCATCTCTCCGACAGGGAATGAGCTCGCGG | 4490 |
| QY | 2762 | TCGCCACCGTACGCTTCGGGATCGGTTCACCGTCCCAATCCAAACATCGAGAGGTGG | 2821 | QY | 3842 | ATGAGTGGAGAGTGGCGCTCACACCTCTCTTACATCGAACAGGGAATGAGCTCGCGG | 3901 |
| Db | 3411 | TCGCCACCGTACGCTTCGGGATCGGTTCACCGTCCCAATCCAAACATCGAGAGGTGG | 3470 | Db | 4491 | ATGAGTGGAGAGTGGCGCTCACACCTCTCTTACATCGAACAGGGAATGAGCTCGCGG | 4550 |
| QY | 2822 | CTCTGTCCAGCACTGGAGAAATCCCTTTTATGCAAGGACCATCCCATCGAGACCATCA | 2881 | QY | 3902 | AACAATTTCAAACAGAGGCAATCGGTTGCTTGAACAGCCACCAAGCAGCGAGGCTG | 3961 |
| Db | 3471 | CTCTGTCCAGCACTGGAGAAATCCCTTTTATGCAAGGACCATCCCATCGAGACCATCA | 3530 | Db | 4551 | AACAATTTCAAACAGAGGCAATCGGTTGCTTGAACAGCCACCAAGCAGCGAGGCTG | 4610 |
| | | | | QY | 3962 | CTGCTCCGCTGGTGAATCCAGTGGCGGACCTCTCGAAGCCTTCTGGGCGAAGCATATGT | 4021 |

| | | | | | | | |
|----|------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|------|
| Qy | 7262 | CTCATTTCTTCTCCATCTTCTAGCTCAGAA | CAA | CTTGA | AAAAAGCCCTAGATTGT | CAGA | 7322 |
| Db | 7911 | CTCATTTCTTCTCCATCTTCTAGCTCAGAA | CAACT | TGAAAA | AGCCCTAGATTGT | CAGA | 7970 |
| Qy | 7322 | TCTACGGGGCTGT | TACTCC | ATTGAG | CCACTTGC | ACTTACCTCAGATCATTTCAACGACTCC | 7381 |
| Db | 7971 | TCTACGGGGCTGT | TACTCC | ATTGAG | CCACTTGC | ACTTACCTCAGATCATTTCAACGACTCC | 8030 |
| Qy | 7382 | ATGGCCTTAGCGCATTTTCACTCCATAGT | PACTCT | CCAGT | GAGATCAAT | PAGGGTGGCTT | 7441 |
| Db | 8031 | ACGGCCTTAGCGCATTTTCACTCCATAGT | TACTCT | CCAGT | GAGATCAAT | PAGGGTGGCTT | 8090 |
| Qy | 7442 | CATGCTCAGGAAACTTTGGGGTAC | CGCCCT | TTCG | AGTCTGG | AGACATCGGGCCAGAGTG | 7501 |
| Db | 8091 | CATGCTCAGGAAACTTTGGGGTAC | CGCCCT | TTCG | AGTCTGG | AGACATCGGGCCAGAGTG | 8150 |
| Qy | 7502 | TCCGCGCTAGGCTACTGTCTCCACGGGGG | AGGGCT | GC | CACTTCTGG | CAAGTACTCTTCA | 7561 |
| Db | 8151 | TCCGCGCTAGGCTACTGTCTCCACGGGGG | AGGGCT | GCC | ACTTCTGG | CAAGTACTCTTCA | 8210 |
| Qy | 7562 | ACTGGGAGTAAGGACCAAGCTCAAA | CTACT | CCAAT | CCCGGT | TGGGTCCAGTTGGATT | 7621 |
| Db | 8211 | ACTGGGAGTAAGGACCAAGCTCAAA | CTACT | CCAAT | CCCGGT | TGGGTCCAGTTGGATT | 8270 |
| Qy | 7622 | TATCCAGCTGGTGTCTGTCTACAGCGGG | GAGACATATAT | CACAG | CTGTCTCGT | CGT | 7681 |
| Db | 8271 | TATCCAGCTGGTGTCTGTCTACAGCGGG | GAGACATATAT | CACAG | CTGTCTCGT | CGT | 8330 |
| Qy | 7682 | CCGACCCCGCTGGTTCATGTGTGCTACT | CTCTACT | TCTCTG | TAGGGGTAGG | CATCTATC | 7741 |
| Db | 8331 | CCGACCCCGCTGGTTCATGTGTGCTACT | CTCTA | CTTCTG | TAGGGGTAGG | CATCTATC | 8390 |
| Qy | 7742 | TACTTCCCAACCGATGAACGGGAGCT | TAAAC | ACTTCC | AGGCCAAT | PAGGCCATCTCTTTTT | 7801 |
| Db | 8391 | TACTTCCCAACCGATGAACGGGAGCT | TAAAC | ACTTCC | AGGCCAAT | PAGGCCATCTCTTTTT | 8450 |
| Qy | 7802 | TTCCCTTTTCTTTTCTTTTCTTTTCTTTT | TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | 7861 |
| Db | 8451 | TTCCCTTTTCTTTTCTTTTCTTTTCTTTT | TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | 8510 |
| Qy | 7862 | TTTTCCTTTTCTTTTCTTTTCTTTTCTTTT | TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | 7921 |
| Db | 8511 | TTTTCCTTTTCTTTTCTTTTCTTTTCTTTT | TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | 8570 |
| Qy | 7922 | AGCTGTGAAAGGTCCGTGAGCCGTTT | GACTTGC | AGAGAGT | GCTGAT | ACTGGCCCTCTCTGCA | 7981 |
| Db | 8571 | AGCTGTGAAAGGTCCGTGAGCCGTTT | GACTTGC | AGAGAGT | GCTGAT | ACTGGCCCTCTCTGCA | 8630 |
| Qy | 7982 | GATCAAGT | 7989 | | | | |
| Db | 8631 | GATCAAGT | 8638 | | | | |

RESULT 10

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US/10-029-907-7
/ Sequence 7, Application US/10029907
/ Patent No. 6706874
/ GENERAL INFORMATION:
/ APPLICANT: BOEHRINGER INGELHEIM (CANADA)
/ TITLE OF INVENTION: SELF REPLICATING RNA
/ TITLE OF INVENTION: HEPATITIS C VIRUS
/ FILE REFERENCE: 13/083
/ CURRENT APPLICATION NUMBER: US/10/029,907
/ CURRENT FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 60/257,857
/ PRIOR FILING DATE: 2000-12-22
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7
/ LENGTH: 8638
/ TYPE: DNA
/ ORGANISM: HCV
/ FEATURE:

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| | | | | | |
|-----------------|------|---|------|---|--|
| | | NAME/KEY: CDS | | 90.7%; Score 7249.8; DB 4; Length 8638; | |
| | | LOCATION: (1802) ... (8407) | | Best Local Similarity 92.0%; Pred. No. 0; | |
| US-10-029-907-7 | | Matches 7961; Conservative 0; Mismatches 17; Indels 671; Gaps 3; | | | |
| Qy | 1 | GCCAGCCCCGATTTGGGGGCGACACTCCACCATAGATCACTCCCTCGTGGAGAACTACTG | 60 | | |
| | 1 | GCCAGCCCCGATTTGGGGGCGACACTCCACCATAGATCACTCCCTCGTGGAGAACTACTG | 60 | | |
| Qy | 61 | TCCTTCAGCGAAGACGCTTAGCCGATGCTAGAGTGTAGTATGAGTGTCTGAGCTCCAGGAC | 120 | | |
| | 61 | TCCTTCAGCGAAGACGCTTAGCCGATGCTAGAGTGTAGTATGAGTGTCTGAGCTCCAGGAC | 120 | | |
| Qy | 121 | CCCCCTCCCGGAGAGCCATAGTGTCTGCGAACCGGTGAGTACACCGAAATGGCAG | 180 | | |
| | 121 | CCCCCTCCCGGAGAGCCATAGTGTCTGCGAACCGGTGAGTACACCGAAATGGCAG | 180 | | |
| Qy | 181 | GACGACCGGCTCTTCTTGATCAACCCGCTCAATGCTCGAGATTGGGCGTGCCTCC | 240 | | |
| | 181 | GACGACCGGCTCTTCTTGATCAACCCGCTCAATGCTCGAGATTGGGCGTGCCTCC | 240 | | |
| Qy | 241 | GCGAGACTGTAGCCGAGTAGTGTGGTCCGAAAGCCCTTGTGTACTGCTGATAGG | 300 | | |
| | 241 | GCGAGACTGTAGCCGAGTAGTGTGGTCCGAAAGCCCTTGTGTACTGCTGATAGG | 300 | | |
| Qy | 301 | GTGCTTCGAGTGCCTCCGGAGGCTCTGTAGACCGTGCACCATGAGCACGAACTCTAAAC | 360 | | |
| | 301 | GTGCTTCGAGTGCCTCCGGAGGCTCTGTAGACCGTGCACCATGAGCACGAACTCTAAAC | 360 | | |
| Qy | 361 | CTCAAGAAACCAAAAGGGCGCCCATGATTGAACAAAGATGGATTGCAGCAGGCTCTC | 420 | | |
| | 361 | CTCAAGAAACCAAAAGGGCGCCCATGATTGAACAAAGATGGATTGCAGCAGGCTCTC | 420 | | |
| Qy | 421 | CGGCGCTGTGGGTGAGAGGCTATTCCGCTATGACTGGGCAACACAGCAATCGGCTGCT | 480 | | |
| | 421 | CGGCGCTGTGGGTGAGAGGCTATTCCGCTATGACTGGGCAACACAGCAATCGGCTGCT | 480 | | |
| Qy | 481 | CTGATCCGCGCTGCTCCGGCTGTGAGGAGGCTGTCAGGAGGCGCGCGCTTCTTTTGTCAAGACCG | 540 | | |
| | 481 | CTGATCCGCGCTGCTCCGGCTGTGAGGAGGCTGTCAGGAGGCGCGCGCTTCTTTTGTCAAGACCG | 540 | | |
| Qy | 541 | ACCTGTCCGCTGCTCCGCTGAATGAATCTGAGGAGGCGCGCGCTATCGTGGCTGCGCA | 600 | | |
| | 541 | ACCTGTCCGCTGCTCCGCTGAATGAATCTGAGGAGGCGCGCGCTATCGTGGCTGCGCA | 600 | | |
| Qy | 601 | CGAGCGGCTTCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGACTGGC | 660 | | |
| | 601 | CGAGCGGCTTCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGACTGGC | 660 | | |
| Qy | 661 | TGCTATTGGGCGAAGTCCCGGGCAGGATCTCCTGTCTATCTCACTTGTCTCTCCGCGAGA | 720 | | |
| | 661 | TGCTATTGGGCGAAGTCCCGGGCAGGATCTCCTGTCTATCTCACTTGTCTCTCCGCGAGA | 720 | | |
| Qy | 721 | AAGTATCCATATGCTGATGCAATCGGCGGCTGCACTAGCTTGTATCCGCTACCTGCTC | 780 | | |
| | 721 | AAGTATCCATATGCTGATGCAATCGGCGGCTGCACTAGCTTGTATCCGCTACCTGCTC | 780 | | |
| Qy | 781 | CATTTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCACTGCTGATGGAAGCGGTC | 840 | | |
| | 781 | CATTTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCACTGCTGATGGAAGCGGTC | 840 | | |
| Qy | 841 | TTGTTCGATCAGGATGATCTGACGAAAGCATGAGGGGCTCGGCGACCGCACTGTTCG | 900 | | |
| | 841 | TTGTTCGATCAGGATGATCTGACGAAAGCATGAGGGGCTCGGCGACCGCACTGTTCG | 900 | | |
| Qy | 901 | CCAGGCTCAAGGCGCGCATCCGAGCGGAGGATCTCTGCTGACCCATGGCGATGCTCCT | 960 | | |
| | 901 | CCAGGCTCAAGGCGCGCATCCGAGCGGAGGATCTCTGCTGACCCATGGCGATGCTCCT | 960 | | |
| Qy | 961 | GCTTGGCGAATATATGTTGGGAAATGGCGGCTTTTCTGGATTATCGACTGTGGCGGC | 1020 | | |
| | 961 | GCTTGGCGAATATATGTTGGGAAATGGCGGCTTTTCTGGATTATCGACTGTGGCGGC | 1020 | | |
| Qy | 1021 | TGGGTGGCGGACCGCTATCAGACATAGGCTTGGCTACCCGTGATATGCTGAAGAGC | 1080 | | |
| | 1021 | TGGGTGGCGGACCGCTATCAGACATAGGCTTGGCTACCCGTGATATGCTGAAGAGC | 1080 | | |
| Qy | 1081 | TTGGCGGCAATGGCTGACCGCTTCTCGTTCCTTACGTTACGGTATCGCGCTCCGATTCGC | 1140 | | |
| | 1081 | TTGGCGGCAATGGCTGACCGCTTCTCGTTCCTTACGTTACGGTATCGCGCTCCGATTCGC | 1140 | | |
| Qy | 1141 | AGCGATCGCCTTCTATCGCCTTCTTGACGAGTTCCTTCTGAGTT-----TAAA | 1188 | | |
| | 1141 | AGCGATCGCCTTCTATCGCCTTCTTGACGAGTTCCTTCTGAGTTGCGGCCAGATGTAA | 1200 | | |
| Qy | 1189 | CAGACCAACAGGTTTCCCTCTAGCGGATCAATTCGCCCTCTCCCTCCGCCCCCT | 1248 | | |
| | 1201 | CAGACCAACAGGTTTCCCTCTAGCGGATCAATTCGC-----CCCCCCCCCT | 1249 | | |
| Qy | 1249 | AACGTTACTGGCGGACCGCTTGGATTAAGGCGGCTGCGTTGTCTATATGTTATTT | 1308 | | |
| | 1250 | AACGTTACTGGCGGACCGCTTGGATTAAGGCGGCTGCGTTGTCTATATGTTATTT | 1309 | | |
| Qy | 1309 | TCCACCATATTGCGCTCTTTTGGCAATGTGAGGCGCGGAAACCTGCGCTCTCTCTTG | 1368 | | |
| | 1310 | TCCACCATATTGCGCTCTTTTGGCAATGTGAGGCGCGGAAACCTGCGCTCTCTCTTG | 1369 | | |
| Qy | 1369 | ACGAGCATCTTAGGGGTCTTTCCCTCTCGCMAAGGAATGCAAGTCTGTTGAATGTC | 1428 | | |
| | 1370 | ACGAGCATCTTAGGGGTCTTTCCCTCTCGCMAAGGAATGCAAGTCTGTTGAATGTC | 1429 | | |
| Qy | 1429 | GTGAAGAACAGCTTCTCTGAGAGCTTCTTGAGACAAACAGCTCTGAGCACCTTT | 1488 | | |
| | 1430 | GTGAAGAACAGCTTCTCTGAGAGCTTCTTGAGACAAACAGCTCTGAGCACCTTT | 1489 | | |
| Qy | 1489 | TGCGGAGCGGAAACCCCTGCGACAGGCTCTGCGGCCCAAAAGCCACAGTGA | 1548 | | |
| | 1490 | TGCGGAGCGGAAACCCCTGCGACAGGCTCTGCGGCCCAAAAGCCACAGTGA | 1549 | | |
| Qy | 1549 | TAGATACACTGCAAGGCGGCAACCCAGTGCACCGTGTGAGTGGATAGTTGTG | 1608 | | |
| | 1550 | TAGATACACTGCAAGGCGGCAACCCAGTGCACCGTGTGAGTGGATAGTTGTG | 1609 | | |
| Qy | 1609 | GAAAGCTCAATGGCTCTCTCAAGCTATTCAACAGGGGCTGAGGATGCCAGAAG | 1668 | | |
| | 1610 | GAAAGCTCAATGGCTCTCTCAAGCTATTCAACAGGGGCTGAGGATGCCAGAAG | 1669 | | |
| Qy | 1669 | GTACCCCATTTGATGGGATCTGATCTGGGCTCTCGGTGCAATGCTTATGTTTGTAG | 1728 | | |
| | 1670 | GTACCCCATTTGATGGGATCTGATCTGGGCTCTCGGTGCAATGCTTATGTTTGTAG | 1729 | | |
| Qy | 1729 | TGAGGTTAAAAAGCTTAGGCCCCCGAAACACAGGGGAGCTGTTTCTTTGAAAAA | 1788 | | |
| | 1730 | TGAGGTTAAAAAGCTTAGGCCCCCGAAACACAGGGGAGCTGTTTCTTTGAAAAA | 1789 | | |
| Qy | 1789 | CAGATAATAACATG----- | 1803 | | |
| | 1790 | CAGATAATAACATGACCGGAGATGGCAGCATCGTGGGAGCGGCTTTTCGTAGGT | 1849 | | |
| Qy | 1804 | ----- | 1803 | | |
| | 1850 | CTGATACTCTTGACCTTGTACCGCATATAAGCTGTTCTCTCGTAGGCTCATATGTTGG | 1909 | | |
| Qy | 1804 | ----- | 1803 | | |
| | 1910 | TTACAATATTTTATCACCAGGCGGAGGACACTTGCAGTGTGGATCCCCCCCCCTCAAC | 1969 | | |
| Qy | 1804 | ----- | 1803 | | |
| | 1970 | GTTTCGGGGGGCGCGATGCGCTCATCTCTCACTGCGCGATCCACCGAGAGTAATC | 2029 | | |
| Qy | 1804 | ----- | 1803 | | |

QY 3601 TATAGGCTGGAGCCGTTCAAAACAGGTTACTACACACACCCATAACCAAATACATC 3660
Db 4250 TATAGGCTGGAGCCGTTCAAAACAGGTTACTACACACACCCATAACCAAATACATC 4309
QY 3661 ATGGCATGATGTCGCTGACCTGGAGTCGTCACAGACACCTGGGTGCTGTAGCGGA 3720
Db 4310 ATGGCATGATGTCGCTGACCTGGAGTCGTCACAGACACCTGGGTGCTGTAGCGGA 4369
QY 3721 GTCTTAGAGCTCTGSCCGCGTATTGCTGACAAACAGGAGCGTGTGCTATTGTGGCAGG 3780
Db 4370 GTCTTAGAGCTCTGSCCGCGTATTGCTGACAAACAGGAGCGTGTGCTATTGTGGCAGG 4429
QY 3781 ATCATCTTCTCGGAAAGCGCGCATCATTCGCGACAGGAAAGTCCTTTACCGGAGTTC 3840
Db 4430 ATCATCTTCTCGGAAAGCGCGCATCATTCGCGACAGGAAAGTCCTTTACCGGAGTTC 4489
QY 3841 GATGAGTGAAGAGTGCCTCTACACCTCCCTTACATCGACAGGAGTGCAGCTCGCC 3900
Db 4490 GATGAGTGAAGAGTGCCTCTACACCTCCCTTACATCGACAGGAGTGCAGCTCGCC 4549
QY 3901 GAACAATTCAACAGAGGCAATCGGGTTGCTGCAAAACAGCCACCAAGCAAGCGAGGCT 3960
Db 4550 GAACAATTCAACAGAGGCAATCGGGTTGCTGCAAAACAGCCACCAAGCAAGCGAGGCT 4609
QY 3961 GCTGCTCCGCTGGTGAATCGAAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG 4020
Db 4610 GCTGCTCCGCTGGTGAATCGAAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG 4669
QY 4021 TGGAAATTCATCAGCGGGATACAATATTAGCAGGCTGTCCACCTCGCTGGCAACCCC 4080
Db 4670 TGGAAATTCATCAGCGGGATACAATATTAGCAGGCTGTCCACCTCGCTGGCAACCCC 4729
QY 4081 GCGATAGCATCATGATGGCAATCAGCCTCTATCACCAGCCGCTCACCACCCAAACAT 4140
Db 4730 GCGATAGCATCATGATGGCAATCAGCCTCTATCACCAGCCGCTCACCACCCAAACAT 4789
QY 4141 ACCCTCCTGTTTAAATCCTGGGGGATGGGTGGCGGCCCAACTTGCTCTCCAGCGCT 4200
Db 4790 ACCCTCCTGTTTAAATCCTGGGGGATGGGTGGCGGCCCAACTTGCTCTCCAGCGCT 4849
QY 4201 GCTTCGTCTTCTGATAGCGCGGATCGCTGAGCGGCTGTGGCAGTATAGGCTTTGGG 4260
Db 4850 GCTTCGTCTTCTGATAGCGCGGATCGCTGAGCGGCTGTGGCAGTATAGGCTTTGGG 4909
QY 4261 AAGGTGCTTGTGGATATTTGGCAGGTTATGAGCAGGGGTGGCAGCGCGCTGCTGGCC 4320
Db 4910 AAGGTGCTTGTGGATATTTGGCAGGTTATGAGCAGGGGTGGCAGCGCGCTGCTGGCC 4969
QY 4321 TTTAAGTTCATGAGCGCGAGATGCCCTCCACCGAGGACCTGGTTAACCTTACCTGCT 4380
Db 4970 TTTAAGTTCATGAGCGCGAGATGCCCTCCACCGAGGACCTGGTTAACCTTACCTGCT 5029
QY 4381 ATCTCTCTCCCTGGCGCCCTAGTCTGCGGGTCTGTGCGCAGCGATATCGCTGGCAC 4440
Db 5030 ATCTCTCTCCCTGGCGCCCTAGTCTGCGGGTCTGTGCGCAGCGATATCGCTGGCAC 5089
QY 4441 GTGGGCCAGGGAGGGGCTGTGCAGTGAATGAACCGGCTGTAGCGTTGCTTCCGG 4500
Db 5090 GTGGGCCAGGGAGGGGCTGTGCAGTGAATGAACCGGCTGTAGCGTTGCTTCCGG 5149
QY 4501 GGTAAACACGCTCTCCCGACGACATGTGCTGAGAGCGACGCTGAGCAGCTGTCACT 4560
Db 5150 GGTAAACACGCTCTCCCGACGACATGTGCTGAGAGCGACGCTGAGCAGCTGTCACT 5209
QY 4561 CAGATCTCTCTAGTCTTACCATCAGCTGCTGAGAGGCTTACCCAGTGAATCAAC 4620
Db 5210 CAGATCTCTCTAGTCTTACCATCAGCTGCTGAGAGGCTTACCCAGTGAATCAAC 5269
QY 4621 GAGGACTGCTCCAGCCATGCTCCGGCTGCTGGCTAAGAGATGTTTGGGATTTGATATGC 4680
Db 5270 GAGGACTGCTCCAGCCATGCTCCGGCTGCTGGCTAAGAGATGTTTGGGATTTGATATGC 5329
QY 4681 ACGGTGTTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCTCTGCGCGGATGCGGGA 4740

Db 5330 ACGGTGTTGACTGATTTCAAGGCTTGGCTCCAGTCCAGCTCTGCGCGATTTGCCGGA 5389
QY 4741 GTCCCTTCTTCTCATGTCAACGTGGGTACAAGGAGTCTGGCGGGCGACGCGCATCATG 4800
Db 5390 GTCCCTTCTTCTCATGTCAACGTGGGTACAAGGAGTCTGGCGGGCGACGCGCATCATG 5449
QY 4801 CAAAACACCTGCGCATGTGGAGCAGATCAACGTGGCATGGAACATTTCCCATTAACCGGTAC 4860
Db 5450 CAAAACACCTGCGCATGTGGAGCAGATCAACGTGGCATGGAACATTTCCCATTAACCGGTAC 5509
QY 4861 ATCTGTTGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTTCCCATTAACCGGTAC 4920
Db 5510 ATCTGTTGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTTCCCATTAACCGGTAC 5569
QY 4921 ACCAGGGGCTTGCACGCGCTTCCCGGCGCAAAATTTATTTAGGCGCTGTGGCGGGTG 4980
Db 5570 ACCAGGGGCTTGCACGCGCTTCCCGGCGCAAAATTTATTTAGGCGCTGTGGCGGGTG 5629
QY 4981 GCTGCTGAGGAGTACGTGGAGTTACGGGGTGGGGGATTTCCACTAGTGAAGGCGCATG 5040
Db 5630 GCTGCTGAGGAGTACGTGGAGTTACGGGGTGGGGGATTTCCACTAGTGAAGGCGCATG 5689
QY 5041 ACCACTGACAAAGTAAAGTGGCGCTGTAGGTTCCGGGCGCCCAATTTCTTACAGAAAGTG 5100
Db 5690 ACCACTGACAAAGTAAAGTGGCGCTGTAGGTTCCGGGCGCCCAATTTCTTACAGAAAGTG 5749
QY 5101 GATGGGGTGGGTTGCCACAGGTACGCTCAGGTCGAAACCCCTCCTACGGGAGGAGTTC 5160
Db 5750 GATGGGGTGGGTTGCCACAGGTACGCTCAGGTCGAAACCCCTCCTACGGGAGGAGTTC 5809
QY 5161 ACATTCCTGCTGGGCTCAATCAATACCTGTTGGTTCACAGTCCCATGCGAGCCGGA 5220
Db 5810 ACATTCCTGCTGGGCTCAATCAATACCTGTTGGTTCACAGTCCCATGCGAGCCGGA 5869
QY 5221 CCGGAGTGAAGTGTCTCACTTCCATGCTCACCAGCCCTCCCACTTACCGCGGAGACG 5280
Db 5870 CTGGAGGTAGCAGTGTCTCACTTCCATGCTCACCAGCCCTCCCACTTACCGCGGAGACG 5929
QY 5281 GCTAAGCGTGAAGTGTGGCGAGGATCTCCCGCTTCTTGGCCAGCTCATAGTACCGAG 5340
Db 5930 GCTAAGCGTGAAGTGTGGCGAGGATCTCCCGCTTCTTGGCCAGCTCATAGTACCGAG 5989
QY 5341 CTGCTCGGCTTCTTGAAGGCAACATGCTACTACCTGCTATGCTTCCCGGAGCCTGAC 5400
Db 5990 CTGCTCGGCTTCTTGAAGGCAACATGCTACTACCTGCTATGCTTCCCGGAGCCTGAC 6049
QY 5401 CTCATCGAGGCAACCTCTCTGCGCGCAGGAGATGGCGGGAAACATCACCCGCTGGAG 5460
Db 6050 CTCATCGAGGCAACCTCTCTGCGCGCAGGAGATGGCGGGAAACATCACCCGCTGGAG 6109
QY 5461 TCAGAAATAAGGTAGTAAATTTGGAGCTTTTCGAGCGCTTCCAGCGGAGGAGATGAG 5520
Db 6110 TCAGAAATAAGGTAGTAAATTTGGAGCTTTTCGAGCGCTTCCAGCGGAGGAGATGAG 6169
QY 5521 AGGGAAGTATCCGTTCCGGGGAGATCTCGGAGGTCCAGGAAATTTCCCTCGAGCGATG 5580
Db 6170 AGGGAAGTATCCGTTCCGGGGAGATCTCGGAGGTCCAGGAAATTTCCCTCGAGCGATG 6229
QY 5581 CCCATATGGGCAACCGCGGATTAACAACCTCTCACTGTTAGAGTCTCTGGAAGGACCCGAC 5640
Db 6230 CCCATATGGGCAACCGCGGATTAACAACCTCTCACTGTTAGAGTCTCTGGAAGGACCCGAC 6289
QY 5641 TAGCTCCTCCAGTGTGTAACCGGTGCTCAATGCGGCTTCCAGGCGCCCTCCGATACCA 5700
Db 6290 TAGCTCCTCCAGTGTGTAACCGGTGCTCAATGCGGCTTCCAGGCGCCCTCCGATACCA 6349
QY 5701 CCTCCAGGAGGAGGAGGAGGAGTGTCTGCTCAGAAATCTACCGTGTCTTCTGCTTGGG 5760
Db 6350 CCTCCAGGAGGAGGAGGAGGAGTGTCTGCTCAGAAATCTACCGTGTCTTCTGCTTGGG 6409
QY 5761 GAGCTGCCCAAAAGACCTTTCGCGAGCTCCGAATTCGTCGCGCGCTCGACAGGCGCACGGA 5820

QY 7981 AGATCAAGT 7989
Db 8630 AGATCAAGT 8638

RESULT 11

US-10-029-907-25
; Sequence 25, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: 2001-12-21
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802) ... (8407)
US-10-029-907-25

Query Match 90.7%; Score 7248.8; DB 4; Length 8638;
Best Local Similarity 92.0%; Pred. No. 0;
Matches 7960; Conservative 0; Mismatches 17; Indels 671; Gaps 3;

| | | | |
|----|-----|--|-----|
| QY | 2 | CCAGCCCCGATTGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAACACTACTGT | 61 |
| Db | 2 | CCAGCCCCCGATTGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAACACTACTGT | 61 |
| QY | 62 | CTTCACGAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTGTCGACGCTCCAGGACC | 121 |
| Db | 62 | CTTCACGAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTGTCGACGCTCCAGGACC | 121 |
| QY | 122 | CCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACACCGGAATTGCCAGG | 181 |
| Db | 122 | CCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACACCGGAATTGCCAGG | 181 |
| QY | 182 | ACGACCGGCTCTTCTTGATCAACCGCTCAATGCTGAGATTTGGGCTGCCCCCG | 241 |
| Db | 182 | ACGACCGGCTCTTCTTGATCAACCGCTCAATGCTGAGATTTGGGCTGCCCCCG | 241 |
| QY | 242 | CGAGACTGCTAGCCGAGTAGTGTGGTTCGGAAGGCTTGTGCTACTGCTGATAGG | 301 |
| Db | 242 | CGAGACTGCTAGCCGAGTAGTGTGGTTCGGAAGGCTTGTGCTACTGCTGATAGG | 301 |
| QY | 302 | TGCTTGGAGTGCCCGGAGGCTCTGCTAGACCGGTGACCAATGCAATCTTAAAC | 361 |
| Db | 302 | TGCTTGGAGTGCCCGGAGGCTCTGCTAGACCGGTGACCAATGCAATCTTAAAC | 361 |
| QY | 362 | TCAAGAAACAAAGGGCGCCATGATTGAACAAGATGATTGACGAGGTTCTCC | 421 |
| Db | 362 | TCAAGAAACAAAGGGCGCCATGATTGAACAAGATGATTGACGAGGTTCTCC | 421 |
| QY | 422 | GGCGCTTGGTGGAGAGGCTATTTCGGCTATGATCGGCAACACAGACAATCGGCTGCT | 481 |
| Db | 422 | GGCGCTTGGTGGAGAGGCTATTTCGGCTATGATCGGCAACACAGACAATCGGCTGCT | 481 |
| QY | 482 | TGATGCGCGCTGTTCGGCTGTGAGGCGAGGCGCCGCTTCTTTTGTCAAGACCGA | 541 |
| Db | 482 | TGATGCGCGCTGTTCGGCTGTGAGGCGAGGCGCCGCTTCTTTTGTCAAGACCGA | 541 |
| QY | 542 | CCTTCGGCTCCCTGATGAACTGCAGGACGAGGCGGCTATCGTGGCTGGCCAC | 601 |
| Db | 542 | CCTGTCCGGTCCCTGATGAACTGCAGGACGAGGCGGCTATCGTGGCTGGCCAC | 601 |

| | | | |
|----|------|---|------|
| QY | 602 | GACGGCGCTTCTCTGCGCAGCTGTGCTCAGCGTGTCTCACTGAAGCGGAAGGACTGGCT | 661 |
| Db | 602 | GACGGCGCTTCTCTGCGCAGCTGTGCTCAGCGTGTCTCACTGAAGCGGAAGGACTGGCT | 661 |
| QY | 662 | GCTATTGGCGAAGTGCOCGGGCGAGGATCTCTGTCACTCACCTTGTCTCTGCGGAGAA | 721 |
| Db | 662 | GCTATTGGCGAAGTGCOCGGGCGAGGATCTCTGTCACTCACCTTGTCTCTGCGGAGAA | 721 |
| QY | 722 | AGTATCCATCATGCTGATCAATGCGCGGCGCTGATACGCTGTGATCGGCTACCTGCC | 781 |
| Db | 722 | AGTATCCATCATGCTGATCAATGCGCGGCGCTGATACGCTGTGATCGGCTACCTGCC | 781 |
| QY | 782 | ATTTCGACCAACGAAACATCGCATCGAGCGAGCATCTCGATCGGATGGAAGCGGCT | 841 |
| Db | 782 | ATTTCGACCAACGAAACATCGCATCGAGCGAGCATCTCGATCGGATGGAAGCGGCT | 841 |
| QY | 842 | TGTCGATCAGGATGATCTGACGAGAGCATCAGGGCTCGCGCAGCGCAACTGTCGC | 901 |
| Db | 842 | TGTCGATCAGGATGATCTGACGAGAGCATCAGGGCTCGCGCAGCGCAACTGTCGC | 901 |
| QY | 902 | CAGGCTCAAGCGGCGCATGCGCGAGGATCTCGTGTGACCATGCGGATGCGCTG | 961 |
| Db | 902 | CAGGCTCAAGCGGCGCATGCGCGAGGATCTCGTGTGACCATGCGGATGCGCTG | 961 |
| QY | 962 | CTTCCGGAATATCATGTGGAATGCGCGCTTTTCTGGAATTCATCGACTGTGCGCGCT | 1021 |
| Db | 962 | CTTCCGGAATATCATGTGGAATGCGCGCTTTTCTGGAATTCATCGACTGTGCGCGCT | 1021 |
| QY | 1022 | GGTGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCGTGATATTGCTGAAGAGCT | 1081 |
| Db | 1022 | GGTGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCGTGATATTGCTGAAGAGCT | 1081 |
| QY | 1082 | TGGCGGGAATGGGCTGACCGCTTCTGCTGCTTTACGGTATGCGCGCTCCGATTCGA | 1141 |
| Db | 1082 | TGGCGGGAATGGGCTGACCGCTTCTGCTGCTTTACGGTATGCGCGCTCCGATTCGA | 1141 |
| QY | 1142 | CGCATCGCTTCTATCGCTTCTGAGAGTCTTCTGAGT-----TAAAC | 1189 |
| Db | 1142 | CGCATCGCTTCTATCGCTTCTGAGAGTCTTCTGAGT-----TAAAC | 1201 |
| QY | 1190 | AGACCAACACGGTTTCCCTCTAGCGGATCAATTCGCGCTTCCCTCCCGCCCTA | 1249 |
| Db | 1202 | AGACCAACACGGTTTCCCTCTAGCGGATCAATTCGCG-----CCCCCCCCCTA | 1250 |
| QY | 1250 | ACGTTACTGCGCGAAGCGCTTGAATAAGCGCGGTGCGTTGTCTATATGTTATTTT | 1309 |
| Db | 1251 | ACGTTACTGCGCGAAGCGCTTGAATAAGCGCGGTGCGTTGTCTATATGTTATTTT | 1310 |
| QY | 1310 | CCACATATTGCGCTTCTTTGGCAATGTAGGCGCGGAAACCTGCGCTCTCTTTGA | 1369 |
| Db | 1311 | CCACATATTGCGCTTCTTTGGCAATGTAGGCGCGGAAACCTGCGCTCTCTTTGA | 1370 |
| QY | 1370 | CGAGCATTCCTAGGGGTCTTTTCCCTCTCGCAAGGAATGCAAGGTCTGTTGAATGTCG | 1429 |
| Db | 1371 | CGAGCATTCCTAGGGGTCTTTTCCCTCTCGCAAGGAATGCAAGGTCTGTTGAATGTCG | 1430 |
| QY | 1430 | TGAAGGAAGAGTTCCTCTGGAAGCTTCTGAAGACAAAACACGTCTGTAGGACCTTT | 1489 |
| Db | 1431 | TGAAGGAAGAGTTCCTCTGGAAGCTTCTGAAGACAAAACACGTCTGTAGGACCTTT | 1490 |
| QY | 1490 | GCAGGACGGAACCCCCACCTGCGACAGGTGCTCTGCGGCAAAAGCCAGCTGAT | 1549 |
| Db | 1491 | GCAGGACGGAACCCCCACCTGCGACAGGTGCTCTGCGGCAAAAGCCAGCTGAT | 1550 |
| QY | 1550 | AAGATACCTGCAAGGCGGCAACCCAGTGCACCTTGTGAGTTGATAGTTGTTGG | 1609 |
| Db | 1551 | AAGATACCTGCAAGGCGGCAACCCAGTGCACCTTGTGAGTTGATAGTTGTTGG | 1610 |
| QY | 1610 | AAAGAGTCAATGCTCTCTCAAGCGTATTCACAAAGGGGCTGAAGATGCCAGAGG | 1669 |
| Db | 1611 | AAAGAGTCAATGCTCTCTCAAGCGTATTCACAAAGGGGCTGAAGATGCCAGAGG | 1670 |
| QY | 1670 | TACCCATTGTATGGGATCTGATCTGGGCTCGGTGCACATGCTTTACATGCTTTAGT | 1729 |

1671 TACCCATTGTATGGGATCTGATCTGGGCGCTCGGTGCACATGCTTTACATGTTAGT 1730
1730 CGAGGTAAACACGCTAGGCCCCCGAACCACCGGGAGCGTGTTCCTTTGAAAAAC 1789
1731 CGAGGTAAACACGCTAGGCCCCCGAACCACCGGGAGCGTGTTCCTTTGAAAAAC 1790
1790 ACATAATACCATG----- 1803
1791 ACATATATACCATGGACCGGAGATGGCAGCATCGTGGGAGCGCGGTTTCGTAGGTC 1850
1804 ----- 1803
1851 TGATACTCTTGACCTTGTACCGCACTATAAGCTGTTCTCGTAGGCTCATATGGTGT 1910
1804 ----- 1803
1911 TACAATATTTATACAGGGCGGAGGACACATTGCAAGTGTGGATCCCCCCCCCTCAACG 1970
1804 ----- 1803
1971 TTCGGGGGGCGGATCGGTTCATCTCTCACGTGGCGATCCACCCAGAGCTAATCT 2030
1804 ----- 1803
2031 TTACCATACCAAAATCTTGTCTCGCCATACTCGGTCCACTCATGTGCTCCAGGCTGGTA 2090
1804 ----- 1803
2091 TAACCAAGTGCGGTACTTGTGCGCGCACAGGGGTCAATTCGTGATGATGCTGGTGC 2150
1804 ----- 1803
2151 GGNAGTTGCTGGGGTCATTATGTCCAAATGGCTCTCATGAAGTTGGCGGCACTGACAG 2210
1804 ----- 1803
2211 GTACGTACGTTTATGACCATTCTCACCCCACTCGGGGACTGGGCCACGCGGGCTACGAG 2270
1804 ----- 1803
2271 ACCTTCGGTGGAGTTGAGCCGCTGCTCTTCTGTATATGAGACCAAGTTATCACCT 2330
1804 ----- 1803
2331 GGGGGGACACACCGCGCGTGTGGGACATCATCTTGGCCCTGCCCGTCTCCGCCGCA 2390
1804 ----- 1803
2391 GGGGGAGGAGATACATCTGGGACCGGACAGACAGCCTTTGAAGGGCAGGGGTGGCGACTCC 2450
1804 --GCGCTATTAGCGCTACTCCCAACAGACGAGCGGCTACTTGGCTGCATCATCACTA 1861
2451 TCGCGCTATTAGCGCTACTCCCAACAGACGCGAGCGCTACTTGGCTGCATCATCACTA 2510
1862 GCCTCACAGCCCGGACAGGAACAGGTCCAGGGGAGGTCCAAAGTGTCTCCACCGCAA 1921
2511 GCCTCACAGCCCGGACAGGAACAGGTCCAGGGGAGGTCCAAAGTGTCTCCACCGCAA 2570
1922 CAAATCTTTCCTGGGACCTGCGTCAATGGCGTGTGTTGGACTGTCTATCATGTGTCGG 1981
2571 CAAATCTTTCCTGGGACCTGCGTCAATGGCGTGTGTTGGACTGTCTATCATGTGTCGG 2630
1982 GCTCAAAGACCTTTCGCGGCCAAAGGGGCCAATCACCCAAATGTACCAATGTGGACC 2041
2631 GCTCAAAGACCTTTCGCGGCCAAAGGGGCCAATCACCCAAATGTACCAATGTGGACC 2690
2042 AGGACCTCGTGGTGGCAAGCGCCCCCGGGCGCGTTCCTTGACACCATGACCTGGG 2101
2691 AGGACCTCGTGGTGGCAAGCGCCCCCGGGCGCGTTCCTTGACACCATGACCTGGG 2750
2102 GAGCTCGGACCTTACTTGGTACAGGCGATGCCGATGTTCATTCGGTGGCGCGGG 2161

2751 GCAGCTCGGACCTTTACTTGGTCAAGACATGCCGATGTCAATTCGGTGGCGCGGG 2810
2162 GCGACAGAGGGAGCGCTACTCTCCCGCAGGCGCGCTCTCTTAAAGGGCTCTTCGG 2221
2811 GCGACAGAGGGAGCGCTACTCTCCCGCAGGCGCGCTCTCTTAAAGGGCTCTTCGG 2870
2222 GGGTCTACTGTCTCTCCCTCGGGCACGCTGTGGGCACTTCTTCGGGTGGCGTGTGA 2281
2871 GGGTCTACTGTCTCTCCCTCGGGCACGCTGTGGGCACTTCTTCGGGTGGCGTGTGA 2930
2282 CCGAGGGGTGGGAAGCGGTGGACTTTGTACCCGTCCAGTCTATGGAAAACCATATGC 2341
2931 CCGAGGGGTGGGAAGCGGTGGACTTTGTACCCGTCCAGTCTATGGAAAACCATATGC 2990
2342 GGTCCCGGTCTTTCAGGACAACTCGTCCCTCCGCGCGTACCGACAGACATTCAGGTGG 2401
2991 GGTCCCGGTCTTTCAGGACAACTCGTCCCTCCGCGCGTACCGACAGACATTCAGGTGG 3050
2402 CCAATCTACCGCCCCCTACTGTGTAGCGGAAGAGCACTAAGGTGCCGTGCGTATGCGAG 2461
3051 CCAATCTACCGCCCCCTACTGTGTAGCGGAAGAGCACTAAGGTGCCGTGCGTATGCGAG 3110
2462 CCAAGGTATTAAGGTCTTGTCTGAACCGGTCCGTCCGCGCACCTAGAGTTTCGGGG 2521
3111 CCAAGGTATTAAGGTCTTGTCTGAACCGGTCCGTCCGCGCACCTAGAGTTTCGGGG 3170
2522 CGTATATGTCTAAGGCACATGGTATCGACCCCTAAACATCAGAACCGGGSTAAGACCATCA 2581
3171 CGTATATGTCTAAGGCACATGGTATCGACCCCTAAACATCAGAACCGGGSTAAGACCATCA 3230
2582 CCACGGGTCCCCCATCACTACTCCACCTATGGCAAGTTTCTTGGCGAGCGGTGGTGTCT 2641
3231 CCACGGGTCCCCCATCACTACTCCACCTATGGCAAGTTTCTTGGCGAGCGGTGGTGTCT 3290
2642 CTGGGGCGCTATGACATCATATATGTATGAGTGCACCTCAACTGACTCCGACCATCA 2701
3291 CTGGGGCGCTATGACATCATATATGTATGAGTGCACCTCAACTGACTCCGACCATCA 3350
2702 TCTCGGGCATCGGACAGTCTTGGACCAAGCGGAGACGGGTGGAGCGGACTCGTGTGC 2761
3351 TCTCGGGCATCGGACAGTCTTGGACCAAGCGGAGACGGGTGGAGCGGACTCGTGTGC 3410
2762 TGCCACCGCTAGCTCTCGGGATCGGTCAACCGTGCACATCCAAACATCGAGAGGTGG 2821
3411 TGCCACCGCTAGCTCTCGGGATCGGTCAACCGTGCACATCCAAACATCGAGAGGTGG 3470
2822 CTCTGTCCAGCACTGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATCA 2881
3471 CTCTGTCCAGCACTGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATCA 3530
2882 AGGGGGGAGGCACTTCTTCTGCCATTTCCAAAGAAATGTATGATGAGCTCCGCGCGA 2941
3531 AGGGGGGAGGCACTTCTTCTGCCATTTCCAAAGAAATGTATGATGAGCTCCGCGCGA 3590
2942 AGCTGTCCGCGCTCGGACTCAATGTGTAGCATATTACCGGGCGCTTGTATTCGCTCA 3001
3591 AGCTGTCCGCGCTCGGACTCAATGTGTAGCATATTACCGGGCGCTTGTATTCGCTCA 3650
3002 TACCAACTAGCGAGACGTCTTGTGTAGCAACGCGCTCTAATGACGGGCTTTACCG 3061
3651 TACCAACTAGCGAGACGTCTTGTGTAGCAACGCGCTCTAATGACGGGCTTTACCG 3710
3062 GCGATTTCCAGTCACTGATGCAATATCTGTGTACCCAGACAGTGCAGCTTCAGCC 3121
3711 GCGATTTCCAGTCACTGATGCAATATCTGTGTACCCAGACAGTGCAGCTTCAGCC 3770
3122 TGGAACCGGCTTTCACCATTTGAGACGACCGTGCACAAAGCGGGTGTACGCTCCG 3181
3771 TGGAACCGGCTTTCACCATTTGAGACGACCGTGCACAAAGCGGGTGTACGCTCCG 3830
3182 AGCGGCGAGGACGCTGGTAGGGGAGGATGGCAATTTACAGGTTTGTGACTCCAGGAG 3241
3831 AGCGGCGAGGACGCTGGTAGGGGAGGATGGCAATTTACAGGTTTGTGACTCCAGGAG 3890

QY 3242 AACGCCCTCGGCGATGTTTCGATTCCTCGGTTCTGTGCGAGTGCATATGACGGGGCTGTG 3301
Db
QY 3891 AACGCCCTCGGCGATGTTTCGATTCCTCGGTTCTGTGCGAGTGCATATGACGGGGCTGTG 3950
Db
QY 3302 CTTGTACAGACTACGCCCGCGGAGACCTCAGTTAGGTGTTGGGGCTTACCTAAACACAC 3361
Db
QY 3951 CTTGTGTACAGACTACGCCCGCGGAGACCTCAGTTAGGTGTTGGGGCTTACCTAAACACAC 4010
QY 3362 CAGGGTTGCCCTCTGCGCAGGACCACTCTGGAGTCTTGGGAGAGCGTCTTTACAGGCTCA 3421
Db
QY 4011 CAGGGTTGCCCTCTGCGCAGGACCACTCTGGAGTCTTGGGAGGCGCTTTTACAGGCTCA 4070
QY 3422 CCCACATAGACGCCCATTTCTTGTGCCAGACTAAGCAGCAGCAGAGACAACTTCCCTTACC 3481
Db
QY 4071 CCCACATAGACGCCCATTTCTTGTGCCAGACTAAGCAGCAGCAGAGACAACTTCCCTTACC 4130
QY 3482 TGGTAGCATACAGAGTACGGTGTGGCGCAGGGCTCAGGCTCCACTCCCTCGTGGGACC 3541
Db
QY 4131 TGGTAGCATACAGAGTACGGTGTGGCGCAGGGCTCAGGCTCCACTCCCTCGTGGGACC 4190
QY 3542 AAATGTGGAAGTGTCTCATACGGCTAAAGCCTACGCTGACCGGCCCAACCGCCCTGCTGT 3601
Db
QY 4191 AAATGTGGAAGTGTCTCATACGGCTAAAGCCTACGCTGACCGGCCCAACCGCCCTGCTGT 4250
QY 3602 ATAGGCTGGGAGCCGTTCAAAAAGAGGTTTACTACACACACACCCCATAAACAAATACATCA 3661
Db
QY 4251 ATAGGCTGGGAGCCGTTCAAAAAGAGGTTTACTACACACACACCCCATAAACAAATACATCA 4310
QY 3662 TGGCATGATGTGCGCTGACCTGGAGGTGCTGACGAGACCTGGGTGTGGTAGCGGAG 3721
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QY 4311 TGGCATGATGTGCGCTGACCTGGAGGTGCTGACGAGACCTGGGTGTGGTAGCGGAG 4370
QY 3722 TCCTAGCAGCTGTCGCCGCTATTCGCTGACAAACAGGAGCGTGTCTATTTGGGACAGA 3781
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QY 4371 TCCTAGCAGCTGTCGCCGCTATTCGCTGACAAACAGGAGCGTGTCTATTTGGGACAGA 4430
QY 3782 TCATCTTGTCCGGAAGCGGCGCATCATTTCCCGACAGGGAAGTCTCTTACCGGAGGTTCG 3841
Db
QY 4431 TCATCTTGTCCGGAAGCGGCGCATCATTTCCCGACAGGGAAGTCTCTTACCGGAGGTTCG 4490
QY 3842 ATGAGATGGAAGTGTGGCTCACAACCTCCCTTATCATCGAAGAGGAAATGCAAGTTCGCG 3901
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QY 4491 ATGAGATGGAAGTGTGGCTCACAACCTCCCTTATCATCGAAGAGGAAATGCAAGTTCGCG 4550
QY 3902 AACAAATCAACAGAGGCAATCGGTTGCTGCAAAACAGCCACCAAGCAAGCGGAGGCTG 3961
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QY 4551 AACAAATCAACAGAGGCAATCGGTTGCTGCAAAACAGCCACCAAGCAAGCGGAGGCTG 4610
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QY 4611 CTGCTCCGCTGTGGAATCCAGTGGCGGACCTCGAAGCCCTTCTGGCGGAAGCATATGT 4670
QY 4022 GGAATTTTCATAGCGGGATCAATATTTAGCGGCTGTGCACTCTGCTGCTGCGCAACCCG 4081
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QY 4671 GGAATTTTCATAGCGGGATCAATATTTAGCGGCTGTGCACTCTGCTGCTGCGCAACCCG 4730
QY 4082 CGATAGCATCACTGATGCAATTCAGAGCTCTATCACCAGCCGCTCACCACCCCAACATA 4141
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QY 4262 AGGTGCTTGTGATATTTTGCAGGTTATGAGCAGGGGTGCGAGCGCGCTGCTGGCT 4321
Db
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QY 4322 TTAAAGTCATAGCGCGAGATGCCCTCCACGAGACCTGTTTAACTACTCCCTGCTA 4381
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QY 5991 TGTCTGCGCTTCTTGAAGCAATGCACTACCGCTCATGACTCCCGGAGCGCTGACC 6050
QY 5402 TCATCGAGGCCAACCTCTCTGTGGCGGAGAGATGGGGGGAACATCACCCCGCTGGAGT 5461

| | | | |
|------|----|--|------|
| 6051 | Db | TCA TCGAGGCCAA CCTCCTCTGGCGG CAGGAGATGGCGGGGAA CATCACCCGGTGGAGT | 6110 |
| 5462 | Qy | CAGAAATAGGTAGTAA TTTGAC TCTTTCGAGCGCTCC AAGCGGAGGAGATGAGA | 5521 |
| 6111 | Db | CAGAGATAAGGTAGTAA TTTGGAC TCTTTCGAGCCGCTCC AAGCGGAGGAGATGAGA | 6170 |
| 5522 | Qy | GGGAAGTATCCG TTCCGCGCGAGATCCTGGGAGGTCC AGAAATTCCTCGAGCGATGC | 5581 |
| 6171 | Db | GGGAAGTATCCG TTCCGCGCGAGATCCTGGGAGGTCC AGAAATTCCTCGAGCGATGC | 6230 |
| 5582 | Qy | CCATATGGG CAGCGCGGATTA CAACCTCCAC TTTAGAGTCTCTG AAGAACCCGSACT | 5641 |
| 6231 | Db | CCATATGGG CAGCGCGGATTA CAACCTCCAC TTTAGAGTCTCTG AAGAAAGACCCGSACT | 6290 |
| 5642 | Qy | ACGTCCCTCCAGTGGT ACACGGGTGTCC ATTGCCGCTGCTCC AAGCCCCCTCCGATACCA | 5701 |
| 6291 | Db | ACGTCCCTCCAGTGGT ACACGGGTGTCC ATTGCCGCTGCTCC AAGCCCCCTCCGATACCA | 6350 |
| 5702 | Qy | CTCCAGGAGAA GAGAGCGTTGTCTGT CAGAAATCTAC CGTGTCTTCTG CCTTGGCGG | 5761 |
| 6351 | Db | CTCCAGGAGAA GAGAGCGTTGTCTGT CAGAAATCTAC CGTGTCTTCTG CCTTGGCGG | 6410 |
| 5762 | Qy | AGCTCGCACAAAGAC TTCCGCGAGCTCC GAATCGTGGCGCTCGA CAGCGGACGCA | 5821 |
| 6411 | Db | AGCTCGCACAAAGAC TTCCGCGAGCTCC GAATCGTGGCGCTCGA CAGCGGACGCA | 6470 |
| 5822 | Qy | CGGCTCTCTG ACCAGCCCTCC AGCAGCGCGAGCGGGATCC GATGAGTCTG ACT | 5881 |
| 6471 | Db | CGGCTCTCTG ACCAGCCCTCC AGCAGCGCGAGCGGGATCC GATGAGTCTG ACT | 6530 |
| 5882 | Qy | CCTCCATGCCCCCTTTGAGGGGAGCGGGGATCC CGATCTCAGCGACGGGTCTTGGT | 5941 |
| 6531 | Db | CCTCCATGCCCCCTTTGAGGGGAGCGGGGATCC CGATCTCAGCGACGGGTCTTGGT | 6590 |
| 5942 | Qy | CTACCGTAAGCGAGGAGCT AGTGAAGACGTCTG CTGCTCGATGTC TACACATGGA | 6001 |
| 6591 | Db | CTACCGTAAGCGAGGAGCT AGTGAAGACGTCTG CTGCTCGATGTC TACACATGGA | 6650 |
| 6002 | Qy | CAGGGCCCTGATC AGCGCATGCGTTCGGAGGAA CCAAGCTGCCATCAATGCACTGA | 6061 |
| 6651 | Db | CAGGGCCCTGATC AGCGCATGCGTTCGGAGGAA CCAAGCTGCCATCAATGCACTGA | 6710 |
| 6062 | Qy | GCAACTTTTGTCTCGT CACACAACTTTGGTCTA TGCTACAA CATCTCGACGCGAAGCC | 6121 |
| 6711 | Db | GCAACTTTTGTCTCGT CACACAACTTTGGTCTA TGCTACAA CATCTCGACGCGAAGCC | 6770 |
| 6122 | Qy | TGCGCAGAAAGTCA CCTTTTGA CAGACTG CAGTCTCTG GACGACCACTACCGGAGC | 6181 |
| 6771 | Db | TGCGCAGAAAGTCA CCTTTTGA CAGACTG CAGTCTCTG GACGACCACTACCGGAGC | 6830 |
| 6182 | Qy | TGCTCAAGGATGAAGCG GAAGCGTCC ACAGTTTAA GGCTAA ACTTCTATCCGTGGAGG | 6241 |
| 6831 | Db | TGCTCAAGGATGAAGCG GAAGCGTCC ACAGTTTAA GGCTAA ACTTCTATCCGTGGAGG | 6890 |
| 6242 | Qy | AAGCCTGTAAGTGA CGCCGCCACATTC CGGCAGATCTA AATTTGGCTATCGGGCAAGG | 6301 |
| 6891 | Db | AAGCCTGTAAGTGA CGCCGCCACATTC CGGCAGATCTA AATTTGGCTATCGGGCAAGG | 6950 |
| 6302 | Qy | AGTCCGGAA CCTATCCAGCAAGCGGT TAACCATCGCTCCG GTGGAAGCACTTGC | 6361 |
| 6951 | Db | AGTCCGGAA CCTATCCAGCAAGCGGT TAACCATCGCTCCG GTGGAAGCACTTGC | 7010 |
| 6362 | Qy | TGGAAGACACTGAGAC ACCAATTTGAC CACCATCATGGC AAAAAATGAGTTTTCTGCG | 6421 |
| 7011 | Db | TGGAAGACACTGAGAC ACCAATTTGAC CACCATCATGGC AAAAAATGAGTTTTCTGCG | 7070 |
| 6422 | Qy | TCCAA CCAGAGAGGGGGCG CAGCAGCTG CGCTTATCGTATTC CCAGATTTGGGGG | 6481 |
| 7071 | Db | TCCAA CCAGAGAGGGGGCG CAGCAGCTG CGCTTATCGTATTC CCAGATTTGGGGG | 7130 |
| 6482 | Qy | TTCTGTGTGTCAGAAAAAT GGCCCTTTAC GATGGTCTCC ACCCCTCCCTCAGGCGGTGA | 6541 |

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QY 7622 TATCCAGTGGTTCGTTGCTGTTTACAGCGGGGAGACATATATACAGCCTGTCTCGTG 7681
D 8271 TATCCAGTGGTTCGTTGCTGTTTACAGCGGGGAGACATATATACAGCCTGTCTCGTG 8330
QY 7682 CCCGACCCCGTGTTCATGTTGGTTCCTACTCTCTTCTGTAGGGTAGGCATCTATC 7741
D 8331 CCCGACCCCGTGTTCATGTTGGTTCCTACTCTCTTCTGTAGGGTAGGCATCTATC 8390
QY 7742 TACTCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAAATAGGCCATCTCTTTT 7801
D 8391 TACTCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAAATAGGCCATCTCTTTT 8450
QY 7802 TTCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 7861
D 8451 TTCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 8510
QY 7862 TTTTCTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 7921
D 8511 TTTTCTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 8570
QY 7922 AGCTGTGAAAGTCCGAGCGCTTCACTGCAGAGAGTGTGATAGTGGCTCTCTGCA 7981
D 8571 AGCTGTGAAAGTCCGAGCGCTTCACTGCAGAGAGTGTGATAGTGGCTCTCTGCA 8630
QY 7982 GATCAAGT 7989
D 8631 GATCAAGT 8638

RESULT 12
US-10-029-907-2
; Sequence 2, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 8642
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
; NAME/KEY: variation
; LOCATION: 6268
; OTHER INFORMATION: r = a or g
; NAME/KEY: variation
; LOCATION: 4446
; OTHER INFORMATION: r = a or g
US-10-029-907-2

Query Match 90.7%; Score 7246.8; DB 4; Length 8642;
Best Local Similarity 92.1%; Pred. No. 0;
Matches 7966; Conservative 2; Mismatches 9; Indels 675; Gaps 4;

QY 2 CCAGCCCCGATTTGGGGGACACTCCACATAGATCACTCCCTGTGAGGAACACTACTGT 61
D 2 CCAGCCCCGATTTGGGGGACACTCCACATAGATCACTCCCTGTGAGGAACACTACTGT 61
QY 62 CTTTACGACAGAAAGCTGTAGCCATGCGTTCATGATGATGCTGCGAGCTCCAGACC 121
D 62 CTTTACGACAGAAAGCTGTAGCCATGCGTTCATGATGATGCTGCGAGCTCCAGACC 121
QY 122 CCCCTTCCGGGAGAGCCATAGTGGTCTGCGAACCAGGTGAGTACACCGGAATTGCCAGG 181
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Db 122 CCCCTTCCGGGAGAGCCATAGTGGTCTGCGAACCAGGTGAGTACACCGGAATTGCCAGG 181
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D 182 ACGACCGGGTCTTTTCTTGGATCAACCCGCTCAATGCTGTGAGATTTGGGGGTGCCCCCG 241
QY 242 CGAGACTGCTAGCCGATAGTGTGGTTCGGAAGGCTTGTGTTACTGCTGATAGGG 301
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QY 302 TGTGTTGCGAGTGCCTCCGCGAGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAACC 361
D 302 TGTGTTGCGAGTGCCTCCGCGAGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAACC 361
QY 362 TCAAGAAAAACCAAGGGCGGCTATGATGAACAAGATGGATTGCAACGCAAGTTCTTC 421
D 362 TCAAGAAAAACCAAGGGCGGCTATGATGAACAAGATGGATTGCAACGCAAGTTCTTC 421
QY 422 GCGCGTGGTGGAGAGGCTATTCGGCTATGACTGGGCAACAGACAATCGGCTGCTC 481
D 422 GCGCGTGGTGGAGAGGCTATTCGGCTATGACTGGGCAACAGACAATCGGCTGCTC 481
QY 482 TGATGCGCGCTGTTCGGCTGTGAGCGCAGGGGCGCCGGTCTCTTTTGTCAAGACCGA 541
D 482 TGATGCGCGCTGTTCGGCTGTGAGCGCAGGGGCGCCGGTCTCTTTTGTCAAGACCGA 541
QY 542 CTTGTCGGTGGCTTGAATGAATGAGGAGGAGCGCGCTATCGTGGTGGCCAC 601
D 542 CTTGTCGGTGGCTTGAATGAATGAGGAGGAGCGCGCTATCGTGGTGGCCAC 601
QY 602 GACGGGCTTCTTGGCAGCTGTGTCGAGCTGTGCTCACTGAAAGCGGAGGAGCTGGCT 661
D 602 GACGGGCTTCTTGGCAGCTGTGTCGAGCTGTGCTCACTGAAAGCGGAGGAGCTGGCT 661
QY 662 GCTATTGGGCGAAGTCCGGGCGAGGATCTCTGTCTATCTCACCTTCTCTCTGCGGAA 721
D 662 GCTATTGGGCGAAGTCCGGGCGAGGATCTCTGTCTATCTCACCTTCTCTCTGCGGAA 721
QY 722 AGTATCCATCATGGCTGTGCAATGCGGGGTGCTATGCTGCTGATCCGGTACCTGCCC 781
D 722 AGTATCCATCATGGCTGTGCAATGCGGGGTGCTATGCTGCTGATCCGGTACCTGCCC 781
QY 782 ATTTCGACCCACCAAGCGAATCGATCGAGCGAGCAGTACTCGGATGGAACCGGTCT 841
D 782 ATTTCGACCCACCAAGCGAATCGATCGAGCGAGCAGTACTCGGATGGAACCGGTCT 841
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D 842 TGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCGGAACTGTCG 901
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D 902 CAGGCTCAAGGCGCGCATGCGCGAGCGAGGATCTGTCGTGACCCCATGGCGATGCGCTG 961
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D 962 CTTGCGCAATATCATGTTGGAATGCGCGCTTTTCTGGATTCATCGACTGTGCGCGCT 1021
QY 1022 GGTGTTGGCGGACCGCTATCAGGACATAGCTTGGCTACCCGCTGATATTGCTCAAGAGCT 1081
D 1022 GGTGTTGGCGGACCGCTATCAGGACATAGCTTGGCTACCCGCTGATATTGCTCAAGAGCT 1081
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Qy 1804 ----- 1803
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Qy 1804 ----- 1803
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Db 2031 TTACCATCACAAATCTTGTCTCGCATCTCGGTCCACTCATGTGTCTCCAGGCTGGTA 2090
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Db 2451 TCGSCCTATTACGSCCTTACTCCAAACAGACGCGAGGCTACTTGGCTGCATCATCTA 2510
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Db 2511 GCCTCACAGGCGGGACAGGAACCAAGTCTGAGGGGAGGTCCAAAGTGTCTCCACGCAA 2570
Qy 1922 CACAACTCTTCTGCGGACCTGCTCAATGGGCTGTGTGACTCTCTATCATGTGCGG 1981
Db 2571 CACAACTCTTCTGCGGACCTGCTCAATGGGCTGTGTGACTCTCTATCATGTGCGG 2630
Qy 1982 GCTCAAGACCTTCTCGGCGCCAAAGGCGCCCAATCACCCAAATGTACACCAATGTGACC 2041
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Qy 2702 TCTTGGGCTCGGACAGTCTTGGACCAAGCGGAGCGCTGGAGCGGACTCGTGTGC 2761
Db 3351 TCTTGGGCTCGGACAGTCTTGGACCAAGCGGAGCGCTGGAGCGGACTCGTGTGC 3410

QY 2762 TCGCCACCGCTACGCTCGGGATCGGTACCGTGCACATCAATCAAAATCGAGAGGTGG 2821
 Db 3411 TCGCCACCGCTACGCTCGGGATCGGTACCGTGCACATCAAAATCGAGAGGTGG 3470
 QY 2822 CTCCTGTCAGACCTCGAGAAATCCCTTTTATGGAAGCCATCCCATCGAGACATCA 2881
 Db 3471 CTCCTGTCAGACCTCGAGAAATCCCTTTTATGGAAGCCATCCCATCGAGACATCA 3530
 QY 2882 AGGGGGGAGGACCTCAATTTCTGCCATTCCTCAAGAGAAATGTGATGAGTTCGCGCGA 2941
 Db 3531 AGGGGGGAGGACCTCAATTTCTGCCATTCCTCAAGAGAAATGTGATGAGTTCGCGCGA 3590
 QY 2942 AGCTGTCGGGCTCGGACTCAATGTGTAGCATATTAACGGGGCCCTTGATGTATCCGTCA 3001
 Db 3591 AGCTGTCGGGCTCGGACTCAATGTGTAGCATATTAACGGGGCCCTTGATGTATCCGTCA 3650
 QY 3002 TACCAACTAGCGGAGACGTCATGTCGTAGCAACCGACGCTCTAATGACGGCTTTACGG 3061
 Db 3651 TACCAACTAGCGGAGACGTCATGTCGTAGCAACCGACGCTCTAATGACGGCTTTACGG 3710
 QY 3062 GCGATTTTCGACTCAGTGATCGACTGCAATACATGTGTCAACCCAGACAGTCACTTTACGCC 3121
 Db 3711 GCGATTTTCGACTCAGTGATCGACTGCAATACATGTGTCAACCCAGACAGTCACTTTACGCC 3770
 QY 3122 TGGACCCGACCTTACCAATTGAGACGACGACGCTGCCACAGACCGGTGTCAACGCTCGC 3181
 Db 3771 TGGACCCGACCTTACCAATTGAGACGACGACGCTGCCACAGACCGGTGTCAACGCTCGC 3830
 QY 3182 AGCGGAGGAGGAGCTGCTAGGGGACGATGCGCAATTTACAGTTTGTGACTCCAGGAG 3241
 Db 3831 AGCGGAGGAGGAGCTGCTAGGGGACGATGCGCAATTTACAGTTTGTGACTCCAGGAG 3890
 QY 3242 AACGGCCCTCGGGATGTTGATTCCTCGTTCTGTGCGAGTGTATGACGCGGCTGTG 3301
 Db 3891 AACGGCCCTCGGGATGTTGATTCCTCGTTCTGTGCGAGTGTATGACGCGGCTGTG 3950
 QY 3302 CTTGGTAGAGCTACGCGCCGCGAGACCTCAGTTAGTTGCGGCTTACCTAAACACAC 3361
 Db 3951 CTTGGTAGAGCTACGCGCCGCGAGACCTCAGTTAGTTGCGGCTTACCTAAACACAC 4010
 QY 3362 CAGGTTGCGGCTGTCAGGACCATCTGGAGTTCTGGAGAGGCTCTTTACAGGCTCA 3421
 Db 4011 CAGGTTGCGGCTGTCAGGACCATCTGGAGTTCTGGAGAGGCTCTTTACAGGCTCA 4070
 QY 3422 CCCACATAGACCCCAATTTCTGTCGCCAGCTTAAGCAGGAGAGACAACTTCCCTACC 3481
 Db 4071 CCCACATAGACCCCAATTTCTGTCGCCAGCTTAAGCAGGAGAGACAACTTCCCTACC 4130
 QY 3482 TGGTAGATACAGGCTACGGTGTGCGCCAGGCTCAGGCTCCACCTCCATCGTGGGACC 3541
 Db 4131 TGGTAGATACAGGCTACGGTGTGCGCCAGGCTCAGGCTCCACCTCCATCGTGGGACC 4190
 QY 3542 AAATGTGGAAGTGTCTATAGGCTTAAGCTAGCTGACGCGGCGCAACGCGCTGTGT 3601
 Db 4191 AAATGTGGAAGTGTCTATAGGCTTAAGCTAGCTGACGCGGCGCAACGCGCTGTGT 4250
 QY 3602 ATAGGCTGGGAGCGGCTTCAAAACGAGGTTACTACACACACCCCATCAACCAATACATCA 3661
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 Db 4311 TGGCATGATGTGCGGCTGACCTGAGGTCGTACAGACACCTGGGTGTGGTAGCGGAG 4370
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 Db 4371 TCCTAGAGCTTCGGCGGCTATTTGCTTACCAACAGGAGGCTGTGATTTGGGAGGA 4430
 QY 3782 TCATCTTGTTCGGAAAGCCGCTCATCTTCCGACAGGAGTCTTTTACCGGAGTTTCG 3841
 Db 4431 TCATCTTGTTCGGAAAGCCGCTCATCTTCCGACAGGAGTCTTTTACCGGAGTTTCG 4490
 QY 3842 ATGAGATGGAAGAGTGGCTTCACACCTCCCTTACATCGAAGGAAATGAGCTCGCGG 3901

Db 4491 ATGAGATGGAAGAGTGGCTTCACACCTCCCTTACATCGAAGGAAATGAGCTCGCGG 4550
 QY 3902 AACAAATCAACAGAAAGCAATCGGTTGCTGCAAAAGCCACCAAGCAAGCGAGGCTG 3961
 Db 4551 AACAAATCAACAGAAAGCAATCGGTTGCTGCAAAAGCCACCAAGCAAGCGAGGCTG 4610
 QY 3962 CTGCTCCCGTGGTGAATCCCAAGTCGCGGACCTCGAAGCCTTCTGGGGAAGCATATGT 4021
 Db 4611 CTGCTCCCGTGGTGAATCCCAAGTCGCGGACCTCGAAGCCTTCTGGGGAAGCATATGT 4670
 QY 4022 GGAATTTTCATCAGCGGGGATCAAAATTTTAGCAGGCTTGTCACTCTGCTGCTGCAACCCCG 4081
 Db 4671 GGAATTTTCATCAGCGGGGATCAAAATTTTAGCAGGCTTGTCACTCTGCTGCTGCAACCCCG 4730
 QY 4082 CGATAGCATCACTGATGCAATTCACAGCTCTATCACCAGCCCGCTCACCACCAACATA 4141
 Db 4731 CGATAGCATCACTGATGCAATTCACAGCTCTATCACCAGCCCGCTCACCACCAACATA 4790
 QY 4142 CCCTCCTGTTTAAACATCCTGGGGGATGGGTGGCGGCCCAACTTGTCTCTCCAGCGCTG 4201
 Db 4791 CCCTCCTGTTTAAACATCCTGGGGGATGGGTGGCGGCCCAACTTGTCTCTCCAGCGCTG 4850
 QY 4202 CTTCTGCTTTCTAGGCGCGCATTCGCTGGAGCGGCTGTTGGCAGCATAGGCTTTGGA 4261
 Db 4851 CTTCTGCTTTCTAGGCGCGCATTCGCTGGAGCGGCTGTTGGCAGCATAGGCTTTGGA 4910
 QY 4262 AGGTGCTTTGCGATATTTTGGCAGGTTATGAGCAGGGGTGGCAGCGCTCGTGGCT 4321
 Db 4911 AGGTGCTTTGCGATATTTTGGCAGGTTATGAGCAGGGGTGGCAGCGCTCGTGGCT 4970
 QY 4322 TTAAGGTATCAGCGGCGAGATGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCTA 4381
 Db 4971 TTAAGGTATCAGCGGCGAGATGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCTA 5030
 QY 4382 TCCTCTCCCTCGGCGCCCTAGTCTCGGGGTGCTGTGCGCAGCATATCTGCTGCGGACG 4441
 Db 5031 TCCTCTCCCTCGGCGCCCTAGTCTCGGGGTGCTGTGCGCAGCATATCTGCTGCGGACG 5090
 QY 4442 TGGGCCAGGGGAGGGGCTGTGCAAGTGGATGAACCCGCTGATAGCGTTCTCGCGG 4501
 Db 5091 TGGGCCAGGGGAGGGGCTGTGCAAGTGGATGAACCCGCTGATAGCGTTCTCGCGG 5150
 QY 4502 GTACACAGCTCTCCCGACCGACTATGTCTGAGAGCGAGCTGACGACGCTGCTCACTC 4561
 Db 5151 GTACACAGCTCTCCCGACCGACTATGTCTGAGAGCGAGCTGACGACGCTGCTCACTC 5210
 QY 4562 AGATCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTCAACAGTGGATCAACG 4621
 Db 5211 AGATCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTCAACAGTGGATCAACG 5270
 QY 4622 AGGATGCTTCAACCGCATGTCTCGGCTCGTGGCTTAAGAGATGTTTGGGATTTGATGCA 4681
 Db 5271 AGGATGCTTCAACCGCATGTCTCGGCTCGTGGCTTAAGAGATGTTTGGGATTTGATGCA 5330
 QY 4682 CGGTGTTGACTGATTTCAAGACCTGGCTCCAGTCCAGTCCAGCTCTCTCCCGGATTTGCGGAG 4741
 Db 5331 CGGTGTTGACTGATTTCAAGACCTGGCTCCAGTCCAGTCCAGCTCTCTCCCGGATTTGCGGAG 5390
 QY 4742 TCCCTCTCTCTCATGTCAACGTTGAGTACAAAGGAGTCTGGCGGGCGACGCGCATATGC 4801
 Db 5391 TCCCTCTCTCTCATGTCAACGTTGAGTACAAAGGAGTCTGGCGGGCGACGCGCATATGC 5450
 QY 4802 AAACCACTGCCATGTGGAGCAGATCACCAGACATGTGAATAAAGCTTCCATGAGGA 4861
 Db 5451 AAACCACTGCCATGTGGAGCAGATCACCAGACATGTGAATAAAGCTTCCATGAGGA 5510
 QY 4862 TCGTGGGCGCTAGACCTGTAGTAAACGTTGGCATGGAACATTTCCCATTAACCGGTACA 4921
 Db 5511 TCGTGGGCGCTAGACCTGTAGTAAACGTTGGCATGGAACATTTCCCATTAACCGGTACA 5570
 QY 4922 CCACGGGCCCTCGACGCGCTCCCGCGGCCAAATTTATTCTAGGGCGCTGTGGCGGTGG 4981

| | | | |
|----|------|--|------|
| Db | 5571 | CCACGGGCGCTGCAAGCGCTCCCGCGCCAAATTAATTCTAGGGCGCTGTGCGGGTGG | 5630 |
| Qy | 4982 | CTGCTGAGGAGTACGTGAGGTTTACCGGGGTGGGGAATTTCCATACGTGACGGGATCA | 5041 |
| Db | 5631 | CTGCTGAGGAGTACGTGAGGTTTACCGGGGTGGGGAATTTCCATACGTGACGGGATCA | 5690 |
| Qy | 5042 | CCACTGACAAAGTAAAGTGCCTGTGAGTTCCGGGCCCGGAAATTTCTTCAAGAAAGTGG | 5101 |
| Db | 5691 | CCACTGACAAAGTAAAGTGCCTGTGAGTTCCGGGCCCGGAAATTTCTTCAAGAAAGTGG | 5750 |
| Qy | 5102 | ATGGGTGGGGTTCACAGGTACGCTCCAGCGTGCAAAACCCCTCTTACGGGAGGAGTCA | 5161 |
| Db | 5751 | ATGGGTGGGGTTCACAGGTACGCTCCAGCGTGCAAAACCCCTCTTACGGGAGGAGTCA | 5810 |
| Qy | 5162 | CATTCTGTGCGGGTCAATCAATACCTGTGTTGGGTACAGCTCCCATGGAGCCCGAAC | 5221 |
| Db | 5811 | CATTCTGTGCGGGTCAATCAATACCTGTGTTGGGTACAGCTCCCATGGAGCCCGAAC | 5870 |
| Qy | 5222 | CGGAGCTAGCAGTGTCACTTCCATGCTCACCGACCCCTCCACATTAAGCGCGAGACGG | 5281 |
| Db | 5871 | CGGAGCTAGCAGTGTCACTTCCATGCTCACCGACCCCTCCACATTAAGCGCGAGACGG | 5930 |
| Qy | 5282 | CTAAGCGTAGGCTGGCGAGGGATCTCCCGCTCTTGGCGAGCTCATCAGCTAGCGAGC | 5341 |
| Db | 5931 | CTAAGCGTAGGCTGGCGAGGGATCTCCCGCTCTTGGCGAGCTCATCAGCTAGCGAGC | 5990 |
| Qy | 5342 | TGTTCTGGGCTTCTTTGAAGGCAACATGCTACTACCGCTCATGACTCCCGGAGCGTGACC | 5401 |
| Db | 5991 | TGTTCTGGGCTTCTTTGAAGGCAACATGCTACTACCGCTCATGACTCCCGGAGCGTGACC | 6050 |
| Qy | 5402 | TCATCAGGCGCAACCTCTCTGTGCGGAGGAGATGGCGGGAAACATCACCGCGTGGAGT | 5461 |
| Db | 6051 | TCATCAGGCGCAACCTCTCTGTGCGGAGGAGATGGCGGGAAACATCACCGCGTGGAGT | 6110 |
| Qy | 5462 | CAGAAATAAGGTAGTAATTTGGACTTTTGGACTTTTGGAGCGCTTCCAGCGGAGGAGTGA | 5521 |
| Db | 6111 | CAGAAATAAGGTAGTAATTTGGACTTTTGGACTTTTGGAGCGCTTCCAGCGGAGGAGTGA | 6170 |
| Qy | 5522 | GGGAGTATCCGTTCCGGCGGAGATCTGGGAGGTCCAGGAAATTCCTTCGAGCGATGC | 5581 |
| Db | 6171 | GGGAGTATCCGTTCCGGCGGAGATCTGGGAGGTCCAGGAAATTCCTTCGAGCGATGC | 6230 |
| Qy | 5582 | CCATATGGGCAAGCGCGGATTAACCCCTCCACTGTTAGAGTCTCTGGAAGGACCCGGACT | 5641 |
| Db | 6231 | CCATATGGGCAAGCGCGGATTAACCCCTCCACTGTTAGAGTCTCTGGAAGGACCCGGACT | 6290 |
| Qy | 5642 | ACGTCCCTCCAGTGGTACACGGGTGTCATATGCGCGCTGCCAAGGCGCTTCCGATACAC | 5701 |
| Db | 6291 | ACGTCCCTCCAGTGGTACACGGGTGTCATATGCGCGCTGCCAAGGCGCTTCCGATACAC | 6350 |
| Qy | 5702 | CTCAGCGGAGGAGGAGGAGTGTCTCTGTGAGTCTAGGATCTCTTCTGCTTGGCGG | 5761 |
| Db | 6351 | CTCAGCGGAGGAGGAGGAGTGTCTCTGTGAGTCTAGGATCTCTTCTGCTTGGCGG | 6410 |
| Qy | 5762 | AGCTCGGCAACAAGACCTTCGGCAGCTCCGAATCGTGGCGGTCCGACAGCGGACCGCAA | 5821 |
| Db | 6411 | AGCTCGGCAACAAGACCTTCGGCAGCTCCGAATCGTGGCGGTCCGACAGCGGACCGCAA | 6470 |
| Qy | 5822 | CGGCGTCTCTGACCAAGCCCTCCGACAGCGCGGATCCGAGCTTGAFTGCTACT | 5891 |
| Db | 6471 | CGGCGTCTCTGACCAAGCCCTCCGACAGCGCGGATCCGAGCTTGAFTGCTACT | 6530 |
| Qy | 5892 | CCTTCATGCCCCCTTGGGGGAGCGGGGATCCGATCTCAGCGAGCGGTCTTGGT | 5941 |
| Db | 6531 | CCTTCATGCCCCCTTGGGGGAGCGGGGATCCGATCTCAGCGAGCGGTCTTGGT | 6590 |
| Qy | 5942 | CTACCGTAAAGCGAGGAGTGTGAGGACGTGCTGTCTGTCTCGATGTCTTACATGGA | 6001 |
| Db | 6591 | CTACCGTAAAGCGAGGAGTGTGAGGACGTGCTGTCTGTCTCGATGTCTTACATGGA | 6650 |
| Qy | 6002 | CAGCGCGCTGATCAGCGCATGCGTGGGAGGAAACAGCTGCCCATCAATGACTGA | 6061 |
| Db | 6651 | CAGCGCGCTGATCAGCGCATGCGTGGGAGGAAACAGCTGCCCATCAATGACTGA | 6710 |
| Qy | 6062 | GCAACTCTTTGCTCCGTACCAACAACCTTGTCTATGCTACAACTTCGACGCGCAAGCC | 6121 |
| Db | 6711 | GCAACTCTTTGCTCCGTACCAACAACCTTGTCTATGCTACAACTTCGACGCGCAAGCC | 6770 |
| Qy | 6122 | TGCGGAGAAAGGTACCTTTGACAGCTGAGTCTGAGGACCACTACCGGAGC | 6181 |
| Db | 6771 | TGCGGAGAAAGGTACCTTTGACAGCTGAGTCTGAGGACCACTACCGGAGC | 6830 |
| Qy | 6182 | TGCTCAAGGAGTGAAGGCGAAGGCGTCCACAGTTAAGCTTAACTTCTATCCGTGGAG | 6241 |
| Db | 6831 | TGCTCAAGGAGTGAAGGCGAAGGCGTCCACAGTTAAGCTTAACTTCTATCCGTGGAG | 6890 |
| Qy | 6242 | AAGCCTGTAAAGTGAAGCGCCCACTTCGCGCCAGATCTAAATTTGGCTATGGGGCAAGG | 6301 |
| Db | 6891 | AAGCCTGTAAAGTGAAGCGCCCACTTCGCGCCAGATCTAAATTTGGCTATGGGGCAAGG | 6950 |
| Qy | 6302 | AGTCCGGAACCTATCCAGAAAGCGGTTAAACACATCCGCTCCGTTGGAAGGACTTGC | 6361 |
| Db | 6951 | AGTCCGGAACCTATCCAGAAAGCGGTTAAACACATCCGCTCCGTTGGAAGGACTTGC | 7010 |
| Qy | 6362 | TGGAAGACACTGAGACCAATTTGACACCACTCATGCAAAATAGAGTTTCTGCG | 6421 |
| Db | 7011 | TGGAAGACACTGAGACCAATTTGACACCACTCATGCAAAATAGAGTTTCTGCG | 7070 |
| Qy | 6422 | TCCAAACAGAGAGGGGCGGCAAGCCAGCTCGCTTATCGTATTTCCAGATTTGGGG | 6481 |
| Db | 7071 | TCCAAACAGAGAGGGGCGGCAAGCCAGCTCGCTTATCGTATTTCCAGATTTGGGG | 7130 |
| Qy | 6482 | TTGCTGTGCGGAGAAATTTGGGCTTTACATGTTGCTTCCACCTCCCTCAGGCGTGA | 6541 |
| Db | 7131 | TTGCTGTGCGGAGAAATTTGGGCTTTACATGTTGCTTCCACCTCCCTCAGGCGTGA | 7190 |
| Qy | 6542 | TGGGCTCTTCAACGAGTTCCCAATCTCTCTGACAGCGGCTCGAGTTTCTGCTGAATG | 6601 |
| Db | 7191 | TGGGCTCTTCAACGAGTTCCCAATCTCTCTGACAGCGGCTCGAGTTTCTGCTGAATG | 7250 |
| Qy | 6602 | CCTGGAAGCGAAGAAATGCTTATGGCTTCCATATGACACCCGCTGTTTGTACTCAA | 6661 |
| Db | 7251 | CCTGGAAGCGAAGAAATGCTTATGGCTTCCATATGACACCCGCTGTTTGTACTCAA | 7310 |
| Qy | 6662 | CGGTCACTGAGATGACATCCGCTGTTGAGAGTCAATCTACCAATGTTGACTTGGCC | 6721 |
| Db | 7311 | CGGTCACTGAGATGACATCCGCTGTTGAGAGTCAATCTACCAATGTTGACTTGGCC | 7370 |
| Qy | 6722 | CCGAGCCACAGGCGCATTAAGTTCGCTACAGAGCGCTTTACATCGGCGGCCCTCGA | 6781 |
| Db | 7371 | CCGAGCCACAGGCGCATTAAGTTCGCTACAGAGCGCTTTACATCGGCGGCCCTCGA | 7430 |
| Qy | 6782 | CTAATTTCTAAGGGCAGAACTGCGGCTTATCGCGGTTCGCGGAGCGGTGTACTGACGA | 6841 |
| Db | 7431 | CTAATTTCTAAGGGCAGAACTGCGGCTTATCGCGGTTCGCGGAGCGGTGTACTGACGA | 7490 |
| Qy | 6842 | CGAGCTGCGGTATACCTCAGATGTTTGAAGGCGCTTGGGCGCTGTCGAGCTCGGA | 6901 |
| Db | 7491 | CGAGCTGCGGTATACCTCAGATGTTTGAAGGCGCTTGGGCGCTGTCGAGCTCGGA | 7550 |
| Qy | 6902 | AGCTCCAGGAGTGCACGATGCTGTATGCGGAGACGACCTTGTCTGTTATCTGTGAAAGCG | 6961 |
| Db | 7551 | AGCTCCAGGAGTGCACGATGCTGTATGCGGAGACGACCTTGTCTGTTATCTGTGAAAGCG | 7610 |
| Qy | 6962 | CGGCGACCCCAAGAGGACGAGCGGCTTACGGGCTTTCAGGAGCTTATGACTAGTACT | 7021 |
| Db | 7611 | CGGCGACCCCAAGAGGACGAGCGGCTTACGGGCTTTCAGGAGCTTATGACTAGTACT | 7670 |
| Qy | 7022 | CTGCCCCCTTGGGAGCCCGCCAAACCAAGTACGACTTGGAGTTGATTAACATCATGCT | 7081 |
| Db | 7671 | CTGCCCCCTTGGGAGCCCGCCAAACCAAGTACGACTTGGAGTTGATTAACATCATGCT | 7730 |
| Qy | 7082 | CCTTCAATGTGTGAGTCCGCGACGATGCTATGCAAAAGGCTTACTTATCTCACCCGCTG | 7141 |
| Db | 7731 | CCTTCAATGTGTGAGTCCGCGACGATGCTATGCAAAAGGCTTACTTATCTCACCCGCTG | 7790 |

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QY 7142 ACCGACACCCCTTGGCGGGCTGCGTGGAGACAGTACACACTCCAGTCAATT 7201
Db 7791 ACCGACACCCCTTGGCGGGCTGCGTGGAGACAGTACACACTCCAGTCAATT 7850
QY 7202 CTGGCTAGGCAACATCATGATGCGCCACCTTGTGGCAAGGATGATCTGATGA 7261
Db 7851 CTGGCTAGGCAACATCATGATGCGCCACCTTGTGGCAAGGATGATCTGATGA 7910
QY 7262 CTCAITTTCTTCCATCTTCTAGCTCAGGAACAACTTGAAGAGCCCTAGATTGTCAGA 7321
Db 7911 CTCAITTTCTTCCATCTTCTAGCTCAGGAACAACTTGAAGAGCCCTAGATTGTCAGA 7970
QY 7322 TCTAGGGGCGCTGTTACTCCATGAGCCACTTGAACTACTCAGATCATTAACGACTCC 7381
Db 7971 TCTAGGGGCGCTGTTACTCCATGAGCCACTTGAACTACTCAGATCATTAACGACTCC 8030
QY 7382 ATGGCTTAGCGCATTTTCACTCCATAGTACTCTCCAGGTGAGATCAATAGGTGGCTT 7441
Db 8031 ACGGCTTAGCGCATTTTCACTCCATAGTACTCTCCAGGTGAGATCAATAGGTGGCTT 8090
QY 7442 CATGCTCAGGAACACTTGGGGTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAAGTG 7501
Db 8091 CATGCTCAGGAACACTTGGGGTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAAGTG 8150
QY 7502 TCCGGCTAGGCTACTGCTCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACCTTTCA 7561
Db 8151 TCCGGCTAGGCTACTGCTCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACCTTTCA 8210
QY 7562 ACTGGGCTAGTAGGACCAAGCTCAAACTCACTCCAACTCCCGCTGGTCCGAGTTGGATT 7621
Db 8211 ACTGGGCTAGTAGGACCAAGCTCAAACTCACTCCAACTCCCGCTGGTCCGAGTTGGATT 8270
QY 7622 TATCCAGCTGGTTCGTTGCTGTATACGCGGGGAGACATATATACAGCCCTGTCTCGTG 7681
Db 8271 TATCCAGCTGGTTCGTTGCTGTATACGCGGGGAGACATATATACAGCCCTGTCTCGTG 8330
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Db 8331 CCGGACCCCGCTGGTTCATGCTGCTACTCTACTTCTGTAGGGGTAGGCATCTATC 8390
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QY 7802 TTCCC ---TTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCT 7857
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QY 7858 TTTTTTTTCTCTTTTTTTCTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTCC 7917
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QY 7918 GGCTAGCTGTGAAGGTCGCTGAGCGCTTGACTGCAGAGAGTGTGATCTAGGCTCTC 7977
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QY 7978 TGCAGATCAAGT 7989
Db 8631 TGCAGATCAAGT 8642
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RESULT 13
US-10-029-907-6
; Sequence 6, Application US/10029907
; Patent No. 6706874
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/029,907
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857

; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-029-907-6

Query Match 90.7%; Score 7245.6; DB 4; Length 8638;
Best Local Similarity 92.0%; Pred. No. 0;
Matches 7958; Conservative 0; Mismatches 19; Indels 671; Gaps 3;
QY 2 CCAGCCCCGATTTGGGGCGACACTCCACATAGATCACTCCCCTGTGAGGAACACTCT 61
Db 2 CCAGCCCCGATTTGGGGCGACACTCCACATAGATCACTCCCCTGTGAGGAACACTCT 61
QY 62 CTTACGCGAGAAAGCGTCTAGCCATGGGTTAGTATAGTGTGTCGACGCTCCAGGACC 121
Db 62 CTTACGCGAGAAAGCGTCTAGCCATGGGTTAGTATAGTGTGTCGACGCTCCAGGACC 121
QY 122 CCCCCCTCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGG 181
Db 122 CCCCCCTCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGG 181
QY 182 ACGACCGGCTCTTTCTTTGGATCAACCCGCTCAATGCCCTGGAGATTGGGCGTGCCTCC 241
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QY 242 CGAGACTCTAGCCGAGTAGTGTTCGGTTCGCGAAAGGCTTTGTGCTACTGCTGATAGGG 301
Db 242 CGAGACTCTAGCCGAGTAGTGTTCGGTTCGCGAAAGGCTTTGTGCTACTGCTGATAGGG 301
QY 302 TCGTTGCGAGTGCCTCCGGGAGGCTCTCGTAGACCGGTGACCATGAGCAGCAATCTTAAACC 361
Db 302 TCGTTGCGAGTGCCTCCGGGAGGCTCTCGTAGACCGGTGACCATGAGCAGCAATCTTAAACC 361
QY 362 TCAAGAAAAACCAAGGCGCGCCATGATTGAACAAGATGATGACGAGGTTCTCC 421
Db 362 TCAAGAAAAACCAAGGCGCGCCATGATTGAACAAGATGATGACGAGGTTCTCC 421
QY 422 GCGCGCTTGGTGGAGAGGCTATTGCGCTATGACTGGGCAACAGACAATCGGCTGTC 481
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QY 482 TGATGCCCGCTGTTCCGGCTGTGAGCGCAGGGCGCGCGCTTTCTTTTGTCAAGACCGA 541
Db 482 TGATGCCCGCTGTTCCGGCTGTGAGCGCAGGGCGCGCGCTTTCTTTTGTCAAGACCGA 541
QY 542 CTTGTCCGGTCCCTGTAATGAACTGCGAGGACGAGCGCGGCTATCGTGGTGGCCAC 601
Db 542 CTTGTCCGGTCCCTGTAATGAACTGCGAGGACGAGCGCGGCTATCGTGGTGGCCAC 601
QY 602 GACGCGGCTTCTTGGCGAGCTGTGCTGCGATTGTCTAAGCGGGAAGGAGTGGCT 661
Db 602 GACGCGGCTTCTTGGCGAGCTGTGCTGCGATTGTCTAAGCGGGAAGGAGTGGCT 661
QY 662 GCTATTGGGCGAAGTGCCTGGGCGAGGATCTCTGCTCATCTCACCTTGTCTGCGCGAGAA 721
Db 662 GCTATTGGGCGAAGTGCCTGGGCGAGGATCTCTGCTCATCTCACCTTGTCTGCGCGAGAA 721
QY 722 AGTATCCATCATGCTGATGCAATGCGCGGCTCATACGCTTGATCCGGTACTCGTCCC 781
Db 722 AGTATCCATCATGCTGATGCAATGCGCGGCTCATACGCTTGATCCGGTACTCGTCCC 781
QY 782 ATTTCGACCAACCAAGCGAAACATCCATCGAGCGAGAGCTACTCGGATGGAAGCGGCT 841
Db 782 ATTTCGACCAACCAAGCGAAACATCCATCGAGCGAGAGCTACTCGGATGGAAGCGGCT 841
QY 842 TGTGATCAGGATGATCTGGAGCAAGAGCATCAGGGGCTCGCGCCAGCACTGTTCCG 901

| | | | | | | | |
|----|------|--|------|----|------|--|------|
| Db | 842 | TGTCGATCAGGATGATCTGACGAGAGCATCAGGGCTCGGCGACAGCACTGTCG | 901 | Db | 1911 | TACAATATTTTATFACCAAGGCGGAGGACACATTGCAAGTGTGGATCCCCCCTCAACG | 1970 |
| Qy | 902 | CAGGCTCAAGGGCGGCATGCGCGACGGCAGGATCTGCTGCTGACCCATGGGATGCTG | 961 | Qy | 1804 | ----- | 1803 |
| Db | 902 | CAGGCTCAAGGGCGGCATGCGCGACGGCAGGATCTGCTGCTGACCCATGGGATGCTG | 961 | Db | 1971 | TTGCGGGGGCGCGATGCGGTCACTCTCTCAGGTGCGGATCCACCCAGAGCTAATCT | 2030 |
| Qy | 962 | CTTGCCGAATATCATGCTGGAAATGGCGCTTTCTGGATTCATGACTGTGCGCGGT | 1021 | Qy | 1804 | ----- | 1803 |
| Db | 962 | CTTGCCGAATATCATGCTGGAAATGGCGCTTTCTGGATTCATGACTGTGCGCGGT | 1021 | Db | 2031 | TTACCATACCAAAATCTTTGCTGCGCATACTCGGTCCACTCATGTGTCTCAGGCTGTA | 2090 |
| Qy | 1022 | GGGTGTGGGGACCGCTATCAGACATAGCGTTGGCTACCGGTGATATTGCTGAAGAGCT | 1081 | Qy | 1804 | ----- | 1803 |
| Db | 1022 | GGGTGTGGGGACCGCTATCAGACATAGCGTTGGCTACCGGTGATATTGCTGAAGAGCT | 1081 | Db | 2091 | TAACAAAGTGGCGTACTTTGTCGCGCACACGGGCTCATTTGTCGATGATGCTGGTGC | 2150 |
| Qy | 1082 | TGCGCGGAATGGGTGACCGCTTCTGCTGCTTTAGCGTATCGCGCTCCCGATTGCA | 1141 | Qy | 1804 | ----- | 1803 |
| Db | 1082 | TGCGCGGAATGGGTGACCGCTTCTGCTGCTTTAGCGTATCGCGCTCCCGATTGCA | 1141 | Db | 2151 | GGNAGTTGCTGGGGTCAATTATGTCCAAATGCTCTCATGAAGTTGGCGCACTGACAG | 2210 |
| Qy | 1142 | GCSCATCGCTTCTATCGCTTCTTGACGAGTTCTTCTGAGTT-----TAAAC | 1189 | Qy | 1804 | ----- | 1803 |
| Db | 1142 | GCSCATCGCTTCTATCGCTTCTTGACGAGTTCTTCTGAGTT-----TAAAC | 1189 | Db | 2211 | GTACGTACGTTTATGACCATCTCACCCACTGCGGACTGGGCCACGCGGGCTACGAG | 2270 |
| Qy | 1190 | AGACCAACACGGTTTCCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCCCCCCCTA | 1249 | Qy | 1804 | ----- | 1803 |
| Db | 1202 | AGACCAACACGGTTTCCCTCTAGCGGATCAATTCG-----CCCCCCCCCTA | 1250 | Db | 2271 | ACCTTCGGTGGCAGTTGAGCCCGTCTTCTCTGATATGAGACCAAGTTATCACCT | 2330 |
| Qy | 1250 | ACGTTACTGGCGAAGCGCTTGGATAGAGCGGCTGCTGTTGCTATATGTTATTT | 1309 | Qy | 1804 | ----- | 1803 |
| Db | 1251 | ACGTTACTGGCGAAGCGCTTGGATAGAGCGGCTGCTGTTGCTATATGTTATTT | 1310 | Db | 2331 | GGGGGCGAGACCGCGGCGTGTGGGACATCATCTTGGGCTGCGCGTCTCGCGCCGCA | 2390 |
| Qy | 1310 | CCACCATATTCGCGTCTTTTGGCAATGTAGGCGCGGAACTGGCCCTGCTCTTTGA | 1369 | Qy | 1804 | ----- | 1803 |
| Db | 1311 | CCACCATATTCGCGTCTTTTGGCAATGTAGGCGCGGAACTGGCCCTGCTCTTTGA | 1370 | Db | 2391 | GGGGGAGGAGATACATCTGGGACCGCGACAGACCTTGAAGGCGAGGGGTGGCGACTCC | 2450 |
| Qy | 1370 | CGAGCATTCCTAGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGTCTGTTGAATGTCG | 1429 | Qy | 1804 | ----- | 1803 |
| Db | 1371 | CGAGCATTCCTAGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGTCTGTTGAATGTCG | 1430 | Db | 2451 | TCGCGCTATTAATCGGCTACTCCCAACAGACGAGGCTCTTGGCTGATCATCACTA | 2510 |
| Qy | 1430 | TGAAGGAGCAGTCTCTGAGAGCTTTTGAAGACAAACAGTCTGAGCGACCTTT | 1489 | Qy | 1862 | GCCTCAAGGCGCGGACAGGAAACAGGTCTGAGGGGAGGTCCAAAGTGGTCTCCACCGCAA | 1921 |
| Db | 1431 | TGAAGGAGCAGTCTCTGAGAGCTTTTGAAGACAAACAGTCTGAGCGACCTTT | 1490 | Db | 2511 | GCCTCAAGGCGCGGACAGGAAACAGGTCTGAGGGGAGGTCCAAAGTGGTCTCCACCGCAA | 2570 |
| Qy | 1490 | GCAGGACGCGAACCCCGCTCTGGACAGTCCCTCTCGGCGCAAAAGCCACGTGTAT | 1549 | Qy | 1922 | CACAAATTTTCTGGCGACCTGCGTCAATGGCGTGTGGACTGTCTATCATGGTCCG | 1981 |
| Db | 1491 | GCAGGACGCGAACCCCGCTCTGGACAGTCCCTCTCGGCGCAAAAGCCACGTGTAT | 1550 | Db | 2571 | CACAAATTTTCTGGCGACCTGCGTCAATGGCGTGTGGACTGTCTATCATGGTCCG | 2630 |
| Qy | 1550 | AAGATACACCTGCAAGGGCGCAACCCCGTGTGAGTGTGAGTGTGATGTTGG | 1609 | Qy | 1982 | GCTCAAGACCTTGGCGCCCAAGGGCCCAATCACCAAAATGTACCAATGTGGACC | 2041 |
| Db | 1551 | AAGATACACCTGCAAGGGCGCAACCCCGTGTGAGTGTGAGTGTGATGTTGG | 1610 | Db | 2631 | GCTCAAGACCTTGGCGCCCAAGGGCCCAATCACCAAAATGTACCAATGTGGACC | 2690 |
| Qy | 1610 | AAAGAGTCAATGGCTCTCTCAAGCGTATTCACAGGGGCTCAAGGATGCCAGAGG | 1669 | Qy | 2042 | AGGACCTCTGCTGGCTGGCAAGCGCCCCCGGGCGCTTCTTGACACCATGCACTGCG | 2101 |
| Db | 1611 | AAAGAGTCAATGGCTCTCTCAAGCGTATTCACAGGGGCTCAAGGATGCCAGAGG | 1670 | Db | 2691 | AGGACCTCTGCTGGCTGGCAAGCGCCCCCGGGCGCTTCTTGACACCATGCACTGCG | 2750 |
| Qy | 1670 | TACCCCATTTGATGGGATCTGATCTGGGCTCGGTGACATGCTTTACATGTTTGT | 1729 | Qy | 2102 | GCAGCTCGGACCTTTTACTTGGTCAAGGATGCGCGATGTCTTCCCGTGGCGCGGG | 2161 |
| Db | 1671 | TACCCCATTTGATGGGATCTGATCTGGGCTCGGTGACATGCTTTACATGTTTGT | 1730 | Db | 2751 | GCAGCTCGGACCTTTTACTTGGTCAAGGATGCGCGATGTCTTCCCGTGGCGCGGG | 2810 |
| Qy | 1730 | CGAGGTTAAAAACGTTAGGCCCGCCGACCAAGGAGCGTGTGTTTCTTTGAAAAAC | 1789 | Qy | 2162 | GCAGCTCGGACCTTTTACTTGGTCAAGGATGCGCGATGTCTTCCCGTGGCGCGGG | 2221 |
| Db | 1731 | CGAGGTTAAAAACGTTAGGCCCGCCGACCAAGGAGCGTGTGTTTCTTTGAAAAAC | 1790 | Db | 2811 | GCAGCTCGGACCTTTTACTTGGTCAAGGATGCGCGATGTCTTCCCGTGGCGCGGG | 2870 |
| Qy | 1790 | ACGATATACCATG----- | 1803 | Qy | 2222 | GCAGCTCGGACCTTTTACTTGGTCAAGGATGCGCGATGTCTTCCCGTGGCGCGGG | 2281 |
| Db | 1791 | ACGATATACCATG----- | 1803 | Db | 2871 | GCAGCTCGGACCTTTTACTTGGTCAAGGATGCGCGATGTCTTCCCGTGGCGCGGG | 2930 |
| Qy | 1804 | ----- | 1803 | Qy | 2282 | CCGAGGGGTTGCGAAGCGGTGACATTTGTACCGCTCGAGTCTATGGAACCACTATGC | 2341 |
| Db | 1851 | TGATACTCTTGACCTTGTACCGCACTATAGCTGTTTCTCGCTAGGCTCATATGGTGT | 1910 | Db | 2931 | CCGAGGGGTTGCGAAGCGGTGACATTTGTACCGCTCGAGTCTATGGAACCACTATGC | 2990 |
| Qy | 1804 | ----- | 1803 | Qy | 2342 | GGTCCCGGTTCTTCAAGGACCACTCGTCCCTCCCGCGTACCGCAGACATTCAGGTGG | 2401 |

| | | | |
|----|------|---|------|
| QY | 2402 | CCCATCTACACGCCCCCTACTGTTAGCGCAGAGCACTAAGAGTGC CGGCTCGGTATCGAG | 2461 |
| Db | 3051 | CCCATCTACACGCCCTTACTGGTAGCGGCAAGACACTAAGAGTGC CGGCTCGGTATCGAG | 3110 |
| QY | 2462 | CCCAAGGGTATAAGGTCTTGTCTCTGAACCCGTCCTGTCGCCGCCACCTTAGGTTTTCGGGG | 2521 |
| Db | 3111 | CCCAAGGGTATAAGGTCTTGTCTCTGAACCCGTCCTGTCGCCGCCACCTTAGGTTTTCGGGG | 3170 |
| QY | 2522 | CGTATATGTCTTAAGGCACATGGTATCAGACCTTAACATCAGAAACCGGGTAAAGCAACATCA | 2581 |
| Db | 3171 | CGTATATGTCTTAAGGCACATGGTATCAGACCTTAACATCAGAAACCGGGTAAAGCAACATCA | 3230 |
| QY | 2582 | CCACGGGTGCCCCCATCAGGTACTCCACCTATATGGCAAGTTTCTTTGCCGACGGTGGTTGCT | 2641 |
| Db | 3231 | CCACGGGTGCCCCCATCAGGTACTCCACCTATATGGCAAGTTTCTTTGCCGACGGTGGTTGCT | 3290 |
| QY | 2642 | CTGGGGGGCGCTATGACATCATATAATATGTGATGAGTGCCACTCAACTGACTCGACCACTA | 2701 |
| Db | 3291 | CTGGGGGGCGCTATGACATCATATAATATGTGATGAGTGCCACTCAACTGACTCGACCACTA | 3350 |
| QY | 2702 | TCCTGGGCATCGGCACAGTCTCTGACCAAGGGAGACGGCTGGAGCGGACTCGTCTGTGC | 2761 |
| Db | 3351 | TCCTGGGCATCGGCACAGTCTCTGACCAAGGGAGACGGCTGGAGCGGACTCGTCTGTGC | 3410 |
| QY | 2762 | TCGCCACCGGTACGCCCTCCGGATCGGTACCGTGCCACATCCAAACATCGAGAGAGTGG | 2821 |
| Db | 3411 | TCGCCACCGGTACGCCCTCCGGATCGGTACCGTGCCACATCCAAACATCGAGAGAGTGG | 3470 |
| QY | 2822 | CTCTGTCCAGACTGGAGAAATCCCTTTTATGGCAAAAGCCATCCCATCGAGACCATCA | 2881 |
| Db | 3471 | CTCTGTCCAGACTGGAGAAATCCCTTTTATGGCAAAAGCCATCCCATCGAGACCATCA | 3530 |
| QY | 2882 | AGGGGGGAGGCACCTCATTTCTGCCATTCCAGAGAAATGTGATGAGCTCGCCGCGA | 2941 |
| Db | 3531 | AGGGGGGAGGCACCTCATTTCTGCCATTCCAGAGAAATGTGATGAGCTCGCCGCGA | 3590 |
| QY | 2942 | AGCTGTCCGGCCCTCGGACTCAATGCTGTAGCATATTACCGGGGCTTTGATGTATCCGTCA | 3001 |
| Db | 3591 | AGCTGTCCGGCCCTCGGACTCAATGCTGTAGCATATTACCGGGGCTTTGATGTATCCGTCA | 3550 |
| QY | 3002 | TACCAACTAGCGGAGAGCTCATTTGCTGTAGCAACGGACGCTCTTAATGACGGGCTTTACCG | 3061 |
| Db | 3651 | TACCAACTAGCGGAGAGCTCATTTGCTGTAGCAACGGACGCTCTTAATGACGGGCTTTACCG | 3710 |
| QY | 3062 | GCGATTTGCACTCAGTGATCGACTGCNAATCATGTGTCAACCGACAGACGTGCACTTCAGCC | 3121 |
| Db | 3711 | GCGATTTGCACTCAGTGATCGACTGCNAATCATGTGTCAACCGACAGACGTGCACTTCAGCC | 3770 |
| QY | 3122 | TGACCCGACCTTCAACATTGAGACGACGACCGTGCCCAAGACGGGCTGTCAAGCTCGC | 3181 |
| Db | 3771 | TGACCCGACCTTCAACATTGAGACGACGACCGTGCCCAAGACGGGCTGTCAAGCTCGC | 3830 |
| QY | 3182 | AGCGGGAGCGAGGACTGTGTAGGGGACGAGATGGGCATTTACAGTTTGTGATCTCCAGGAG | 3241 |
| Db | 3831 | AGCGGGAGCGAGGACTGTGTAGGGGAGGATGGGCATTTACAGTTTGTGATCTCCAGGAG | 3890 |
| QY | 3242 | AACGGCCCTCGGGCATGTTCCATTCTCTCGTTCTGTGCGAGTGTCTATGACGCGGGCTGTG | 3301 |
| Db | 3891 | AACGGCCCTCGGGCATGTTCCATTCTCTCGTTCTGTGCGAGTGTCTATGACGCGGGCTGTG | 3950 |
| QY | 3302 | CTTTGGTACGAGCTCAAGCCCGCGAGACCTCAGTTAGTTTGGGGCTTACTTAAACACAC | 3361 |
| Db | 3951 | CTTTGGTACGAGCTCAAGCCCGCGAGACCTCAGTTAGTTTGGGGCTTACTTAAACACAC | 4010 |
| QY | 3362 | CAGGTTGCCGCTGTGCCAGGACATCTGGAGTTCTGGGAGAGCGTCTTTTACAGGCGCTCA | 3421 |
| Db | 4011 | CAGGTTGCCGCTGTGCCAGGACATCTGGAGTTCTGGGAGAGCGTCTTTTACAGGCGCTCA | 4070 |
| QY | 3422 | CCCACTAGAGCGCCATTTCTTGTCCGACTTAAGCAGCAGCAGAGACAACTTCCCTACC | 3481 |
| Db | 4071 | CCCACTAGAGCGCCATTTCTTGTCCGACTTAAGCAGCAGCAGAGACAACTTCCCTACC | 4130 |

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|----|------|---|------|
| QY | 3482 | TGTTAGCATATACGAGGCTACGGTGTGCGCAGGGCTCAGGCTCCACCTGCCATCGTGGGACC | 3541 |
| DB | 4131 | TGGTAGCATATACAGGCTACGGTGTGCGCCAGGGCTCAGGCTCCACCTCCATCGTGGGACC | 4190 |
| QY | 3542 | AAATGTGGAAGTGTCTCATACGGCTAAAGCCTACGCTGCACGGGCCAACGCCCTGCTGT | 3601 |
| DB | 4191 | AAATGTGGAAGTGTCTCATACGGCTAAAGCCTACGCTGCACGGGCCAACGCCCTGCTGT | 4250 |
| QY | 3602 | ATAGGCTGGGAGCCGTTTCAAAACGAGGTTTACTACACACACCCCATAAACAAATACATCA | 3661 |
| DB | 4251 | ATAGGCTGGGAGCCGTTTCAAAACGAGGTTTACTACACACACCCCATAAACAAATACATCA | 4310 |
| QY | 3662 | TGGCATGATGTCCGGCTGACCTGAGAGTGTTCAGCAGACACTCGGTCTGTTAGGCGGAG | 3721 |
| DB | 4311 | TGGCATGATGTCCGGCTGACCTGAGAGTGTTCAGCAGACACTCGGTCTGTTAGGCGGAG | 4370 |
| QY | 3722 | TCCTAGCAGCTCTCGCCCGGTATTGCCCTGACAAACAGGACGCGTGTTCATTGTGGGACGGA | 3781 |
| DB | 4371 | TCCTAGCAGCTCTCGCCCGGTATTGCCCTGACAAACAGGACGCGTGTTCATTGTGGGACGGA | 4430 |
| QY | 3782 | TCATCTTTCCGGAAGCCGCGCCATCATTCGCCGACAGGGAAGTCCTTTACCGGGAGTTCG | 3841 |
| DB | 4431 | TCATCTTTCCGGAAGCCGCGCCATCATTCGCCGACAGGGAAGTCCTTTACCGGGAGTTCG | 4490 |
| QY | 3842 | ATGAGATGGAAGAGTGGCCCTCACACCTCCCTTACATCGAACAGGAGTATCGAGCTGC | 3901 |
| DB | 4491 | ATGAGATGGAAGAGTGGCCCTCACACCTCCCTTACATCGAACAGGAGTATCGAGCTGC | 4550 |
| QY | 3902 | AACAAATTCAAACAGAGGCAATCGGTTGCTGCAACACAGCCACCAAGCAAGCGGAGGCTG | 3961 |
| DB | 4551 | AACAAATTCAAACAGAGGCAATCGGTTGCTGCAACACAGCCACCAAGCAAGCGGAGGCTG | 4610 |
| QY | 3962 | CTGCTCCCTGGTGGAAATCCAAGTGGCGGACCCCTCGAAAGCCTTCTGGCGGAACATATGT | 4021 |
| DB | 4611 | CTGCTCCCTGGTGGAAATCCAAGTGGCGGACCCCTCGAAAGCCTTCTGGCGGAACATATGT | 4670 |
| QY | 4022 | GGAAATTCATCAGGGGATACAAATTTAGCAGGCTTGTCCAATCTGCTCTGGCAACCCCG | 4081 |
| DB | 4671 | GGAAATTCATCAGGGGATACAAATTTAGCAGGCTTGTCCAATCTGCTCTGGCAACCCCG | 4730 |
| QY | 4082 | CGATAGCATCACATGATGGCATTCACAGCCTCTATCACCAGCCGCTCACCCACCAATTA | 4141 |
| DB | 4731 | CGATAGCATCACATGATGGCATTCACAGCCTCTATCACCAGCCGCTCACCCACCAATTA | 4790 |
| QY | 4142 | CCCTCCCTGTTTAAACATCCTGGGGGATGGGTGGCCGCCCAAATTTGCTCTCCACAGCGCTG | 4201 |
| DB | 4791 | CCCTCCCTGTTTAAACATCCTGGGGGATGGGTGGCCGCCCAAATTTGCTCTCCACAGCGCTG | 4850 |
| QY | 4202 | CTTCTGCTTTTCGTAGGCGCGGATCGCTGGAGCGCTGTGTGCAGCATAGGCCCTTGGGA | 4261 |
| DB | 4851 | CTTCTGCTTTTCGTAGGCGCGGATCGCTGGAGCGCTGTGTGCAGCATAGGCCCTTGGGA | 4910 |
| QY | 4262 | AGTGCTTGTGGATATTTTGGCAGGTTATGGACAGGGGTGGCAGGGCGCTCGTGGCCT | 4321 |
| DB | 4911 | AGTGCTTGTGGATATTTTGGCAGGTTATGGACAGGGGTGGCAGGGCGCTCGTGGCCT | 4970 |
| QY | 4322 | TTAAGGTCATGAGCGCGAGATCCCTCCACCGAGGACCTGGTTAACTACTCCCTGGCTTA | 4381 |
| DB | 4971 | TTAAGGTCATGAGCGCGAGATCCCTCCACCGAGGACCTGGTTAACTACTCCCTGGCTTA | 5030 |
| QY | 4382 | TCCTCTCCCTCGGGCCCTAGTCTGTCGGGTGTGTGCGCAGCATATCTGCGTTCGCAACG | 4441 |
| DB | 5031 | TCCTCTCCCTCGGGCCCTAGTCTGTCGGGTGTGTGCGCAGCATATCTGCGTTCGCAACG | 5090 |
| QY | 4442 | TGGGCCACAGGGAGGGGCTGTGCACTGTGATGAACCGGCTGATAGCGTTTCGCTTCGCGG | 4501 |
| DB | 5091 | TGGGCCACAGGGAGGGGCTGTGCACTGTGATGAACCGGCTGATAGCGTTTCGCTTCGCGG | 5150 |
| QY | 4502 | GTAACACAGCTCTCCCCACGCACTATGTGCTCTGAGAGCGACGCTGCAGCAGCTGTCACTC | 4561 |
| DB | 5151 | GTAACACAGCTCTCCCCACGCACTATGTGCTCTGAGAGCGACGCTGCAGCAGCTGTCACTC | 5210 |
| QY | 4562 | AGATCCTCTCTAGTCTTATCCATCCTCAGCTGTGTGAAGAGGCTTTCACCAAGTGGATCAACG | 4621 |

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|----|------|--|------|----|------|---|------|
| QY | 481 | CTGATCCCGCGCTGTTCGGCTGTTCAGCGACGGGCGCCCGTCTTTTGTCAAGACG | 540 | Db | 1550 | TAAGATACACCTGCAAGGCGGCAACACCCAGTCCACGTTGTGTAGTTGATGTTGTG | 1609 |
| Db | 481 | CTGATCCCGCGCTGTTCGGCTGTTCAGCGACGGGCGCCCGTCTTTTGTCAAGACG | 540 | QY | 1609 | GAAGAGTCAAAATGGCTCTCTCAAGCGTATTCAACAAGGGCTGAAGGATCCCAAG | 1668 |
| QY | 541 | ACCTGTCCGGTCCCTGATGAATGAATGCAGAGACGAGCGCGGCTATCGTGGCTGGCA | 600 | Db | 1610 | GAAGAGTCAAAATGGCTCTCTCAAGCGTATTCAACAAGGGCTGAAGGATCCCAAG | 1669 |
| Db | 541 | ACCTGTCCGGTCCCTGATGAATGAATGCAGAGACGAGCGCGGCTATCGTGGCTGGCA | 600 | QY | 1669 | GTACCCCATTTGATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTGTTAG | 1728 |
| QY | 601 | CGACGGCGCTTCTTTCGCGAGCTGTCTCGAGCTGTCTCACTGAAGCGGAAGGACTGCG | 660 | Db | 1670 | GTACCCCATTTGATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTGTTAG | 1729 |
| Db | 601 | CGACGGCGCTTCTTTCGCGAGCTGTCTCGAGCTGTCTCACTGAAGCGGAAGGACTGCG | 660 | QY | 1729 | TCGAGTTTAAAAAGCTGTAGGCCCGCCGAAACACGAGGACGTGGTTTCTTCTTGA | 1788 |
| QY | 661 | TGCTATTTGGCGAAGTGCOCGGGCGAGATCTCTGTCTCTCACTTGTCTTGTGCGAGA | 720 | Db | 1730 | TCGAGTTTAAAAAGCTGTAGGCCCGCCGAAACACGAGGACGTGGTTTCTTCTTGA | 1789 |
| Db | 661 | TGCTATTTGGCGAAGTGCOCGGGCGAGATCTCTGTCTCTCACTTGTCTTGTGCGAGA | 720 | QY | 1789 | CACGATAATACCATG | 1803 |
| QY | 721 | AGTATCCATCATGGCTGATGCAATGCGCGGCTGCATACGTTGATCCGGCTACCTGCC | 780 | Db | 1790 | CACGATAATACCATGCAACGGGAGATGGCAGCATCGTGGGAGGCGGGTTTTCGTAGGT | 1849 |
| Db | 721 | AGTATCCATCATGGCTGATGCAATGCGCGGCTGCATACGTTGATCCGGCTACCTGCC | 780 | QY | 1804 | ----- | 1803 |
| QY | 781 | CATTGACCAACCAAGCGAAACATCGCATCGAGCGACGTAATCTCGATGGAAGCCGGTC | 840 | Db | 1850 | CTGATACTCTTGACCTTGTACCGCATATAAGCTGTTCTCGTAGGCTCATATGGTGG | 1909 |
| Db | 781 | CATTGACCAACCAAGCGAAACATCGCATCGAGCGACGTAATCTCGATGGAAGCCGGTC | 840 | QY | 1804 | ----- | 1803 |
| QY | 841 | TTGTGATCAGGATGATCTGACGAAAGAGCATCAGGGGCTCGCGCAGCGAACTGTTCC | 900 | Db | 1910 | TTACAATATTTTATCACCAGGCGGAGGCACACTTGCAGTGTGGATCCCCCCTCAAC | 1969 |
| Db | 841 | TTGTGATCAGGATGATCTGACGAAAGAGCATCAGGGGCTCGCGCAGCGAACTGTTCC | 900 | QY | 1804 | ----- | 1803 |
| QY | 901 | CCAGGCTCAAGCGCGCATGCCCCGACGCGAGGATCTCGTGTGACCCATGGCGATGCC | 960 | Db | 1970 | GTTCGGGGGGCGGATGCCGTCATCTCTCTCAGTGGCGCATCCACCAGAGCTAATC | 2029 |
| Db | 901 | CCAGGCTCAAGCGCGCATGCCCCGACGCGAGGATCTCGTGTGACCCATGGCGATGCC | 960 | QY | 1804 | ----- | 1803 |
| QY | 961 | GCTTCCGGAATCATGTGGGAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGC | 1020 | Db | 2030 | TTTACCATCACCAAAATCTTGTCGCATACCTCGTCCACTCATGTGTGCTCCAGGTG | 2089 |
| Db | 961 | GCTTCCGGAATCATGTGGGAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGC | 1020 | QY | 1804 | ----- | 1803 |
| QY | 1021 | TGGGTGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCGCTGATATGCTGAAGAGC | 1080 | Db | 2090 | ATAACAAAGTCCGTACTTGTGCGCGCACAGGGCTCAITTCGTGCAATGCTGTTG | 2149 |
| Db | 1021 | TGGGTGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCGCTGATATGCTGAAGAGC | 1080 | QY | 1804 | ----- | 1803 |
| QY | 1081 | TTGGGCGGAATGGGTGACCGCTCTCGTCTTTACGGTATCGCGCTCCCGATTCCG | 1140 | Db | 2150 | CGAAGTTGTGGGGTCAITATGTCCAAATGGCTCTCATGAGTTGGCCGACGAC | 2209 |
| Db | 1081 | TTGGGCGGAATGGGTGACCGCTCTCGTCTTTACGGTATCGCGCTCCCGATTCCG | 1140 | QY | 1804 | ----- | 1803 |
| QY | 1141 | AGCGCATCGCTTCTATCGCTTCTTGAAGTCTTCTGAGTT-----TAAA | 1188 | Db | 2210 | GGTACGTAGTTTATGACCATCTCACCCACTGCGGCACTGGGCCCAACGCGGCTACGA | 2269 |
| Db | 1141 | AGCGCATCGCTTCTATCGCTTCTTGAAGTCTTCTGAGTT-----TAAA | 1200 | QY | 1804 | ----- | 1803 |
| QY | 1189 | CAGACCAACCGTTTCCCTTAGCGGGATCAATTCGCGCCCTCTCCCTCCCGCCCTCT | 1248 | Db | 2270 | GACCTTGGGTTGGGATGAGCCCGTCTTCTCTGATATGGAGACCAAGTTATCAC | 2329 |
| Db | 1201 | CAGACCAACCGTTTCCCTTAGCGGGATCAATTCGCG-----CCCGCCCTCT | 1249 | QY | 1804 | ----- | 1803 |
| QY | 1249 | AACGTTACTGGCGGAGCGCTTGGAAATAGCGCGGTGCGTTGCTATATGTTATTT | 1308 | Db | 2330 | TGGGGGCGAGACACCGCGCGCTGTGGGGACATCATCTTGGGCTGCCCTCTCCGCCGC | 2389 |
| Db | 1250 | AACGTTACTGGCGGAGCGCTTGGAAATAGCGCGGTGCGTTGCTATATGTTATTT | 1309 | QY | 1804 | ----- | 1803 |
| QY | 1309 | TCCACCATATGCGCTTCTTGGCAATGTAGGGGCGCGAAACCTGGCCCTGTCTTCTTG | 1368 | Db | 2390 | AGGGGAGGGAGATACATCTGGGACCGGCAGACAGCCTTTAAAGGGCAGGGTGGCGACTC | 2449 |
| Db | 1310 | TCCACCATATGCGCTTCTTGGCAATGTAGGGGCGCGAAACCTGGCCCTGTCTTCTTG | 1369 | QY | 1804 | ---GCGCTTATTCGCGCTACTCCCAACAGACGCGAGGCTACTTGGCTGCATCACT | 1860 |
| QY | 1369 | ACGAGATTCCTAGGGGTCTTCCCTCTCGCCCAAGAGGATGCAAGGTCTGTTGAATGTC | 1428 | Db | 2450 | CTCGCGCTTATTCGCGCTACTCCCAACAGACGCGAGGCTACTTGGCTGCATCACT | 2509 |
| Db | 1370 | ACGAGATTCCTAGGGGTCTTCCCTCTCGCCCAAGAGGATGCAAGGTCTGTTGAATGTC | 1429 | QY | 1861 | AGCCTCACAGCGCGGACAGGAACAGAGTTCGAGGGGAGGTCCAAGTGTCTTCCACCGCA | 1920 |
| QY | 1429 | GTGAAGGAGAGTCTCTCTGGAAGTCTTCTGAAGACAAACAGTCTGTAGCGACCTT | 1488 | Db | 2510 | AGCCTCACAGCGCGGACAGGAACAGAGTTCGAGGGGAGGTCCAAGTGTCTTCCACCGCA | 2569 |
| Db | 1430 | GTGAAGGAGAGTCTCTCTGGAAGTCTTCTGAAGACAAACAGTCTGTAGCGACCTT | 1489 | QY | 1921 | ACAAATCTTCTCGCGACCTGCGTCAATGCGGTGTGTGAGCTGTCTATCATGTGTC | 1980 |
| QY | 1489 | TGCAGCAGCGGAACCCCGCAAGTGTCTTGGCGCAAAAGCAACGCTGTA | 1548 | Db | 2570 | ACAAATCTTCTCGCGACCTGCGTCAATGCGGTGTGTGAGCTGTCTATCATGTGTC | 2629 |
| Db | 1490 | TGCAGCAGCGGAACCCCGCAAGTGTCTTGGCGCAAAAGCAACGCTGTA | 1549 | QY | 1981 | GSCTCAAGACCTTTCGCGGCCCAAGGGCCCAATCACCAATGTACCAATGTGGAC | 2040 |
| QY | 1549 | TAAGATACACCTGCAAGGCGGCAACCCAGTGCACGTTGTGATGTTGTTG | 1608 | | | | |

Db 2630 GGCTAAAGACCTTGC CGGCCCAAGGCCCAATCACCAATGTACCAATGTGGAC 2689
Qy 2041 CAGGACCTCGTGGCTGGCAAGCGCCCCCGGGCGCGTTCCTTGACACCATGCACTCGC 2100
Db 2690 CAGGACCTCGTGGCTGGCAAGCGCCCCCGGGCGCGTTCCTTGACACCATGCACTCGC 2749
Qy 2101 GGCAGCTCGGACCTTACTTGTGTACGAGGATGCGGATGTCAATTCGGTGGCGCGGG 2160
Db 2750 GGCAGCTCGGACCTTACTTGTGTACGAGGATGCGGATGTCAATTCGGTGGCGCGGG 2809
Qy 2161 GGCAGCAGCAGGGGAGCGCTACTCTCCCGCCCGCGCTCTCTACTTGAAGGGCTCTTCG 2220
Db 2810 GGCAGCAGCAGGGGAGCGCTACTCTCCCGCCCGCGCTCTCTACTTGAAGGGCTCTTCG 2869
Qy 2221 GCGGTGCCACTCTCTGCCCCCTCGGGGCAAGCTGTGGGCACTTTTCGGGCTCGCGTGC 2280
Db 2870 GCGGTGCCACTCTCTGCCCCCTCGGGGCAAGCTGTGGGCACTTTTCGGGCTCGCGTGC 2929
Qy 2281 ACCCGAGGGGTGGCAAGCGGTGACCTTTGTACCGGTGAGTCTATGGAACCACTATG 2340
Db 2930 ACCCGAGGGGTGGCAAGCGGTGACCTTTGTACCGGTGAGTCTATGGAACCACTATG 2989
Qy 2341 CCGTCCCCGGTCTTCAAGCAAACTCGTCCCTCCGCGGTACCGCAGACATTCAGGTG 2400
Db 2990 CCGTCCCCGGTCTTCAAGCAAACTCGTCCCTCCGCGGTACCGCAGACATTCAGGTG 3049
Qy 2401 GCCCATCTACCGCCCTACTGTAGCGGCAAGACACTAAGGTCCGCGTGCCTATGCA 2460
Db 3050 GCCCATCTACCGCCCTACTGTAGCGGCAAGACACTAAGGTCCGCGTGCCTATGCA 3109
Qy 2461 GCCCAAGGGTAAAGTCTGTCTCTGAACCGGTCCGTCGCGGCAACCTAGTTCGGG 2520
Db 3110 GCCCAAGGGTAAAGTCTGTCTCTGAACCGGTCCGTCGCGGCAACCTAGTTCGGG 3169
Qy 2521 CGGTATATGTCTAAGGCACATGGTATCGACCTACATCAGAACCGGGTAAAGCACTC 2580
Db 3170 CGGTATATGTCTAAGGCACATGGTATCGACCTACATCAGAACCGGGTAAAGCACTC 3229
Qy 2581 ACCACGGGTGCCCCATCACGTACTTCCACTATGGCAAGTTCCTTCCGCGCGGTGGTGC 2640
Db 3230 ACCACGGGTGCCCCATCACGTACTTCCACTATGGCAAGTTCCTTCCGCGCGGTGGTGC 3289
Qy 2641 TCTGGGGCGCTATGACATCATATATGTGATGATGCCACTCAACTGATCGACCACT 2700
Db 3290 TCTGGGGCGCTATGACATCATATATGTGATGATGCCACTCAACTGATCGACCACT 3349
Qy 2701 ATCTCTGGGCATCGGCACAGTCTCTGACCAAGCGAGCGCTGGAGCGCGACTCGTGTG 2760
Db 3350 ATCTCTGGGCATCGGCACAGTCTCTGACCAAGCGAGCGCTGGAGCGCGACTCGTGTG 3409
Qy 2761 CTCGCCACCGCTACGCTCCGGATCGGTACCGTCCGACATCCCAACATCGAGAGGTG 2820
Db 3410 CTCGCCACCGCTACGCTCCGGATCGGTACCGTCCGACATCCCAACATCGAGAGGTG 3469
Qy 2821 GCTCTGTCCAGCATGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC 2880
Db 3470 GCTCTGTCCAGCATGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC 3529
Qy 2881 AAGGGGGGAGGACCTCATTTCTGCCATTCGAAGAAATGTGATGAGCTCGCCGCG 2940
Db 3530 AAGGGGGGAGGACCTCATTTCTGCCATTCGAAGAAATGTGATGAGCTCGCCGCG 3589
Qy 2941 AAGTGTCCGCTCGGACCTCAATGCTGTAGCATATTTACCGGGGCTTGTATTCGTC 3000
Db 3590 AAGTGTCCGCTCGGACCTCAATGCTGTAGCATATTTACCGGGGCTTGTATTCGTC 3649
Qy 3001 ATACCAACTAGCGAGACGTCAATGCTGTAGCAACGGACGCTCTAATGACGGGCTTTACC 3060
Db 3650 ATACCAACTAGCGAGACGTCAATGCTGTAGCAACGGACGCTCTAATGACGGGCTTTACC 3709
Qy 3061 GGCATTTTCAGTCAAGTATCGAATCATGTGTCAACCAAGACGATTCGCTCCAGCGCT 3120
Db 3710 GGCATTTTCAGTCAAGTATCGAATCATGTGTCAACCAAGACGATTCGCTCCAGCGCT 3769

Qy 3121 CTGGACCCGACCTTACCATTTGAGACGACGACCGTGGCAACAAGCCGGTGTACGCTCG 3180
Db 3770 CTGGACCCGACCTTACCATTTGAGACGACGACCGTGGCAACAAGCCGGTGTACGCTCG 3829
Qy 3181 CAGCGCGAGGCGAGGACCTGGTAGGGGCAAGATGGGCAATTTACAGGTTTGTGATCCAGGA 3240
Db 3830 CAGCGCGAGGCGAGGACCTGGTAGGGGCAAGATGGGCAATTTACAGGTTTGTGATCCAGGA 3889
Qy 3241 GAAACGGCCCTCGGGCATGTTTCTCGGTTCTGAGTGTGAGTGTATGACCGGGCTGT 3300
Db 3890 GAAACGGCCCTCGGGCATGTTTCTCGGTTCTGAGTGTGAGTGTATGACCGGGCTGT 3949
Qy 3301 GCTTGTGACGAGCTCACGCCCGCGAGACCTCAGTTAGTTCGGGCTTACCTAAACACA 3360
Db 3950 GCTTGTGACGAGCTCACGCCCGCGAGACCTCAGTTAGTTCGGGCTTACCTAAACACA 4009
Qy 3361 CCAGGTTGCCGCTCTGCGAGGACCATCTGGAGTTCTGGGAGAGCTCTTTACAGCCCTC 3420
Db 4010 CCAGGTTGCCGCTCTGCGAGGACCATCTGGAGTTCTGGGAGAGCTCTTTACAGCCCTC 4069
Qy 3421 ACCCATAGAGCGCCATTTCTTGTCCAGACTAAGCAGGCGAGGAGACAATTCCTCCCTAC 3480
Db 4070 ACCCATAGAGCGCCATTTCTTGTCCAGACTAAGCAGGCGAGGAGACAATTCCTCCCTAC 4129
Qy 3481 CTGGTAGCATACAGGCTACGCTACGCGTAAAGCTACGCTGACCGGCCCAACCCCTCGTGC 3540
Db 4130 CTGGTAGCATACAGGCTACGCTACGCGTAAAGCTACGCTGACCGGCCCAACCCCTCGTGC 4189
Qy 3541 CAATGTGGAAGTGTCTCATACGCTAAAGCTACGCTGACCGGCCCAACCCCTCGTGC 3600
Db 4190 CAATGTGGAAGTGTCTCATACGCTAAAGCTACGCTGACCGGCCCAACCCCTCGTGC 4249
Qy 3601 TATAGGCTGGAGCGGTTCAAAAGAGGTTACTACCAACACCCCATACCAATACATC 3660
Db 4250 TATAGGCTGGAGCGGTTCAAAAGAGGTTACTACCAACACCCCATACCAATACATC 4309
Qy 3661 ATGCATCATGTCCGTGACCTCGAGTCTCTGAGGACCTCGGTGCTGGTAGGCGGA 3720
Db 4310 ATGCATCATGTCCGTGACCTCGAGTCTCTGAGGACCTCGGTGCTGGTAGGCGGA 4369
Qy 3721 GTCCTAGCAGCTCTGGCGCGCTATTGCTGACAAACAGGACGCTGCTCATTTGTGGGACGG 3780
Db 4370 GTCCTAGCAGCTCTGGCGCGCTATTGCTGACAAACAGGACGCTGCTCATTTGTGGGACGG 4429
Qy 3781 ATCATCTTGTCCGAAAGCGGCGCATCATTTCCGACAGGGAAGTCTTTTACCGGAGTTC 3840
Db 4430 ATCATCTTGTCCGAAAGCGGCGCATCATTTCCGACAGGGAAGTCTTTTACCGGAGTTC 4489
Qy 3841 GATGAGATGGAAGAGTGGCGCTCACCTCCCTTACATCGAAACAGGGAATGCACTCGCC 3900
Db 4490 GATGAGATGGAAGAGTGGCGCTCACCTCCCTTACATCGAAACAGGGAATGCACTCGCC 4549
Qy 3901 GAACAAATCAACAGAGGCAATCGGGTGTGTCAAAACAGCCACCAAGCAGCGAGGCT 3960
Db 4550 GAACAAATCAACAGAGGCAATCGGGTGTGTCAAAACAGCCACCAAGCAGCGAGGCT 4609
Qy 3961 GCTGCTCCCGTGGTGGAAATCGAAGTGGGACCTCGAAGCGCTTCTGGGCGGAACATATG 4020
Db 4610 GCTGCTCCCGTGGTGGAAATCGAAGTGGGACCTCGAAGCGCTTCTGGGCGGAACATATG 4669
Qy 4021 TGGAAATTCATCAGCGGATACAAATTTTAGCAGGCTTGTCCACTCTGCTGGGCAACCCC 4080
Db 4670 TGGAAATTCATCAGCGGATACAAATTTTAGCAGGCTTGTCCACTCTGCTGGGCAACCCC 4729
Qy 4081 GCGATAGCATCACTGATGGCATTCACAGCCTCTATCACACCGCCGCTCACCCACCAACAT 4140
Db 4730 GCGATAGCATCACTGATGGCATTCACAGCCTCTATCACACCGCCGCTCACCCACCAACAT 4789
Qy 4141 ACCCTCTGTTTAACTCTTGGGGGAGTGGTGGCGGCCCAACTTGTCTCTCCAGCGCT 4200
Db 4790 ACCCTCTGTTTAACTCTTGGGGGAGTGGTGGCGGCCCAACTTGTCTCTCCAGCGCT 4849

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|----|------|--|------|----|------|---|------|
| QY | 4201 | GCTTCTGCTTTCTAGCGCCCGGCATCGCTGAGCGGCTGTGTGGCAGCATAGCGCTTGGG | 4260 | Db | 5930 | GCTAAGCGTAGCTGCCAGGGGATCTCCCCCTCTTGGCCAGCTCATCAGTAGCCAG | 5989 |
| Db | 4850 | GCTTCTGCTTTCTAGGCGCCGGCATCGCTGAGCGGCTGTGGCAGCATAGGCGCTTGG | 4909 | QY | 5341 | CTGTCTGCGCCTTCTTTGAAGCAACATGCACTACCCGTCATGACTCCCGGACGCTGAC | 5400 |
| QY | 4261 | AAGGTGCTTTGTGATATTTTGGCAGGTTATGAGCAGAGGGTGCGAGCGGCTGTGGGC | 4320 | Db | 5990 | CTGTCTGCGCCTTCTTTGAAGCAACATGCACTACCCGTCATGACTCCCGGACGCTGAC | 6049 |
| Db | 4910 | AAGGTGCTTTGTGATATTTTGGCAGGTTATGAGCAGAGGGTGCGAGCGGCTGTGGGC | 4969 | QY | 5401 | CTCATCGAGCCCAACCTCTCTGTGGGGCAGGAGATGGGCGGGAACATCAACCCGCTGGAG | 5460 |
| QY | 4321 | TTTAAGGTATGAGCGCGGAGATGCCCTCCACGAGGACTGGTTAACTACTCCCTGCT | 4380 | Db | 6050 | CTCATCGAGCCCAACCTCTCTGTGGGGCAGGAGATGGGCGGGAACATCAACCCGCTGGAG | 6109 |
| Db | 4970 | TTTAAGGTATGAGCGCGGAGATGCCCTCCACGAGGACTGGTTAACTACTCCCTGCT | 5029 | QY | 5461 | TCAGAAATTAAGTAGTAAATTTTGGACTCTTTTCGAGCCGCTCCAGGGAGGAGGATGAG | 5520 |
| QY | 4381 | ATCCTCTCCCTCGCGCCCTAGTCGTCGGGTCGCTGTGCGCAGCGATACTGCGTCGCGAC | 4440 | Db | 6110 | TCAGAAATTAAGTAGTAAATTTTGGACTCTTTTCGAGCCGCTCCAGGGAGGAGGATGAG | 6169 |
| Db | 5030 | ATCCTCTCCCTCGCGCCCTAGTCGTCGGGTCGCTGTGCGCAGCGATACTGCGTCGCGAC | 5089 | QY | 5521 | AGGGAAGTATCCGTTCCGCGGAGATCTCTCGGAGGTCCAGGAAATTTCCCTCCAGCGGATG | 5580 |
| QY | 4441 | GTGGGCCCGAGGAGGGGGCTGTGCAGTGGATGAACCGGCTGATAGGTTTCGCTTCGGG | 4500 | Db | 6170 | AGGGAAGTATCCGTTCCGCGGAGATCTCTCGGAGGTCCAGGAAATTTCCCTCCAGCGGATG | 6229 |
| Db | 5090 | GTGGGCCCGAGGAGGGGGCTGTGCAGTGGATGAACCGGCTGATAGGTTTCGCTTCGGG | 5149 | QY | 5581 | CCCATATGGGCACGCGCCGATTAACAACCTTCACTGTTAGAGTCTTGGAAGGACCCGGAC | 5640 |
| QY | 4501 | GGTAACACAGTCTCCCGCCAGCACTATGTCCTGAGAGCGAGCTGCAGCACGTTGCACT | 4560 | Db | 6230 | CCCATATGGGCACGCGCCGATTAACAACCTTCACTGTTAGAGTCTTGGAAGGACCCGGAC | 6289 |
| Db | 5150 | GGTAACACAGTCTCCCGCCAGCACTATGTCCTGAGAGCGAGCTGCAGCACGTTGCACT | 5209 | QY | 5641 | TAGTCTCCTCCAGTGTACACGGGTGTCCATTGCCCGCTGCCAAGGCCCTCCGATACCA | 5700 |
| QY | 4561 | CAGATCCTCTCTAGTCTTTACCATCACTCAGTCTGTAAGAGGCTTCAACGATGGATCAAC | 4620 | Db | 6290 | TAGTCTCCTCCAGTGTACACGGGTGTCCATTGCCCGCTGCCAAGGCCCTCCGATACCA | 6349 |
| Db | 5210 | CAGATCCTCTCTAGTCTTTACCATCACTCAGTCTGTAAGAGGCTTCAACGATGGATCAAC | 5269 | QY | 5701 | CCTCCACGGAGGAAGGACGGTTGTCTGTCTAGAAATCTACCGTGTCTTCTGCTCTGGCG | 5760 |
| QY | 4621 | GAGGACTGTCCACGCGCATGCTCCGGCTCGTGGCTTAAGAGATGTTGGATTTGGATGTC | 4680 | Db | 6350 | CCTCCACGGAGGAAGGACGGTTGTCTGTCTAGAAATCTACCGTGTCTTCTGCTCTGGCG | 6409 |
| Db | 5270 | GAGGACTGTCCACGCGCATGCTCCGGCTCGTGGCTTAAGAGATGTTGGATTTGGATGTC | 5329 | QY | 5761 | GAGTCTGCCACAAAGACCTTTCGGAGTCCGAATTCGTGCGCCGTTCGACAGCGGACCGCA | 5820 |
| QY | 4681 | ACGGTGTGACTGATTTCAAGACTGCTCCAGTCCAGTCCAGTCTCTCCGCGAATTTGCCGGGA | 4740 | Db | 6410 | GAGTCTGCCACAAAGACCTTTCGGAGTCCGAATTCGTGCGCCGTTCGACAGCGGACCGCA | 6469 |
| Db | 5330 | ACGGTGTGACTGATTTCAAGACTGCTCCAGTCCAGTCCAGTCTCTCCGCGAATTTGCCGGGA | 5389 | QY | 5821 | ACGGCTCTCTCTACACAGCCCTCCGACGCGGAGCGGAGTCCGAGCTTCGAGTCTGATC | 5880 |
| QY | 4741 | GTCCCTCTTCTCATGTCAACCTGGGTACAAGGGAGTCTGGCGGGCGACGCGCATCATG | 4800 | Db | 6470 | ACGGCTCTCTCTACACAGCCCTCCGACGCGGAGCGGAGTCCGAGCTTCGAGTCTGATC | 6529 |
| Db | 5390 | GTCCCTCTTCTCATGTCAACCTGGGTACAAGGGAGTCTGGCGGGCGACGCGCATCATG | 5449 | QY | 5881 | TCCTCCATGCCCGCCCTTGAGGGGGAGCGCGGGGATCCCGATCTCAGCGACGGGTCTTGG | 5940 |
| QY | 4801 | CAAAACACCTGCGCATGTGAGCAGACATCACCGGACATGTGAAGACGTTCCATGAGG | 4860 | Db | 6530 | TCCTCCATGCCCGCCCTTGAGGGGGAGCGCGGGGATCCCGATCTCAGCGACGGGTCTTGG | 6589 |
| Db | 5450 | CAAAACACCTGCGCATGTGAGCAGACATCACCGGACATGTGAAGACGTTCCATGAGG | 5509 | QY | 5941 | TCTACCGTAAGCAGGAGGCTAGTAGGACGCTGTCTGTCTGCTGCTGATGCTTACATG | 6000 |
| QY | 4861 | ATCGTGGGCTTAGGACCTGTAGTAACAGTGGATGAACATTTCCCCATTTAACCGGTAC | 4920 | Db | 6590 | TCTACCGTAAGCAGGAGGCTAGTAGGACGCTGTCTGTCTGCTGCTGATGCTTACATG | 6649 |
| Db | 5510 | ATCGTGGGCTTAGGACCTGTAGTAACAGTGGATGAACATTTCCCCATTTAACCGGTAC | 5569 | QY | 6001 | ACAGGCGCCCTGATCAGCCATCGCTGCGGAGGAAACCAAGCTGCCCATCAATGCACTG | 6060 |
| QY | 4921 | ACCACGGGCCCCCTGACGCGCTCCCGCGCGCCAAATTTATTTAGGGCGCTGTGGCGGGT | 4980 | Db | 6650 | ACAGGCGCCCTGATCAGCCATCGCTGCGGAGGAAACCAAGCTGCCCATCAATGCACTG | 6709 |
| Db | 5570 | ACCACGGGCCCCCTGACGCGCTCCCGCGCGCCAAATTTATTTAGGGCGCTGTGGCGGGT | 5629 | QY | 6061 | AGCAACTCTTTGCTCCGTCACCACTTGTGTCTATGCTTCAACATCTCGAGCGCAAGC | 6120 |
| QY | 4981 | GCTGCTCAGAGTACGTGGAGTTACCGGGTGGGGATTTCCACTACGTGACGGGCATG | 5040 | Db | 6710 | AGCAACTCTTTGCTCCGTCACCACTTGTGTCTATGCTTCAACATCTCGAGCGCAAGC | 6769 |
| Db | 5630 | GCTGCTCAGAGTACGTGGAGTTACCGGGTGGGGATTTCCACTACGTGACGGGCATG | 5689 | QY | 6121 | CTCGGCGAGGAAGGTCACCTTTTGACAGACTGCGAGTCTCTGAGCAGCACTACCGGAC | 6180 |
| QY | 5041 | ACCACGTACAACGTAAAGTGCCTGTTCAGTTCCTGGCCCGCCGAATTTCTTCAAGAAAGT | 5100 | Db | 6770 | CTCGGCGAGGAAGGTCACCTTTTGACAGACTGCGAGTCTCTGAGCAGCACTACCGGAC | 6829 |
| Db | 5690 | ACCACGTACAACGTAAAGTGCCTGTTCAGTTCCTGGCCCGCCGAATTTCTTCAAGAAAGT | 5749 | QY | 6181 | GTGCTCAAGGAGATGAAGCGGAGGCGTCCACAGTTAAGGCTAACTTCTATCCGTCGAG | 6240 |
| QY | 5101 | GATGGGTGCGGTTGCAAGGTACGCTCCAGCGTGCAGAAACCCCTCTTACGGGAGGATC | 5160 | Db | 6830 | GTGCTCAAGGAGATGAAGCGGAGGCGTCCACAGTTAAGGCTAACTTCTATCCGTCGAG | 6889 |
| Db | 5750 | GATGGGTGCGGTTGCAAGGTACGCTCCAGCGTGCAGAAACCCCTCTTACGGGAGGATC | 5809 | QY | 6241 | GAAGCCTGTAAAGTGTGACGCCCCCACTTCGCGCAGATCTTAAATTTGGCTATGGGGCAAG | 6300 |
| QY | 5161 | ACATTCCTGTCGGGCTCAATCAATACCTGTTGGGTTCAGGCTCCCATGGAGCCGAA | 5220 | Db | 6890 | GAAGCCTGTAAAGTGTGACGCCCCCACTTCGCGCAGATCTTAAATTTGGCTATGGGGCAAG | 6949 |
| Db | 5810 | ACATTCCTGTCGGGCTCAATCAATACCTGTTGGGTTCAGGCTCCCATGGAGCCGAA | 5869 | QY | 6301 | GACGTCCGGAACCTTATCCAGCAAGGCGGTTAAACCATCCGCTCCGCTGCGAGGACTTG | 6360 |
| QY | 5221 | CCGAGCCTGACGAGTGTCTTCCATGCTTCCAGGACCCCTCCCATTTACGGCGGAGACG | 5280 | Db | 6950 | GACGTCCGGAACCTTATCCAGCAAGGCGGTTAAACCATCCGCTCCGCTGCGAGGACTTG | 7009 |
| Db | 5870 | CCGAGCCTGACGAGTGTCTTCCATGCTTCCAGGACCCCTCCCATTTACGGCGGAGACG | 5929 | QY | 6361 | CTGGAAGACACTGACACCAATTTGACACCACTCATGGCAAAATAGGTTTCTGTC | 6420 |
| QY | 5281 | GCTAAGCGTAGGCTGGCCAGGGGATCTCCCGCTCTCTGGCGCAGCTCATCAGTAGCCAG | 5340 | | | | |

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|----|------|---|------|
| Db | 7010 | CTGGAAGACACTGAGACACCAATTTGACACCAACCATCATGCAAAAAAATAGGTTTTCTGCG | 7066 |
| Qy | 6421 | GTCCAAACAGAGAAGGGGGCCGCAAGCCAGCTCGCCTTATCGTATTCCAGATTTGGGG | 6480 |
| Db | 7070 | GTCCAAACAGAGAAGGGGGCCGCAAGCCAGCTCGCCTTATCGTATTCCAGATTTGGGG | 7129 |
| Qy | 6481 | GTTCTGTGTGCGAGAAAAATGGCCCTTTACATGTGTCTCCACCTTCCCTCAGGCCGTG | 6540 |
| Db | 7130 | GTTCTGTGTGCGAGAAAAATGGCCCTTTAGCATGTGTCTCCACCTTCCCTCAGGCCGTG | 7189 |
| Qy | 6541 | ATGGGCTCTTCATACGATTTCCATATCTCTCTGGACAGCGGTCGAGTTCCTGTGTCAT | 6600 |
| Db | 7190 | ATGGGCTCTTCATACGATTTCCATATCTCTCTGGACAGCGGTCGAGTTCCTGTGTCAT | 7249 |
| Qy | 6601 | GCCTGAAAAGCAAGAAATGCCCTATCGGCTTCGCATATGACACCCGCTGTTTGACTCA | 6660 |
| Db | 7250 | GCTTGGAAAGCAAGAAATGCCCTATCGGCTTCGCATATGACACCCGCTGTTTGACTCA | 7309 |
| Qy | 6661 | ACGGTCACTGAGATGATCCGTGTGTGAGAGTCAATCTACCAATGTTGTGACTTGGCC | 6720 |
| Db | 7310 | ACGGTCACTGAGATGATCCGTGTGTGAGAGTCAATCTACCAATGTTGTGACTTGGCC | 7369 |
| Qy | 6721 | CCCGAAGCCAGACAGGCCATAAGTGCCTCACAGAGCGCTTTACATCGGGGGCCCCCTG | 6780 |
| Db | 7370 | CCCGAAGCCAGACAGGCCATAAGTGCCTCACAGAGCGCTTTACATCGGGGGCCCCCTG | 7429 |
| Qy | 6781 | ACTAATTTAAAGGCGAGAACTGCGGCTATCGCGGTGCGCGCGAGCGGTACTGACG | 6840 |
| Db | 7430 | ACTAATTTAAAGGCGAGAACTGCGGCTATCGCGGTGCGCGCGAGCGGTACTGACG | 7489 |
| Qy | 6841 | ACCAGCTCGGTAAATACCCCTCACATGTACTTGAAGGCGCGCTGCGGCTCTCGAGCTGG | 6900 |
| Db | 7490 | ACCAGCTCGGTAAATACCCCTCACATGTACTTGAAGGCGCGCTGCGGCTCTCGAGCTGG | 7549 |
| Qy | 6901 | AAGCTCCAGGACTCCAGATGCTCGTATCGGAGACGACCTTGTCTGTTACTGTGAAAGC | 6960 |
| Db | 7550 | AAGCTCCAGGACTCCAGATGCTCGTATCGGAGACGACCTTGTCTGTTACTGTGAAAGC | 7609 |
| Qy | 6961 | GCGGGACCCAAAGAGGACGAGGCGAGCTACGGGCTTTACGGAGGCTATGACTAGATAC | 7020 |
| Db | 7610 | GCGGGACCCAAAGAGGACGAGGCGAGCTACGGGCTTTACGGAGGCTATGACTAGATAC | 7669 |
| Qy | 7021 | TCTGCCCCCTTGGGGACCCGCCCAACAGAAATACGACTTGGAGTTGTAAACATCATGC | 7080 |
| Db | 7670 | TCTGCCCCCTTGGGGACCCGCCCAACAGAAATACGACTTGGAGTTGTAAACATCATGC | 7729 |
| Qy | 7081 | TCCTCCAAATGTGTAGTCTGCGGCAGATGCTCTGGAAAAGGGTGTTACTATCTCACCCGT | 7140 |
| Db | 7730 | TCCTCCAAATGTGTAGTCTGCGGCAGATGCTCTGGAAAAGGGTGTTACTATCTCACCCGT | 7789 |
| Qy | 7141 | GACCCACACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACCTCCAGATCAAT | 7200 |
| Db | 7790 | GACCCACACCCCTTGGCGGGCTGCGTGGGAGACAGCTAGACACCTCCAGATCAAT | 7849 |
| Qy | 7201 | TCCTGGCTAGGCAACATCATATGATGCGGCCACCTTGTGGGCAAGGATGATCTCTGATG | 7260 |
| Db | 7850 | TCCTGGCTAGGCAACATCATATGATGCGGCCACCTTGTGGGCAAGGATGATCTCTGATG | 7909 |
| Qy | 7261 | ACTCATTTCTTCTCGATCTTCTAGCTCAGGAACAACTTGAAAAGCCCTAGATTTGTGAG | 7320 |
| Db | 7910 | ACTCATTTCTTCTCGATCTTCTAGCTCAGGAACAACTTGAAAAGCCCTAGATTTGTGAG | 7969 |
| Qy | 7321 | ATCTACGGGGCTGTTACTCCATTGAGCCACTTCGACCTACCTCAGATCAATTCAACGACTC | 7380 |
| Db | 7970 | ATCTACGGGGCTGTTACTCCATTGAGCCACTTCGACCTACCTCAGATCAATTCAACGACTC | 8029 |
| Qy | 7381 | CATGGCCCTTAGCGCAATTTTCACTCCATAGTTACTCTCTCAGGTGAGATCAATAGGTTGGCT | 7440 |
| Db | 8030 | CACGGCCCTTAGCGCAATTTTCACTCCATAGTTACTCTCTCAGGTGAGATCAATAGGTTGGCT | 8089 |
| Qy | 7441 | TCATGCCCTCAGAAACTTTGGGGTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAAGT | 7500 |
| Db | 8090 | TCATGCCCTCAGAAACTTTGGGGTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAAGT | 8149 |

| QY | 7501 | GTCCGCGCTAGGCTACTGTCCAGGGGGGAGGGCTCCCACTTGTGCAAGTACTCTTTC | 7560 |
|---|------|---|------|
| Db | 8150 | GTCCGCGCTAGGCTACTGTCCAGGGGGGAGGGCTCCCACTTGTGCAAGTACTCTTTC | 8209 |
| QY | 7561 | AAC TGGG CAGT TAGGAC CAAAGCTCAAAC TCACTCCAATCCCGGTCGCTCCAGTTCGAT | 7620 |
| Db | 8210 | AAC TGGG CAGT TAGGAC CAAAGCTCAAAC TCACTCCAATCCCGGTCGCTCCAGTTCGAT | 8269 |
| QY | 7621 | TTATCCAGCTGGTTTCGTTGTCTGGTTTACAGCGGGGAGACATATATCACAGCCTCTCTCGT | 7680 |
| Db | 8270 | TTATCCAGCTGGTTTCGTTGTCTGGTTTACAGCGGGGAGACATATATCACAGCCTCTCTCGT | 8329 |
| QY | 7681 | GCCCGACCCCGCTGGTTCATGTGTGCTACTCTCTACTTTCTGTAGGGGTAGGCATCTAT | 7740 |
| Db | 8330 | GCCCGACCCCGCTGGTTCATGTGTGCTACTCTCTACTTTCTGTAGGGGTAGGCATCTAT | 8389 |
| QY | 7741 | CTACTCCCCAACCCATGAAGCGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTTT | 7800 |
| Db | 8390 | CTACTCCCCAACCCATGAAGCGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTTT | 8449 |
| QY | 7801 | TTTCCC-----TT | 7850 |
| Db | 8450 | TTTCCCCTTTTTTCCTTT | 8509 |
| QY | 7851 | TTCTCCCTTTTTTTTCTCTTTTTTTTCTTTTTCTTTCTTTCTTTGGTGGCTCCATCTTAGCCC | 7910 |
| Db | 8510 | CCCTCCCTTTTTTTTCCCTTTTTTTTTTTTCTTTCTTTCTTTCTTTGGTGGCTCCATCTTAGCCC | 8569 |
| QY | 7911 | TAGTCACGGCTAGCTGTGAAGGTCCCGTGAGCCGCTTGACTGTCAGAGAGTCTGATCATG | 7970 |
| Db | 8570 | TAGTCACGGCTAGCTGTGAAGGTCCCGTGAGCCGCTTGACTGTCAGAGAGTCTGATCATG | 8629 |
| QY | 7971 | GCCTCTCTGCAGATCAAGT 7989 | |
| Db | 8630 | GCCTCTCTGCAGATCAAGT 8648 | |
| RESULT 15 | | | |
| US-10-029-907-4 | | | |
| ; Sequence 4, Application US/10029907 | | | |
| ; Patent No. 6706874 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD. | | | |
| ; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM | | | |
| ; FILE OF INVENTION: HEPATITIS 'C' VIRUS | | | |
| ; FILE REFERENCE: 13/083 | | | |
| ; CURRENT APPLICATION NUMBER: US/10/029,907 | | | |
| ; CURRENT FILING DATE: 2001-12-21 | | | |
| ; PRIOR APPLICATION NUMBER: 60/257,857 | | | |
| ; PRIOR FILING DATE: 2000-12-22 | | | |
| ; NUMBER OF SEQ ID NOS: 25 | | | |
| ; SOFTWARE: FastSeq for Windows Version 4.0 | | | |
| ; SEQ ID NO 4 | | | |
| ; LENGTH: 8643 | | | |
| ; TYPE: DNA | | | |
| ; ORGANISM: HCV | | | |
| ; FEATURE: | | | |
| ; NAME/KEY: CDS | | | |
| ; LOCATION: (1802)...(8407) | | | |
| US-10-029-907-4 | | | |
| Query Match 90.4%; Score 7222.6; DB 4; Length 8643; | | | |
| Best Local Similarity 91.9%; Pred. No. 0; | | | |
| Matches 7953; Conservative 0; Mismatches 24; Indels 676; Gaps 4 | | | |
| QY | 2 | CCAGCCCCCGATTGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAATCTACTGT | 61 |
| Db | 2 | CCAGCCCCCGATTGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAATCTACTGT | 61 |
| QY | 62 | CTTCAACGAGAAACGGTCTACGCCATGGCGTTAGTATGAGTCTGTGAGGCTCCAGGACC | 121 |
| Db | 62 | CTTCAACGAGAAACGGTCTACGCCATGGCGTTAGTATGAGTCTGTGAGGCTCCAGGACC | 121 |

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| QY | 122 | CCCTCTCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCAGG | 181 |
| Db | 122 | CCCCCTCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCAGG | 181 |
| QY | 182 | ACGACCGGGTCCCTTTCTTGATCAACCGCTCAATGCTGGAATTTGGGCGTGCCTCCG | 241 |
| Db | 182 | ACGACCGGGTCCCTTTCTTGATCAACCGCTCAATGCTGGAATTTGGGCGTGCCTCCG | 241 |
| QY | 242 | CGAGACTGCTAGCCGAGTAGTGGTCCGGAAGGCCCTTGTGCTACCTCCCTGATAGGG | 301 |
| Db | 242 | CGAGACTGCTAGCCGAGTAGTGGTCCGGAAGGCCCTTGTGCTACCTCCCTGATAGGG | 301 |
| QY | 302 | TGCTTGCAGTGCCTCCGGGAGGTCTCGTAGACCGTGCACCATGAGCAGGATCCTAAACC | 361 |
| Db | 302 | TGCTTGCAGTGCCTCCGGGAGGTCTCGTAGACCGTGCACCATGAGCAGGATCCTAAACC | 361 |
| QY | 362 | TCAAGAAACCAAAAGGGCGCCATGATGTAACAAAGATGGAATGACGCGAGTCTCC | 421 |
| Db | 362 | TCAAGAAACCAAAAGGGCGCCATGATGTAACAAAGATGGAATGACGCGAGTCTCC | 421 |
| QY | 422 | GGCCGCTTGGTGGAGAGGTATTCGGCTATGACTGGGCAACACAGACATCGCTGCTC | 481 |
| Db | 422 | GGCCGCTTGGTGGAGAGGTATTCGGCTATGACTGGGCAACACAGACATCGCTGCTC | 481 |
| QY | 482 | TGATGCCGCGGTTCCTCGGCTGTGAGCGCAGGGGCGCCCGTTCTTTTGTCAAGACCGA | 541 |
| Db | 482 | TGATGCCGCGGTTCCTCGGCTGTGAGCGCAGGGGCGCCCGTTCTTTTGTCAAGACCGA | 541 |
| QY | 542 | CTGTCCGCTGCTGAATGAATGTCAGGACGAGGCGCGGCTATGCTGCGGCTGCGCAC | 601 |
| Db | 542 | CTGTCCGCTGCTGAATGAATGTCAGGACGAGGCGCGGCTATGCTGCGGCTGCGCAC | 601 |
| QY | 602 | GACGGCGTTCCTTGGCGAGCTGTGCTCGACGTTGTCATGAGCGGAGGACATCGGCT | 661 |
| Db | 602 | GACGGCGTTCCTTGGCGAGCTGTGCTCGACGTTGTCATGAGCGGAGGACATCGGCT | 661 |
| QY | 662 | GCTATTGGGCGAAGTCCCGGGCAGGATCTCTGTGTCATCTCACTTGTCTCTCCCGAGAA | 721 |
| Db | 662 | GCTATTGGGCGAAGTCCCGGGCAGGATCTCTGTGTCATCTCACTTGTCTCTCCCGAGAA | 721 |
| QY | 722 | AGTATCCATCATGGCTGATGTAATGCGGGCGTGTGATAGCTTGTGCTGCGGCTACCTGCC | 781 |
| Db | 722 | AGTATCCATCATGGCTGATGTAATGCGGGCGTGTGATAGCTTGTGCTGCGGCTACCTGCC | 781 |
| QY | 782 | ATTGCAACCAAGGAAACATCGCATCGAGCGAGCAGTACTCGGATGGAAGCGGCTCT | 841 |
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| Db | 902 | CAGGCTCAAGGCGCGATCGCGAGCGAGGATCTGCTGTCGACCCATGCGGATGCGCTG | 961 |
| QY | 962 | CTTGCGCAATATCATGGTGGAAATGCGCGCTTTTCTGGATTCATCGACTGTGGCGGCT | 1021 |
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| QY | 1022 | GGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCT | 1081 |
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| QY | 1082 | TGGCGCGAATGGCTGACCGCTTCTCGTGTGTTACGATATCGCGCTCCGATTCGCA | 1141 |
| Db | 1082 | TGGCGCGAATGGCTGACCGCTTCTCGTGTGTTACGATATCGCGCTCCGATTCGCA | 1141 |
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| Db | 1142 | GCGCATCGCTTCTATCGCTTCTTTCGACGAGTCTTCTGAGTTCTTCGATTCGCGCCAGATGTAAC | 1201 |
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| Db | 1202 | AGACCACAAACGGTTTCCCTCTAGCGGATCAATTCG-----CCCCCCCCCTA | 1250 |
| QY | 1250 | ACGTTACTGGCCGAAAGCGCTTGGAAATAAGGCGGTGTGGTTGTCTATATGTTATTTT | 1309 |
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| Db | 1371 | CGAGCATTCCTAGGGGTCTTTTCCCTCTGCGCAAGGAATGCAAGTCTGTTGAATGTCG | 1430 |
| QY | 1430 | TGAAGAAGAGTTCCTCTGGAAGCTTTTGAAGAACAACAGCTGTAGGACCCCTTT | 1489 |
| Db | 1431 | TGAAGAAGAGTTCCTCTGGAAGCTTTTGAAGAACAACAGCTGTAGGACCCCTTT | 1490 |
| QY | 1490 | GCAAGCAGCGGAACCCCGACCTGGCGACAGGTGCTCTGCGGCCAAAGCCACGCTAT | 1549 |
| Db | 1491 | GCAAGCAGCGGAACCCCGACCTGGCGACAGGTGCTCTGCGGCCAAAGCCACGCTAT | 1550 |
| QY | 1550 | AAGATACACTGCAAAAGGGCGCACAAACCCAGTGCACCTGTGAGTTGATAGTTGTCG | 1609 |
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| QY | 1670 | TACCCCATTTGATGGGATCTGATCTGGGCTCGGTGCATGCTTTACATGTTTGTAGT | 1729 |
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| Db | 1731 | CGAGGTTAGAAAAACGCTTAGGGCCCCCGAACCAACGCGGACGTTGTTTCTTTGAAAAAC | 1790 |
| QY | 1790 | ACGATTAATACCATG----- | 1803 |
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| QY | 1804 | ----- | 1803 |

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| QY | 4382 | TCCTCTCCCTGGCGCCTAGTCTCGGGGTGCTGCGCAGCGATACTGCTGGCGACG | 4441 | QY | 5462 | CAGAAATAAGGTAGTAAATTTTGGACTCTTTTCGAGCGCTCCAAAGCGGAGGAGATGAGA | 5521 |
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| QY | 4862 | TCGTGGGCGCTTAGGACCTGTAGTAAACACAGTGGATGGAACATTTCCCATTAACGCGTACA | 4921 | QY | 5942 | CTACCTTAAGCGAGGAGGCTAGTAGGACCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 6001 |
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| | | | | QY | 6002 | CAGCGGCGCTGTATCAGCCCATGCGCTGCGGAGGAAACCAAGCTGCCCATCATGCTACATGA | 6061 |

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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 19:35:18 ; Search time 21401 Seconds
(without alignments)
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Perfect score: 7992

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Scoring table: IDENTITY_NUC

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Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_hcg.*
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4: gb_om.*
5: gb_ov.*
6: gb_pat.*
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13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 7989 | 100.0 | 7989 | 6 | AR406043 Sequence |
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ALIGNMENTS

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DEFINITION Sequence 3 from Patent WO20059321.
ACCESSION AX739972
VERSION AX739972.1 GI:30519246
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS de Francesco, R., Migliaccio, G. and Paonessa, G.
TITLE Hepatitis C virus replicons and replicon enhanced cells
JOURNAL Patent: WO 02059321-A 3 01-AUG-2002;
ISTITUTO DI RICERCHE DI BIOLOGIA MOLECOLARE P. ANGELETTI S.P.A.
(IT)
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/note="pHCVNeo.17 coding"

ORIGIN
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Db 1 GCACGCCCCGATTGGGGGACACTCCACCATAGATCACTCCCTGTGAGGAACCTACTG 60
QY 61 TCTTCACGAGAAAGCGTCTAGCCATGGGCTTAGTATGATGTCGTGCGACCTCCAGGAC 120
Db 61 TCTTCACGAGAAAGCGTCTAGCCATGGGCTTAGTATGATGTCGTGCGACCTCCAGGAC 120
QY 121 CCCCCCTCCGGAGAGCCATAGTGGTCTGCGAAACCGGTGAGTACACCGGAATTCGCG 180
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AUTHORS Bartenschlager,R.
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| | | | | | | | |
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| Qy | 841 | TTGTCGATCAGATGATCTGGAAGAGATCAGGGGCTCGGCGCAGCGCACTGTTCG | 900 | Qy | 1921 | ACACAATCTTCTCGGCGACCTGCGTCAATGGGCTGTGTGGACTGTCTATCATGTGTC | 1980 |
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| Qy | 961 | GCTTGGCGAATATCATGTTGGAAATGGCGCTTTTCTGGATTCATCGACTGGCGGC | 1020 | Qy | 2041 | CAGGACTCGTCTGGCTGGCAAGCGCCCCCGGGCGCTTCTCTTGACACCAATGCACTGC | 2100 |
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| Qy | 1021 | TGGTGTGGGACCGCTATCAGGACATAGCGTTGGTACCCGTGATATTGCTGAAGAGC | 1080 | Qy | 2101 | GGCAGTCTCGAATCTTTACTTTGTCACAGGATGCGGATGTCAATCCGGTGGCGCGCGG | 2160 |
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Db 2941 AAGCTGTCCGGCTCGGACTCAATGTGTAGCATATTAACCGGGGCTTGATGTATCCGTC 3000
QY 3001 ATACCAACTAGCGGAGAGCTCAATTCGTGTAGCAACGGAGGCTCTAATGAGGGCTTTTACC 3060
Db 3001 ATACCAACTAGCGGAGAGCTCAATTCGTGTAGCAACGGAGGCTCTAATGAGGGCTTTTACC 3060
QY 3061 GCGGATTTGCACTCAGTGTGATCGACTGCAATATCATGTGTACCCAGACAGTGCACGTGCG 3120
Db 3061 GCGGATTTGCACTCAGTGTGATCGACTGCAATATCATGTGTACCCAGACAGTGCACGTGCG 3120
QY 3121 CTGGACCGGAGTGTACCACTTGTAGAGAGCGACCGTGTCCAAAGAGCGGTGTACAGCTCG 3180
Db 3121 CTGGACCGGAGTGTACCACTTGTAGAGAGCGACCGTGTCCAAAGAGCGGTGTACAGCTCG 3180
QY 3181 CAGCGGCGAGGAGGAGTGTAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGGA 3240
Db 3181 CAGCGGCGAGGAGGAGTGTAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGGA 3240
QY 3241 GAAACGGCCCTCGGGCATGTTCCATTCCTCGGTTCTGTGCGAGTGTATGACGCGGCTGT 3300
Db 3241 GAAACGGCCCTCGGGCATGTTCCATTCCTCGGTTCTGTGCGAGTGTATGACGCGGCTGT 3300
QY 3301 GCTTGTGTAGAGTGTACCGCGCGAGACCTCACTAGTTTTCGGGCTTACCTAAACACA 3360
Db 3301 GCTTGTGTAGAGTGTACCGCGCGAGACCTCACTAGTTTTCGGGCTTACCTAAACACA 3360
QY 3361 CCAGGTTGCGCGCTGCGAGGACCTGTGAGTGTCTGGGAGAGGCTTTTACAGGCTC 3420
Db 3361 CCAGGTTGCGCGCTGCGAGGACCTGTGAGTGTCTGGGAGAGGCTTTTACAGGCTC 3420
QY 3421 ACCACATAGACGCCCATTTCTGTCCAGACTAAGCAGGAGGAGACCACTTCCCTTAC 3480
Db 3421 ACCACATAGACGCCCATTTCTGTCCAGACTAAGCAGGAGGAGACCACTTCCCTTAC 3480
QY 3481 CTGGTAGCATACAGGCTACCGTGTGCGCCAGGCTCAGGCTCCACCTCCATCGTGGAC 3540
Db 3481 CTGGTAGCATACAGGCTACCGTGTGCGCCAGGCTCAGGCTCCACCTCCATCGTGGAC 3540
QY 3541 CAAATGTGGAAGTGTCTCATACGCTAAGCCTACGCTGTGACGCGGCAAGCGCCCTGTG 3600
Db 3541 CAAATGTGGAAGTGTCTCATACGCTAAGCCTACGCTGTGACGCGGCAAGCGCCCTGTG 3600
QY 3601 TATAGGCTGGAGCGGTTCAAAACGAGGTTACTACCAACACCCCAATAACCAATATATC 3660
Db 3601 TATAGGCTGGAGCGGTTCAAAACGAGGTTACTACCAACACCCCAATAACCAATATATC 3660
QY 3661 ATGGCATGATGTGCGGTGACCTGGAGGTGTGTACAGGACCTGGGTGTGTAGGCGGA 3720
Db 3661 ATGGCATGATGTGCGGTGACCTGGAGGTGTGTACAGGACCTGGGTGTGTAGGCGGA 3720
QY 3721 GTCCTAGCAGCTGTGCGCGGTATTTGCTGTACACAGGAGCGGTGTGTGTGGGCGAG 3780
Db 3721 GTCCTAGCAGCTGTGCGCGGTATTTGCTGTGTACACAGGAGCGGTGTGTGTGGGCGAG 3780
QY 3781 ATCATCTTGTCCGAAAGCGGCGCATCATTTCCCGACAGGGAAGTCCCTTTACCGGAGTTC 3840
Db 3781 ATCATCTTGTCCGAAAGCGGCGCATCATTTCCCGACAGGGAAGTCCCTTTTACCGGAGTTC 3840

QY 3841 GATGAGATGAAAGTAGTGCCTCACACCTCCCTTATCATCGAACAGGAATCGAGCTCGCC 3900
Db 3841 GATGAGATGAAAGTAGTGCCTCACACCTCCCTTATCATCGAACAGGAATCGAGCTCGCC 3900
QY 3901 GAAACATTTCAACAGAGCAATCGGGTTGTGCAAAACAGCCACCAAGCAAGCGGAGGCT 3960
Db 3901 GAAACATTTCAACAGAGCAATCGGGTTGTGCAAAACAGCCACCAAGCAAGCGGAGGCT 3960
QY 3961 GCTGTCTCCGCTGGTGGATCCAAAGTGGCGGACCTCTGAAAGCCTTCTGGGCGAAGCATATG 4020
Db 3961 GCTGTCTCCGCTGGTGGATCCAAAGTGGCGGACCTCTGAAAGCCTTCTGGGCGAAGCATATG 4020
QY 4021 TGGAAATTTTCAATCAGCGGGATACAATATTTAGCAGGCTGTGTCCACTCTGCTGCAACCCC 4080
Db 4021 TGGAAATTTTCAATCAGCGGGATACAATATTTAGCAGGCTGTGTCCACTCTGCTGCAACCCC 4080
QY 4081 GCGATAGCATCACTGATGGCATTCACGCTCTATCACCAGCCGCTCACCAACCCAAACAT 4140
Db 4081 GCGATAGCATCACTGATGGCATTCACGCTCTATCACCAGCCGCTCACCAACCCAAACAT 4140
QY 4141 ACCCTCCTGTTTAAACATCTCGGGGGATGGTGGCGGCCCAACTTGTCTCTCCAGCGCT 4200
Db 4141 ACCCTCCTGTTTAAACATCTCGGGGGATGGTGGCGGCCCAACTTGTCTCTCCAGCGCT 4200
QY 4201 GCTTCTGCTTTTGTAGGCGCGGATCGCTGAGCGGCTGTGGCAGCATAGGCTTGGG 4260
Db 4201 GCTTCTGCTTTTGTAGGCGCGGATCGCTGAGCGGCTGTGGCAGCATAGGCTTGGG 4260
QY 4261 AAGGTGCTTGTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCTCGTGCC 4320
Db 4261 AAGGTGCTTGTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCTCGTGCC 4320
QY 4321 TTTAAGGTGATGAGCGGGAGATGCCCTCAACGAGGACCTGGTTAACTTCCCTGCT 4380
Db 4321 TTTAAGGTGATGAGCGGGAGATGCCCTCAACGAGGACCTGGTTAACTTCCCTGCT 4380
QY 4381 ATCTCTCTCCCTGCGCCCTAGTGTGCGGGTGTGTGCGCAGGATACCTGCTGGCAC 4440
Db 4381 ATCTCTCTCCCTGCGCCCTAGTGTGCGGGTGTGTGCGCAGGATACCTGCTGGCAC 4440
QY 4441 GTGGGCCAGGGGAGGGGCTGTGAGTGAATGAACCGGCTGTAGCGCTTCCGTTCCGGG 4500
Db 4441 GTGGGCCAGGGGAGGGGCTGTGAGTGAATGAACCGGCTGTAGCGCTTCCGTTCCGGG 4500
QY 4501 GGTAAACACAGTCTCCCGACGACATATGTGCTGAGAGCGAGCTGAGACAGTGTCACT 4560
Db 4501 GGTAAACACAGTCTCCCGACGACATATGTGCTGAGAGCGAGCTGAGACAGTGTCACT 4560
QY 4561 CAGATCCTCTCTAGTCTTACCATCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4620
Db 4561 CAGATCCTCTCTAGTCTTACCATCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4620
QY 4621 GAGGACTGTCTCAGCGCATGCTCCGGCTCGTGGCTAAGAGATGTTGGGATTTGGATATGC 4680
Db 4621 GAGGACTGTCTCAGCGCATGCTCCGGCTCGTGGCTAAGAGATGTTGGGATTTGGATATGC 4680
QY 4681 ACGGTGTGTAGTGTTCAGAGCTGTGCTCAGTCCAGTCCAGCTTCCCGCATTCGCCGGA 4740
Db 4681 ACGGTGTGTAGTGTTCAGAGCTGTGCTCAGTCCAGTCCAGCTTCCCGCATTCGCCGGA 4740
QY 4741 GTCCCTCTCTCTCATGTCAACGTGGGTCAAGGAGTCTGGCGGGCGAGCGGCTCATG 4800
Db 4741 GTCCCTCTCTCTCATGTCAACGTGGGTCAAGGAGTCTGGCGGGCGAGCGGCTCATG 4800
QY 4801 CAAACACCTTCCGCTGTGAGACAGATCAACCGGACATGTGAACAAACGCTTCCATGAGG 4860
Db 4801 CAAACACCTTCCGCTGTGAGACAGATCAACCGGACATGTGAACAAACGCTTCCATGAGG 4860
QY 4861 ATCGTGGGCGCTTAGGACCTGTGTAGTAAACGTGTGACATTTCCCATTAACGGGTAC 4920
Db 4861 ATCGTGGGCGCTTAGGACCTGTGTAGTAAACGTGTGACATTTCCCATTAACGGGTAC 4920
QY 4921 ACCACGGGCGGCTGTGACGCGCTCCCGGCGCCAAATTTTCTAGGGGCTGTGGGGGTG 4980

| | | | | | | |
|----|------|---|------|------|---|------|
| Db | 841 | TTTTCGATCAGATGATCTGACGAGAGCATCAGGGCTCGCGCAGCGAATCTTCG | 900 | 1921 | ACACAATCTTTCTCGCGCACCTCGCTCAATGGCGTGTGTGGACTGTCTATCATGGTGGC | 1980 |
| Qy | 901 | CCAGGCTCAAGCGCGCATGCCCCGAGAGATCTCGTGTGACCCATGGCGATGCTT | 960 | 1981 | GGCTCAAGAGACCTTTGCGCGCCAAAGGGCCCAATACCCAAATGTACACCAATGTGGAC | 2040 |
| Db | 901 | CCAGGCTCAAGCGCGCATGCCCCGAGAGATCTCGTGTGACCCATGGCGATGCTT | 960 | 1981 | GGCTCAAGAGACCTTTGCGCGCCAAAGGGCCCAATACCCAAATGTACACCAATGTGGAC | 2040 |
| Qy | 961 | GTTTCCGGAATATCATGTGTGAAATGGCCGCTTTTCTGGATTCATCGACTGTGCCG | 1020 | 2041 | CAGGACCTCGTGGTGGCAAGCGCCCCCGGGCGGTTCTTGTGACCATGACACTGC | 2100 |
| Db | 961 | GTTTCCGGAATATCATGTGTGAAATGGCCGCTTTTCTGGATTCATCGACTGTGCCG | 1020 | 2041 | CAGGACCTCGTGGTGGCAAGCGCCCCCGGGCGGTTCTTGTGACCATGACACTGC | 2100 |
| Qy | 1021 | TGGGTGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCGCTGATATGTGAGAGC | 1080 | 2101 | GGCAGCTCGACCTTTACTTGTGTACGAGGATGCGATGTCTATTCGGGTGCGCGCGG | 2160 |
| Db | 1021 | TGGGTGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCGCTGATATGTGAGAGC | 1080 | 2101 | GGCAGCTCGACCTTTACTTGTGTACGAGGATGCGATGTCTATTCGGGTGCGCGCGG | 2160 |
| Qy | 1081 | TTGGGGGGAATGGGCTGACCGCTTCTCGTGTGATTCGGATTCATCGACTGTGCCG | 1140 | 2161 | GGCGACAGCAGGGGAGCCTACTCTCCCGACGCGCTCTCTACTTGAAGGCTCTTCG | 2220 |
| Db | 1081 | TTGGGGGGAATGGGCTGACCGCTTCTCGTGTGATTCGGATTCATCGACTGTGCCG | 1140 | 2161 | GGCGACAGCAGGGGAGCCTACTCTCCCGACGCGCTCTCTACTTGAAGGCTCTTCG | 2220 |
| Qy | 1141 | AGCGATCGCTTCTATCGCTTCTGACGAGTCTCTGAGTTTAAACAGACCAACG | 1200 | 2221 | GGCGGTCCACTGCTCTGCGGCTCGGGGACGCTGTGGGATCTTTGCGGCTGCGGTGC | 2280 |
| Db | 1141 | AGCGATCGCTTCTATCGCTTCTGACGAGTCTCTGAGTTTAAACAGACCAACG | 1200 | 2221 | GGCGGTCCACTGCTCTGCGGCTCGGGGACGCTGTGGGATCTTTGCGGCTGCGGTGC | 2280 |
| Qy | 1201 | GTTTCCCTCTAGCGGATCAATTCGCGCCTCTCTCCCTCCCGCCCTTAACGTTACTGC | 1260 | 2281 | ACCGAGGGGTTGCGAAGCGGTGACCTTTGTACCGTCTGAGTCTATGGAACCACTATG | 2340 |
| Db | 1201 | GTTTCCCTCTAGCGGATCAATTCGCGCCTCTCTCCCTCCCGCCCTTAACGTTACTGC | 1260 | 2281 | ACCGAGGGGTTGCGAAGCGGTGACCTTTGTACCGTCTGAGTCTATGGAACCACTATG | 2340 |
| Qy | 1261 | CGAAGCGCTTGAATAGCGCGGTGTGGTTTGTCTATGTTTATTTCCACCATATTG | 1320 | 2341 | CGGTCCCGGCTTTCACGACAACTCGTCCCTCCCGCCGTACCGCAGACATTCAGGTG | 2400 |
| Db | 1261 | CGAAGCGCTTGAATAGCGCGGTGTGGTTTGTCTATGTTTATTTCCACCATATTG | 1320 | 2341 | CGGTCCCGGCTTTCACGACAACTCGTCCCTCCCGCCGTACCGCAGACATTCAGGTG | 2400 |
| Qy | 1321 | CCGTCTTTTGGCAATCTGAGGCGCGGAAACCTGCGCTCTCTTTGACGACATTCCT | 1380 | 2401 | GCCCATCTACAGCCCTACTGCTAGCGGCAAGAGACCTAAGGTGCGGCTGCGTATGA | 2460 |
| Db | 1321 | CCGTCTTTTGGCAATCTGAGGCGCGGAAACCTGCGCTCTCTTTGACGACATTCCT | 1380 | 2401 | GCCCATCTACAGCCCTACTGCTAGCGGCAAGAGACCTAAGGTGCGGCTGCGTATGA | 2460 |
| Qy | 1381 | AGGGGTCTTTTCCCTCTCGCRAAGGAATGCAAGGTCTGTGTAATGTCTGTAAGGAGCA | 1440 | 2461 | GCCCAAGGTATAGGTGCTTCTCTGAACCGCTCGCGCCGACCTTAGGTTCGGG | 2520 |
| Db | 1381 | AGGGGTCTTTTCCCTCTCGCRAAGGAATGCAAGGTCTGTGTAATGTCTGTAAGGAGCA | 1440 | 2461 | GCCCAAGGTATAGGTGCTTCTCTGAACCGCTCGCGCCGACCTTAGGTTCGGG | 2520 |
| Qy | 1441 | GTTTCTCTGAGAGCTTTCTTGAAGACAAACACCTCTGTAGGACACCTTTGCAAGCAGCG | 1500 | 2521 | GCTATATCTTAAGGACATGGTATCGACCTTAACATCAGAACCGGGTAAAGACCATC | 2580 |
| Db | 1441 | GTTTCTCTGAGAGCTTTCTTGAAGACAAACACCTCTGTAGGACACCTTTGCAAGCAGCG | 1500 | 2521 | GCTATATCTTAAGGACATGGTATCGACCTTAACATCAGAACCGGGTAAAGACCATC | 2580 |
| Qy | 1501 | AACCCCGCCTCGGACAGTGCCTCTCGGCGCAAGGACGCTGTATAGGATACACCT | 1560 | 2581 | ACACGGGTGCGCCCATACGTAATCTGCAAGTATGGAAGTTCCTTTCGCGAGGTGTGC | 2640 |
| Db | 1501 | AACCCCGCCTCGGACAGTGCCTCTCGGCGCAAGGACGCTGTATAGGATACACCT | 1560 | 2581 | ACACGGGTGCGCCCATACGTAATCTGCAAGTATGGAAGTTCCTTTCGCGAGGTGTGC | 2640 |
| Qy | 1561 | GCAAGGCGGCAACCCAGTGCCTGTGAGTGTGATGTTGGAAGAGTCAAA | 1620 | 2641 | TCTGGGGCGCTTACATCATATATGTGATGAGTGCACCTCAACTGACTCGACCAT | 2700 |
| Db | 1561 | GCAAGGCGGCAACCCAGTGCCTGTGAGTGTGATGTTGGAAGAGTCAAA | 1620 | 2641 | TCTGGGGCGCTTACATCATATATGTGATGAGTGCACCTCAACTGACTCGACCAT | 2700 |
| Qy | 1621 | TGGCTCTCAGCGTATTCACAGGGGCTGAGGATGCCAGAGGTACCCATTGT | 1680 | 2701 | ATCCTGGGCATCGGCACAGTCTCTGGACCAAGCGGAGACGCGCTGGAGCGGCTCGTGTG | 2760 |
| Db | 1621 | TGGCTCTCAGCGTATTCACAGGGGCTGAGGATGCCAGAGGTACCCATTGT | 1680 | 2701 | ATCCTGGGCATCGGCACAGTCTCTGGACCAAGCGGAGACGCGCTGGAGCGGCTCGTGTG | 2760 |
| Qy | 1681 | ATGGGATCTGATCTGGGCTCGGTGCAATGCTTTACATGTGTTAGTTCGAGTTAAAA | 1740 | 2761 | CTCGCACCGCTACGCTTCGGGATCGGTACCGTGCACATCCAAACATCGAGGAGGTG | 2820 |
| Db | 1681 | ATGGGATCTGATCTGGGCTCGGTGCAATGCTTTACATGTGTTAGTTCGAGTTAAAA | 1740 | 2761 | CTCGCACCGCTACGCTTCGGGATCGGTACCGTGCACATCCAAACATCGAGGAGGTG | 2820 |
| Qy | 1741 | AACGTCTAGGCCCCCGAACCAAGGAGCTGGTTCCTTTGAAAAACAGTATATACC | 1800 | 2821 | GCTCTGTCCAGACTCGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC | 2880 |
| Db | 1741 | AACGTCTAGGCCCCCGAACCAAGGAGCTGGTTCCTTTGAAAAACAGTATATACC | 1800 | 2821 | GCTCTGTCCAGACTCGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC | 2880 |
| Qy | 1801 | ATGGCGCTTATAGGCTTACTCCACAGACGAGGCTTCTTGGCTGCATCATCT | 1860 | 2881 | AAGGGGGGAGGACCTCATTTTTCTGCCATTCGAAGAAATGTGATAGTCTGCGCGG | 2940 |
| Db | 1801 | ATGGCGCTTATAGGCTTACTCCACAGACGAGGCTTCTTGGCTGCATCATCT | 1860 | 2881 | AAGGGGGGAGGACCTCATTTTTCTGCCATTCGAAGAAATGTGATAGTCTGCGCGG | 2940 |
| Qy | 1861 | AGCCTACAGCGCGGACAGAACCAAGTCTGAGGGGAGGTTCGAAGTGTCTCCACCGCA | 1920 | 2941 | AAGCTGTCCGGCTCGGACTCAATGTGTAGCATATACCGGGCCTTGTATTCGCTC | 3000 |
| Db | 1861 | AGCCTACAGCGCGGACAGAACCAAGTCTGAGGGGAGGTTCGAAGTGTCTCCACCGCA | 1920 | 2941 | AAGCTGTCCGGCTCGGACTCAATGTGTAGCATATACCGGGCCTTGTATTCGCTC | 3000 |
| Qy | 1921 | ACACAATCTTCTGGGACCTGGTCAATGGCGTGTGTGGACTGTCTATCATGGTGGC | 1980 | 3001 | ATACCAACTAGCGGAGACGTCATTTGCTGTAGCAACGACGCTCTTAATAGCGGCTTACC | 3060 |
| Db | 1921 | ACACAATCTTCTGGGACCTGGTCAATGGCGTGTGTGGACTGTCTATCATGGTGGC | 1980 | 3001 | ATACCAACTAGCGGAGACGTCATTTGCTGTAGCAACGACGCTCTTAATAGCGGCTTACC | 3060 |

QY 3061 GCGGATTTGCACTCAGTGATCGACTGCAATACATGTGTCACCAGACAGTGCAGTTCAGC 3120
DB 3061 GCGGATTTGCACTCAGTGATCGACTGCAATACATGTGTCACCAGACAGTGCAGTTCAGC 3120
QY 3121 CTGGACCCGACCTTCACCAATTGAGACGACGACCGGTGCGACAAAGACGCGGTGTCAAGCTCG 3180
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QY 3181 CAGCGGCGAGGACGACTGTGTAGGGGACAGGATGGGCATTTACAGGTTGTGACTCCAGGA 3240
DB 3181 CAGCGGCGAGGACGACTGTGTAGGGGACAGGATGGGCATTTACAGGTTGTGACTCCAGGA 3240
QY 3241 GAAACGCGCTCCGGCATGTTCCGATTTCTCGGTTCCTGCGAGTGTATGACGCGGCTGT 3300
DB 3241 GAAACGCGCTCCGGCATGTTCCGATTTCTCGGTTCCTGCGAGTGTATGACGCGGCTGT 3300
QY 3301 GCTTGGTACGAGCTCACGCCCGCGAGACCTCAGTTAGGTTGCGGCTTACCTAAACACA 3360
DB 3301 GCTTGGTACGAGCTCACGCCCGCGAGACCTCAGTTAGGTTGCGGCTTACCTAAACACA 3360
QY 3361 CCAGGTTGCCCGCTCTGCCAGGACCATCTGGAGTTCTGGGAGAGCTCTTTACAGGCTC 3420
DB 3361 CCAGGTTGCCCGCTCTGCCAGGACCATCTGGAGTTCTGGGAGAGCTCTTTACAGGCTC 3420
QY 3421 ACCACATAGACGCCCATTTCTGTGCCAGACTAAGCAGGAGGAGACAACTTCCCTTAC 3480
DB 3421 ACCACATAGACGCCCATTTCTGTGCCAGACTAAGCAGGAGGAGACAACTTCCCTTAC 3480
QY 3481 CTGGTAGCATACAGGCTACGGTGTGGCCAGGCTCAGGCTCAGCTCATCTGTGGGAC 3540
DB 3481 CTGGTAGCATACAGGCTACGGTGTGGCCAGGCTCAGGCTCAGCTCATCTGTGGGAC 3540
QY 3541 CAATGTGGAAGTGTCTCATACGCTTAAAGCTTACGCTGACGCGGCCAAACCCCTGCTG 3600
DB 3541 CAATGTGGAAGTGTCTCATACGCTTAAAGCTTACGCTGACGCGGCCAAACCCCTGCTG 3600
QY 3601 TATAGGCTGGAGCGGTTCAAAACGAGTTACTACCACACACCCCAACCAATACATC 3660
DB 3601 TATAGGCTGGAGCGGTTCAAAACGAGTTACTACCACACACCCCAACCAATACATC 3660
QY 3661 ATGGCATCATCTCGGCTGACCTGGAGTGTGTACAGAGACCTGGGTGCTGGTAGGGGA 3720
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QY 3721 GTCTAGCAGCTCTGGCGGCTATTGCTGACACAGCAGCGGTGTCATTGTGGCGAG 3780
DB 3721 GTCTAGCAGCTCTGGCGGCTATTGCTGACACAGCAGCGGTGTCATTGTGGCGAG 3780
QY 3781 ATCATCTTGTCCGAAAGCGGCGCATCAITCCCAGAGGAAGTCTTTTACCGGGAGTTC 3840
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DB 4021 TGGAAATTCATCAGCGGATACAAATTTAGCAGGCTTGTCTCATCTGCTGGCAACCC 4080
QY 4081 GCGATAGCATCACTGATGGCATTCACAGCTCTATACACAGCCGCTCACCACCCACAT 4140
DB 4081 GCGATAGCATCACTGATGGCATTCACAGCTCTATACACAGCCGCTCACCACCCACAT 4140

QY 4141 ACCCTCTCTGTTTAAATCATCTCGGGGATGGGTGGCGGCCCAACTTGCTCTCCAGCGCT 4200
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QY 4201 GCTTCTGCTTTTCTGATAGGCGCGGCATCGCTGAGCGGCTGTTGGCAGCATAGGCTTGGG 4260
DB 4201 GCTTCTGCTTTTCTGATAGGCGCGGCATCGCTGAGCGGCTGTTGGCAGCATAGGCTTGGG 4260
QY 4261 AAGGTGCTTGTGGATATTTTGGCAGGTTATGGAGAGGGGTGGAGGCGCTCTGGGCC 4320
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DB 4321 TTTAAGGTTCATGAGCGGCGAGATGCCCTCCACCGAGGACCTGTTAACTATCCCTGCT 4380
QY 4381 ATCTCTCTCCCTGCGGCCCTAGTCTCGGGTCTGTGTGCGCAGCGATATCTCGTCTGGCAC 4440
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DB 4441 GTGGGCGGAGGGGAGGGGCTGTGTCAGTGTGATGAACCGGCTGTAGCGTTGCTTCGGG 4500
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DB 4501 GGTAAACCACTCTCTCCCGCACGCACTATGTGCTCAGAGCGAGCTGACAGCTGTCTACT 4560
QY 4561 CAGATCTCTCTAGTCTTACCATCACTCAGTGTCTGAAGGCTTCCACAGTGGATCAAC 4620
DB 4561 CAGATCTCTCTAGTCTTACCATCACTCAGTGTCTGAAGGCTTCCACAGTGGATCAAC 4620
QY 4621 GAGGACTCTCCAGCGCATGCTCCGGCTCGTGGCTTAAGAGATGTTGGGATGGATATGC 4680
DB 4621 GAGGACTCTCCAGCGCATGCTCCGGCTCGTGGCTTAAGAGATGTTGGGATGGATATGC 4680
QY 4681 ACGGTGTTGACTGATTTCAAGACCTGCTCCAGTCCAAAGCTCTCCCGCGCATTCGCCGGA 4740
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DB 4981 GCTGCTGAGAGTACGTTGAGGTTACCGGGTGGGGATTTTCCACTACGTGACGGGATG 5040
QY 5041 ACCACTGACAACTAAAGTCCCGTGTGAGTTTCGGGCGGCCAAAATTTCTTTCACAGAGTG 5100
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QY 5101 GATGGGCTCGGTTGCAAGGTACCGTCCAGCGTGCAAAACCCCTCTTACGGGAGGAGTTC 5160
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QY 5161 ACATTTCTGCTCGGCTCAATCAATACGTGTTGGGTACAGCTCCCATTCGAGAGCCGAA 5220
DB 5161 ACATTTCTGCTCGGCTCAATCAATACGTGTTGGGTACAGCTCCCATTCGAGAGCCGAA 5220
QY 5221 CCGGACGTAGCAGTGTCTACTTCTCCTCAGCGACCCCTCCACATTCAGCGGCGAGACG 5280

Qy 7441 TCATGCTCAGGAACTTTGGGTACCGCTTGGAGTCTGGAGACATCGGCGCAGAAAGT 7500
 Db 7441 TCATGCTCAGGAACTTTGGGTACCGCTTGGAGTCTGGAGACATCGGCGCAGAAAGT 7500
 Qy 7501 GTCCGCGTAGCTACTGTCCAGGGGGAGGGCTGCCACTTGTGGGAAGTACCTCTTC 7560
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 Qy 7561 AACTGGGAGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCTCCAGTTGAT 7620
 Db 7561 AACTGGGAGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCTCCAGTTGAT 7620
 Qy 7621 TTATCCAGCTGGTTCGTTGCTGTACAGCGGGGAGACATATATACAGCGCTGCTCTCGT 7680
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 Qy 7741 CTACTCCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTT 7800
 Db 7741 CTACTCCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTT 7800
 Qy 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
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 Qy 7861 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
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 Qy 7981 AGATCAAGT 7989
 Db 7981 AGATCAAGT 7989

RESULT 4
 SSEQ242652
 LOCUS
 DEFINITION Hepatitis C virus replicon 1377/NS3-3'UTR.
 ACCESSION AJ242652
 VERSION AJ242652.1 GI:5441834
 KEYWORDS core-neo gene; NS2 gene; NS2 proteinase; NS3 gene; NS3 proteinase/helicase; NS3/4A proteinase cofactor; NS4A gene; NS4B gene; NS4B protein; NS5a gene; NS5A phosphoprotein; NS5b gene; NS5B RNA dependant RNA polymerase; polyprotein.
 SOURCE Hepatitis C virus replicon 1377/NS3-3'UTR
 ORGANISM Hepatitis C virus replicon 1377/NS3-3'UTR
 REFERENCE 1 artificial sequences; vectors.
 2 Lohmann, V., Korner, F., Koch, J., Herian, U., Theilmann, L. and Bartenschlager, R.
 TITLE Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell line
 JOURNAL Science 285 (5424), 110-113 (1999)
 MEDLINE 93322193
 PUBMED 10390360
 REFERENCE 2 (bases 1 to 7989)
 BARTENSCHLAGER, R.
 DIRECT SUBMISSION
 TITLE Submitted (26-MAY-1999) Bartenschlager R., Institute for Virology, Johannes Gutenberg - University Mainz, Obere Zahlbacher Strasse 67, 55131 Mainz, GERMANY
 JOURNAL Location/Qualifiers
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| Dd | 61 | TCTTCACGCAGAACGCTCTAGCCATGCGGTTAGTATGAGTGTCGTGAGCCTCCAGGAC 120 |
| Qy | 121 | CCCCCTCCCGGGAGAGCCATAGTGGTCTCGGGAACCGTGTAGTACACCGGAATGCCAG 180 |
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| Qy | 361 | CTAAAGAAAAACCAAGGGCGCGCCATGATTGAACAAGATGATTTGACCGCAGGTTCTC 420 |
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| Qy | 421 | CGGCGGCTTGGGTGAGAGGCTATTTCGGCTATGACTGGGCAACAAGCAATTCGGCTGCT 480 |
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| Qy | 481 | CTGATCCGCGCTGTTTCGGCTGTCCAGCGCAGGGGCGCCGGTTCCTTTTGTCAAGA 540 |
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| DB | 3901 | GAACAAATTCAAAACAGAGGCAATCGGTTCTCTGCAAAACAGCCACCAAGCAAGCGGAGGCT | 3960 |
| QY | 3961 | GCTGCTCCCGTGGTGGAAATCCAAAGTGGCGGACCCCTCGAAGCCCTTCTGGGCGAAGCATATG | 4020 |
| DB | 3961 | GCTGCTCCCGTGGTGGAAATCCAAAGTGGCGGACCCCTCGAAGCCCTTCTGGGCGAAGCATATG | 4020 |
| QY | 4021 | TGGAATTTCAACAGCGGGATACAAATATTTAGCAGGCTTGTCCACTCTGCCCTGGCAACCCC | 4080 |
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| QY | 4081 | GGGATAGCATCACTGATGGGATTCACAGCCCTCTATACACAGCCCGCTCACACCCCAACAT | 4140 |
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| QY | 4141 | ACCCCTCTGTTTAAACATCTCTGGGGGATGGGTGGCGCCCAACTTGTCTCCCAAGCGCT | 4200 |
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| QY | 4201 | GCTTCTGCTTTGTTAGGCGCGGATCGCTGGAGCGGCTGTGTGGCAGATAGGCGCTTGGG | 4260 |
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| QY | 4261 | AAGTGTCTGTGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGGCTCGTGGCC | 4320 |
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| QY | 4501 | GGTAACACAGCTCTCCCCCAGCAGCTATGTGCTCGAGAGCAGCGCTGACGACGTTGCACT | 4560 |
| DB | 4501 | GGTAACACAGCTCTCCCCCAGCAGCTATGTGCTCGAGAGCAGCGCTGACGACGTTGCACT | 4560 |
| QY | 4561 | CAGATTCCTCTCTAGTCTTTACCATCACTCAGTCTGTGAAGAGGCTTTCACAGTGGATCAAC | 4620 |
| DB | 4561 | CAGATTCCTCTCTAGTCTTTACCATCACTCAGTCTGTGAAGAGGCTTTCACAGTGGATCAAC | 4620 |
| QY | 4621 | GAGGACTCTCCAGCCATGCTCCGGCTGTGGCTTAAGAGATGTTTGGGATTTGGATATGC | 4680 |
| DB | 4621 | GAGGACTCTCCAGCCATGCTCCGGCTGTGGCTTAAGAGATGTTTGGGATTTGGATATGC | 4680 |
| QY | 4681 | ACGGTGTGACTGATTTCAAGACCTTGGCTCCAGTCCAAAGCTCCTGCCCGGATTCGCGGGA | 4740 |
| DB | 4681 | ACGGTGTGACTGATTTCAAGACCTTGGCTCCAGTCCAAAGCTCCTGCCCGGATTCGCGGGA | 4740 |
| QY | 4741 | GTCCCTCTTCTCATGTCAACAGTGGGTACAAAGGAGTCTGGCGGGGCGAGCGGATCATG | 4800 |
| DB | 4741 | GTCCCTCTTCTCATGTCAACAGTGGGTACAAAGGAGTCTGGCGGGGCGAGCGGATCATG | 4800 |
| QY | 4801 | CMAACACCTGCCATGTGGAGCAGATCAACCGGACATGTGAATAACGCTTCCATGAGG | 4860 |
| DB | 4801 | CMAACACCTGCCATGTGGAGCAGATCAACCGGACATGTGAATAACGCTTCCATGAGG | 4860 |
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| DB | 4861 | ATCGTGGGCGCTAGGACCTGTAGTAACACGCTGGCATGGAACAATTCCTCCCATTAACCGGTAC | 4920 |
| QY | 4921 | ACCACGGGCGCTGACCGCCCTCCCGCGCGCAAAATTAATTTAGGGGCGCTGTGGCGGGTG | 4980 |
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| DB | 1 | GCACGCCCGATTGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAATCTG 60 |
| QY | 61 | TCTTCAGCAGAAAGCGTCTAGCCATGGGTTAGTATGATGTCGTGACGCTCCAGGAC 120 |
| DB | 61 | TCTTCAGCAGAAAGCGTCTAGCCATGGGTTAGTATGATGTCGTGACGCTCCAGGAC 120 |
| QY | 121 | CCCCCTCCCGGAGAGCCATAGTGGTCTCGGAAACCGGTGAGTACACCGGAATTGCCAG 180 |
| DB | 121 | CCCCCTCCCGGAGAGCCATAGTGGTCTCGGAAACCGGTGAGTACACCGGAATTGCCAG 180 |
| QY | 181 | GACGACCGGTCCTTCTTGGAATCAACCCGCTCAATGCTGAGATTTGGCGGTGCCCCC 240 |
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| QY | 301 | GTGCTTCGAGTGCCTCCCGGAGGTCTCGTAGACCGGTGCACCATGAGCAGAAATCCTAAAC 360 |
| DB | 301 | GTGCTTCGAGTGCCTCCCGGAGGTCTCGTAGACCGGTGCACCATGAGCAGAAATCCTAAAC 360 |
| QY | 361 | CTCAAGAAAAACAAA-----GGGCGCGCCATGATTGAACAAGATGGATTGC 408 |
| DB | 361 | CTCAAGAAAAACAAAAGTAAACCAACCGGCGCCATGATTGAACAAGATGGATTGC 420 |
| QY | 409 | ACGACAGTTCTTCGGCGCGCTTGGTGGAGAGGCTATTTCGGCTATGACTGGGCACACAGA 468 |
| DB | 421 | ACGACAGTTCTTCGGCGCGCTTGGTGGAGAGGCTATTTCGGCTATGACTGGGCACACAGA 480 |
| QY | 469 | CAATCGGCTGCTCTGATGCCGCGTGTTCGGGCTGTACGCGAGGGCGCCCGGTTCTTT 528 |
| DB | 481 | CAATCGGCTGCTCTGATGCCGCGTGTTCGGGCTGTACGCGAGGGCGCCCGGTTCTTT 540 |
| QY | 529 | TTGTCAAGACCGACTCTCGGTGCCCTGAAATGAATCGAGCAGGAGCGAGCGCGGCTAT 588 |
| DB | 541 | TTGTCAAGACCGACTCTCGGTGCCCTGAAATGAATCGAGCAGGAGCGAGCGCGGCTAT 600 |
| QY | 589 | CGTGGCTGGCCACGACGCGGCTTCTTTCGCGAGCTGTGCTCGACGTTGTCACTGAAGCGG 648 |
| DB | 601 | CGTGGCTGGCCACGACGCGGCTTCTTTCGCGAGCTGTGCTCGACGTTGTCACTGAAGCGG 660 |
| QY | 649 | GAAAGGACTGGTCTCTATTGGCGAAGTGCAGGCGAGGATCTCTGTCTATCTCACCTTG 708 |
| DB | 661 | GAAAGGACTGGTCTCTATTGGCGAAGTGCAGGCGAGGATCTCTGTCTATCTCACCTTG 720 |
| QY | 709 | CTCTCGCGAGAAAGTATCAATCATGCTGATGCAATGCGCGGCTGCATACGCTTGATC 768 |
| DB | 721 | CTCTCGCGAGAAAGTATCAATCATGCTGATGCAATGCGCGGCTGCATACGCTTGATC 780 |
| QY | 769 | CGGCTACTGCGCATTCGACCAACGAGGAACATTCGCATCGAGCGAGCAGCTACTCGGA 828 |
| DB | 781 | CGGCTACTGCGCATTCGACCAACGAGGAACATTCGCATCGAGCGAGCAGCTACTCGGA 840 |
| QY | 829 | TGGAAGCGGTCCTTGTTCGATCAGGATGATCTGGAACGAAGCATCAGGGGCTCGCGCCAG 888 |
| DB | 841 | TGGAAGCGGTCCTTGTTCGATCAGGATGATCTGGAACGAAGCATCAGGGGCTCGCGCCAG 900 |
| QY | 889 | CCGAATGTTTCGACGAGTCAAGCGCGCATGCCCGCAGCGGAGGATCTCGTGTGACCC 948 |
| DB | 901 | CCGAATGTTTCGACGAGTCAAGCGCGCATGCCCGCAGCGGAGGATCTCGTGTGACCC 960 |
| QY | 949 | ATGGCGATGCCGTTCGCGAATATATCGTGTGAAAAATGGCGCTTTTCTGTGATTCATCG 1008 |
| DB | 961 | ATGGCGATGCCGTTCGCGAATATATCGTGTGAAAAATGGCGCTTTTCTGTGATTCATCG 1020 |
| QY | 1009 | ACTGTGGCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATA 1068 |
| DB | 1021 | ACTGTGGCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATA 1080 |
| QY | 1069 | TTGCTGAAGAGCTTGGCGGCGAATGGGCTGACGCTTCTCTGCTTTTACGCTATCGCG 1128 |
| DB | 1081 | TTGCTGAAGAGCTTGGCGGCGAATGGGCTGACGCTTCTCTGCTTTTACGCTATCGCG 1140 |
| QY | 1129 | CTCCCGATTTCGAGCGCATCGCTTCTATCGCTTCTTACGAGTCTCTCTCAGATTATAA 1188 |
| DB | 1141 | CTCCCGATTTCGAGCGCATCGCTTCTATCGCTTCTTACGAGTCTCTCTCAGATTATAA 1200 |
| QY | 1189 | CAGACCAACAGGTTTCCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCCCT 1248 |
| DB | 1201 | CAGACCAACAGGTTTCCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCCCT 1260 |
| QY | 1249 | AACTGTAATGCGCGAGCGCTTGAATAAGCGCGGTGCGTCTGCTATATGTTATT 1308 |
| DB | 1261 | AACTGTAATGCGCGAGCGCTTGAATAAGCGCGGTGCGTCTGCTATATGTTATT 1320 |
| QY | 1309 | TCCACCATATTGCGGCTTTTTCGCAATGTGAGGCGCGGAAACCTGCGCTCTGTTCTTG 1368 |
| DB | 1321 | TCCACCATATTGCGGCTTTTTCGCAATGTGAGGCGCGGAAACCTGCGCTCTGTTCTTG 1380 |
| QY | 1369 | ACGAGCATTCCTAGGGGCTTTTCCCTCTCGCCAAAGAAATGCAAGGTCTGTTGAATGTC 1428 |
| DB | 1381 | ACGAGCATTCCTAGGGGCTTTTCCCTCTCGCCAAAGAAATGCAAGGTCTGTTGAATGTC 1440 |
| QY | 1429 | GTGAAGGAGAGTTCCTCTGGAAGCTTCTGAAGACAAACACGCTGTGACGACCCCT 1488 |
| DB | 1441 | GTGAAGGAGAGTTCCTCTGGAAGCTTCTGAAGACAAACACGCTGTGACGACCCCT 1500 |
| QY | 1489 | TGCGGACGCGGAAACCCCGCTCTGCGGACAGTGTCTCTGCGGCGCAAAAGCCACGTGA 1548 |
| DB | 1501 | TGCGGACGCGGAAACCCCGCTCTGCGGACAGTGTCTCTGCGGCGCAAAAGCCACGTGA 1560 |
| QY | 1549 | TAAGATACACTGTCAAGGCGGCAAAACCCAGTGTGAGTTGGATGATGTTG 1608 |
| DB | 1561 | TAAGATACACTGTCAAGGCGGCAAAACCCAGTGTGAGTTGGATGATGTTG 1620 |
| QY | 1609 | GAAAGATCAATATGGCTCTCTCAAGCTATTCAACAAGGGGTGAAGGATGCCAGAAG 1668 |
| DB | 1621 | GAAAGATCAATATGGCTCTCTCAAGCTATTCAACAAGGGGTGAAGGATGCCAGAAG 1680 |
| QY | 1669 | GTACCCCATTTGATGGGATCTGATCTGGGCGCTCGGTGCACATGCTTTACATGTTTAG 1728 |
| DB | 1681 | GTACCCCATTTGATGGGATCTGATCTGGGCGCTCGGTGCACATGCTTTACATGTTTAG 1740 |
| QY | 1729 | TCGAGGTTAAAAACCTCTAGGCCCCCGAACACGCGGACGTTGTTTCTTTGAAAAA 1788 |
| DB | 1741 | TCGAGGTTAAAAACCTCTAGGCCCCCGAACACGCGGACGTTGTTTCTTTGAAAAA 1800 |
| QY | 1789 | CACGATAATACCATGCGCTATTACGGCTACTCTCCAAACAGACGCGAGGCTTACTTGGC 1848 |
| DB | 1801 | CACGATAATACCATGCGCTATTACGGCTACTCTCCAAACAGACGCGAGGCTTACTTGGC 1860 |
| QY | 1849 | TGCATCATCACTAGCTTCAAGCGGACAGAACACAGGTGAGGGGAGGTCCAAAGTG 1908 |
| DB | 1861 | TGCATCATCACTAGCTTCAAGCGGACAGAACACAGGTGAGGGGAGGTCCAAAGTG 1920 |
| QY | 1909 | GTCTCCACCGCAACAATCTTTCTGCGGACCTGCTCAATGGCGGTGTTTGGACTGTC 1968 |
| DB | 1921 | GTCTCCACCGCAACAATCTTTCTGCGGACCTGCTCAATGGCGGTGTTTGGACTGTC 1980 |
| QY | 1969 | TATCATGTTGCCGGCTCAAGAGACCTTTCGCGCGCGCAAGGGCCCAATCACCCAAATGTAC 2028 |
| DB | 1981 | TATCATGTTGCCGGCTCAAGAGACCTTTCGCGCGCGCAAGGGCCCAATCACCCAAATGTAC 2040 |

QY 2029 ACCAATGTGACCAAGGACCTCGTCGGCTGGCAAGCGCCCCCGGGCGCGTTTCCTTGACA 2088
Db 2041 ACCAATGTGACCAAGGACCTCGTCGGCTGGCAAGCGCCCCCGGGCGCGTTTCCTTGACA 2100
QY 2089 CCATGCACTCGGCGAGCTCGGACCTTTACTTGTGTACAGAGCATGCCGATGTCAATCCG 2148
Db 2101 CCATGCACTCGGCGAGCTCGGACCTTTACTTGTGTACAGAGCATGCCGATGTCAATCCG 2160
QY 2149 GTGGCCCGGGCGGGCGACAGCAGGGGGAGCCCTACTCTCCCCAGGCCCGCTCTCCTACTTG 2208
Db 2161 GTGGCCCGGGCGGGCGACAGCAGGGGGAGCCCTACTCTCCCCAGGCCCGCTCTCCTACTTG 2220
QY 2209 AAGGGCTTTTCGGCGGTTCACATGCTCTGCCCTCGGGCACGCTGTGGGCATCTTTCCG 2268
Db 2221 AAGGGCTTTTCGGCGGTTCACATGCTCTGCCCTCGGGCACGCTGTGGGCATCTTTCCG 2280
QY 2269 GCTCGCGTGCACCCGAGGGGTTGCGAAGCGGTGGACTTTGTACCCGTCGAGTCTATG 2328
Db 2281 GCTCGCGTGTACCCGAGGGGTTGCGAAGCGGTGGACTTTGTACCCGTCGAGTCTATG 2340
QY 2329 GAAACCACTATGCGGTCCCGGTCTTACAGCAAACTCGTCCCTCGGGCGGTACCGGAG 2388
Db 2341 GAAACCACTATGCGGTCCCGGTCTTACAGCAAACTCGTCCCTCGGGCGGTACCGGAG 2400
QY 2389 ACATTCAGGTGGCCCATCTTACACGCCCTTACTGTTAGCGCAAGAGCACTAAGGTGCG 2448
Db 2401 ACATTCAGGTGGCCCATCTTACACGCCCTTACTGTTAGCGCAAGAGCACTAAGGTGCG 2460
QY 2449 GCTCGGTATGACGCCCAAGGTTAAAGGTGTTGTCTGAACCCGTGCGTCGCCGCCACC 2508
Db 2461 GCTCGGTATGACGCCCAAGGTTAAAGGTGTTGTCTGAACCCGTGCGTCGCCGCCACC 2520
QY 2509 CTAGGTTTCGGGGCGTATATGTTAAAGGCACATGGTATCGACCCTTAACATCAGAACCGGG 2568
Db 2521 CTAGGTTTCGGGGCGTATATGTTAAAGGCACATGGTATCGACCCTTAACATCAGAACCGGG 2580
QY 2569 GTAAGCACTATCACCGGTGCCCCCATCACTGTTTCCACTATGCAAGTTTCCTTGGC 2628
Db 2581 GTAAGCACTATCACCGGTGCCCCCATCACTGTTTCCACTATGCAAGTTTCCTTGGC 2640
QY 2629 GACGTTGTTGCTTGGGGGGCCCTATGACATATATATGTGATGATGCTCACTCAACT 2688
Db 2641 GACGTTGTTGCTTGGGGGGCCCTATGACATATATATGTGATGATGCTCACTCAACT 2700
QY 2689 GACTTCGACCACTATCCTGGGCATCGGCACAGTCTCTGACCAAGCGGAGAGCGGTGGAGCG 2748
Db 2701 GACTTCGACCACTATCCTGGGCATCGGCACAGTCTCTGACCAAGCGGAGAGCGGTGGAGCG 2760
QY 2749 CGACTCGTGTGTCGCCACCGCTACCGCTCCGGGATCGGTCAACCGTGCACATCCAAAC 2808
Db 2761 CGACTCGTGTGTCGCCACCGCTACCGCTCCGGGATCGGTCAACCGTGCACATCCAAAC 2820
QY 2809 ATCGAGAGGTGCTCTGTCCAGCACTGGAGAAATCCCTTTATGTGCAAGCCATCCCC 2868
Db 2821 ATCGAGAGGTGCTCTGTCCAGCACTGGAGAAATCCCTTTATGTGCAAGCCATCCCC 2880
QY 2869 ATCGAGACCACTAAGGGGGGAGGCACTCATTTTCTGCCATTCCTCAAGAAAGAAATGTGAT 2928
Db 2881 ATCGAGACCACTAAGGGGGGAGGCACTCATTTTCTGCCATTCCTCAAGAAAGAAATGTGAT 2940
QY 2929 GAGCTCGCCGAGAGTGTCCGCTCGGACTCAATGCTGTAGCATATTACCGGGGCTT 2988
Db 2941 GAGCTCGCCGAGAGTGTCCGCTCGGACTCAATGCTGTAGCATATTACCGGGGCTT 3000
QY 2989 GATGTATCCGTCATACCACTAGCGGAGAGTCAATTGCTGTAGCAACGAGCTCTTAATG 3048
Db 3001 GATGTATCCGTCATACCACTAGCGGAGAGTCAATTGCTGTAGCAACGAGCTCTTAATG 3060
QY 3049 ACGGGCTTTTACCGCGGATTTTCGACTCAGTGTGATCGACTGCAATATCATGTGTCACCCAGACA 3108
Db 3061 ACGGGCTTTTACCGCGGATTTTCGACTCAGTGTGATCGACTGCAATATCATGTGTCACCCAGACA 3120
QY 3109 GTCGACTTCAGCTGGACCCGACCTTCAACATTTGAGACGACGACCGGTGCCAAGAGCGG 3168

Db 3121 GTCGACTTCAGCTTGGACCCGACCTTACCAATTGAGAGCAACGCTGCCACAGACCGG 3180
QY 3169 GTGTCAAGCTCGCAGCGCGAGGAGAGCTGGTAGGGCAAGATGGGCATTTTACAGGTTT 3228
Db 3181 GTGTCAAGCTCGCAGCGCGAGGAGAGCTGGTAGGGCAAGATGGGCATTTTACAGGTTT 3240
QY 3229 GTGACTCCAGAGAACGSCCTCGGGCATGTTCCATTCCTCGGTTCTGTGAGTGTCTAT 3288
Db 3241 GTGACTCCAGAGAACGSCCTCGGGCATGTTCCATTCCTCGGTTCTGTGAGTGTCTAT 3300
QY 3289 GACCGCGGCTGTGTCTGTGTACGAGCTCACGCCCGCCGAGACCTCAGTTAGGTTCGGGCT 3348
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QY 3349 TACCTAAACACACACAGGGTTGCCCGTCTGCCAGAACCATCTGAGAGTCTTGGGAGAGGTC 3408
Db 3361 TACCTAAACACACACAGGGTTGCCCGTCTGCCAGAACCATCTGAGAGTCTTGGGAGAGGTC 3420
QY 3409 TTTTACGGCTCACCCACATAGACGCCCATTTCTTGTGCCAGACTAAGCAGGCGAGGAGAC 3468
Db 3421 TTTTACGGCTCACCCACATAGACGCCCATTTCTTGTGCCAGACTAAGCAGGCGAGGAGAC 3480
QY 3469 AACTTCCCTTACCTGTGTAGCATACAGGCTACCGGTGTGCCCGCCAGGCTCAGGCTCCACCT 3528
Db 3481 AACTTCCCTTACCTGTGTAGCATACAGGCTACCGGTGTGCCCGCCAGGCTCAGGCTCCACCT 3540
QY 3529 CCATCTGGGAGCAAAATGTGGAGTGTCTCATACGGCTAAAGCTACGCTGCACGGGCCA 3588
Db 3541 CCATCTGGGAGCAAAATGTGGAGTGTCTCATACGGCTAAAGCTACGCTGCACGGGCCA 3600
QY 3589 ACGCCCTGCTGTATAGCTGGGAGCGGTTCAAACAGAGTTACTACACACACCCCAT 3648
Db 3601 ACGCCCTGCTGTATAGCTGGGAGCGGTTCAAACAGAGTTACTACACACACCCCAT 3660
QY 3649 ACCAAATACATCATGTGGCATGTCCGCTACCTCGAGGTCTGTCACAGCAGCACCTGGGTG 3708
Db 3661 ACCAAATACATCATGTGGCATGTCCGCTACCTCGAGGTCTGTCACAGCAGCACCTGGGTG 3720
QY 3709 CTGTTAGCGGAGTCTTAGCAGTCTTGGCCGCGTATTTGCCCTGACAAACAGGACGCTGGTC 3768
Db 3721 CTGTTAGCGGAGTCTTAGCAGTCTTGGCCGCGTATTTGCCCTGACAAACAGGACGCTGGTC 3780
QY 3769 ATTGTGGGAGGATCATCTTGTCCGGAAGCGCGCCATCATTTCCGACAGGGAAGTCTTT 3828
Db 3781 ATTGTGGGAGGATCATCTTGTCCGGAAGCGCGCCATCATTTCCGACAGGGAAGTCTTT 3840
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QY 3889 ATGAGCTCCCGAAACAAATTCAAACAGAGGAAATCGGGTGTGCAAAACAGCCACCAAG 3948
Db 3901 ATGAGCTCCCGAAACAAATTCAAACAGAGGAAATCGGGTGTGCAAAACAGCCACCAAG 3960
QY 3949 CAAGCGAGGCTCTGCTCCCGTGTGGATCAAGTGGGGGACCTCGAAGCTTCTGG 4008
Db 3961 CAAGCGAGGCTCTGCTCCCGTGTGGATCAAGTGGGGGACCTCGAAGCTTCTGG 4020
QY 4009 GCGAAGCATATGTGGAATTTTCATCAGCGGATACAATATTAGCAGGCTTGTCCACTCTG 4068
Db 4021 GCGAAGCATATGTGGAATTTTCATCAGCGGATACAATATTAGCAGGCTTGTCCACTCTG 4080
QY 4069 CTGTGGCAACCCCGCATAGATCATCTGATGGCATTCACAGCTCTTATCACCACCCGCTC 4128
Db 4081 CTGTGGCAACCCCGCATAGATCATCTGATGGCATTCACAGCTCTTATCACCACCCGCTC 4140
QY 4129 ACCACCAACATACCTCTGTTTAAATCCTCGGGGGATGGGTGGCGGCCCACTTGTCT 4188
Db 4141 ACCACCAACATACCTCTGTTTAAATCCTCGGGGGATGGGTGGCGGCCCACTTGTCT 4200
QY 4189 CTCTCCAGCGCTGCTTCTGCTTCTGTTAGGCGCGGCATCGCTGAGCGGCTGTTGGCAGC 4248

| | | | | | | | |
|----|------|---|------|----|------|--|------|
| Db | 4201 | CCTCCAGCGCTGCTTCTGCTTTTCGTAGCGCGGCATCGCTGGAGCGGCTTGTGGCAGC | 4260 | QY | 5329 | TCAGTAGCCAGCTGCTGTGCGCTTCTTGTAAGGCAACATGCACTACCGGTATGACTCC | 5388 |
| QY | 4249 | ATAGAGCTTGGAGAGTCTGTGATATTTTGGCAGGTTATGGAGCAGGGTGCAGGC | 4308 | Db | 5341 | TCAGTAGCCAGCTGCTGTGCGCTTCTTGTAAGGCAACATGCACTACCGGTATGACTCC | 5400 |
| Db | 4261 | ATAGAGCTTGGAGAGTCTGTGATATTTTGGCAGGTTATGGAGCAGGGTGCAGGC | 4320 | QY | 5389 | CGGACGCTGACCTCATGAGGCCAACCTCTGTGCGCGCAGGAGATGGCGGGAAACATC | 5448 |
| QY | 4309 | GGGCTCGTGGCCCTTTAAGGTCAATGAGCGCGAGATGCCCTCCACCGAGGACCTGGTTAAC | 4368 | Db | 5401 | CGGACGCTGACCTCATGAGGCCAACCTCTGTGCGCGCAGGAGATGGCGGGAAACATC | 5460 |
| Db | 4321 | GGGCTCGTGGCCCTTTAAGGTCAATGAGCGCGAGATGCCCTCCACCGAGGACCTGGTTAAC | 4380 | QY | 5449 | ACCCCGCTGGAGTCAGAAAATAAGGTAGTAAATTTTGGACTCTTTTCGAGCGGCTCCAAGCG | 5508 |
| QY | 4369 | CTACTCCCTGCTATCTCTCCCTCGCGCCCTAGTCTGTCGGGGTGTGTGCGCAGGATA | 4428 | Db | 5461 | ACCCCGCTGGAGTCAGAAAATAAGGTAGTAAATTTTGGACTCTTTTCGAGCGGCTCCAAGCG | 5520 |
| Db | 4381 | CTACTCCCTGCTATCTCTCCCTCGCGCCCTAGTCTGTCGGGGTGTGTGCGCAGGATA | 4440 | QY | 5509 | GAGGAGGATGAGAGGAAAGTATCCGTTCCGGCGGAGATCTCTCGGAGGTCACAGGAAATTC | 5568 |
| QY | 4429 | CTGCGTCCGACGTCGGCCCGAGGAGGGGGTGTGCACTGATGAACCGGCTGATAGCG | 4488 | Db | 5521 | GAGGAGGATGAGAGGAAAGTATCCGTTCCGGCGGAGATCTCTCGGAGGTCACAGGAAATTC | 5580 |
| Db | 4441 | CTGCGTCCGACGTCGGCCCGAGGAGGGGGTGTGCACTGATGAACCGGCTGATAGCG | 4500 | QY | 5569 | CCTCAGCGATGCCATATGGCAGCGCGGATTAACCCCTCCACTGTTAGAGTCCTCG | 5628 |
| QY | 4489 | TTTCGCTTCGCGGGTAACACAGCTCTCCCGCCACGCACTATGTGCTGAGAGCGACGTGCA | 4548 | Db | 5581 | CCTCAGCGATGCCATATGGCAGCGCGGATTAACCCCTCCACTGTTAGAGTCCTCG | 5640 |
| Db | 4501 | TTTCGCTTCGCGGGTAACACAGCTCTCCCGCCACGCACTATGTGCTGAGAGCGACGTGCA | 4560 | QY | 5629 | AAGGACCCCGACTAGCTCCCTCCAGTGSTACACGGGTGTTCATTTGCGGCTCCCAAGGCC | 5688 |
| QY | 4549 | GCACTGTCTCAGATCTCTCTAGTCTTACATCACTCAGTCTGATGAGAGGCTTCAAC | 4608 | Db | 5641 | AAGGACCCCGACTAGCTCCCTCCAGTGSTACACGGGTGTTCATTTGCGGCTCCCAAGGCC | 5700 |
| Db | 4561 | GCACTGTCTCAGATCTCTCTAGTCTTACATCACTCAGTCTGATGAGAGGCTTCAAC | 4620 | QY | 5689 | CCTCCGATACCACTCCACCGAGGAGAGGACGGTGTCTCTCAGAACTACCGGTGTCT | 5748 |
| QY | 4609 | CAGTGGATCAACGAGGACTGCTCCAGCCATGCTCCGGCTCGTGGCTAAGAGATGTTGG | 4668 | Db | 5701 | CCTCCGATACCACTCCACCGAGGAGAGGACGGTGTCTCTCAGAACTACCGGTGTCT | 5760 |
| Db | 4621 | CAGTGGATCAACGAGGACTGCTCCAGCCATGCTCCGGCTCGTGGCTAAGAGATGTTGG | 4680 | QY | 5749 | TCCTGCTGGCGAGCTCCGACAAAGACCTTCGCGAGCTCCGAACTGTCGCGCGCTCGAC | 5808 |
| QY | 4669 | GATTGATATGACAGCGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAGGCTCTTGCGC | 4728 | Db | 5761 | TCCTGCTGGCGAGCTCCGACAAAGACCTTCGCGAGCTCCGAACTGTCGCGCGCTCGAC | 5820 |
| Db | 4681 | GATTGATATGACAGCGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAGGCTCTTGCGC | 4740 | QY | 5809 | ACGGCACCGCAACCGCTCTCTGACACAGCCCTCCGACGACGGCGACCGGATCCGAC | 5868 |
| QY | 4729 | CGATTGCGGGAGTCCCTTCTTCTCATGTCAACGTTGGGTACAGGAGTCTGGCGGGC | 4788 | Db | 5821 | ACGGCACCGCAACCGCTCTCTGACACAGCCCTCCGACGACGGCGACCGGATCCGAC | 5880 |
| Db | 4741 | CGATTGCGGGAGTCCCTTCTTCTCATGTCAACGTTGGGTACAGGAGTCTGGCGGGC | 4800 | QY | 5869 | GTTGAGTCTGATCTCTCCATGCCCCCTTGAGGGGGAGCGGGGGATCCGATCTCAGC | 5928 |
| QY | 4789 | GACGGCATATGCAAAACCACTGCGCATGTGGAGCACAGATCAACCGGACATGTGAAAAC | 4848 | Db | 5881 | GTTGAGTCTGATCTCTCCATGCCCCCTTGAGGGGGAGCGGGGGATCCGATCTCAGC | 5940 |
| Db | 4801 | GACGGCATATGCAAAACCACTGCGCATGTGGAGCACAGATCAACCGGACATGTGAAAAC | 4860 | QY | 5929 | GACGGCTCTGCTACCGTAAAGCGAGGAGGTAGTGAGAGCTGCTGCTCTCGATG | 5988 |
| QY | 4849 | GGTTCCATGAGGATCGTGGGGCTAGGACCTGAGTAAACAGTGGATGGAACATTTCCC | 4908 | Db | 5941 | GACGGCTCTGCTACCGTAAAGCGAGGAGGTAGTGAGAGCTGCTGCTCTCGATG | 6000 |
| Db | 4861 | GGTTCCATGAGGATCGTGGGGCTAGGACCTGAGTAAACAGTGGATGGAACATTTCCC | 4920 | QY | 5989 | TCTTACACATGACAGCGCCCTGTATCAGCCATGCGCTCGGAGGAAACCAAGCTGCC | 6048 |
| QY | 4909 | ATTACCGGTACACAGCGGCCCTGACGCCCCCTCCCGCGCCCAATTTCTAGGGCG | 4968 | Db | 6001 | TCTTACACATGACAGCGCCCTGTATCAGCCATGCGCTCGGAGGAAACCAAGCTGCC | 6060 |
| Db | 4921 | ATTACCGGTACACAGCGGCCCTGACGCCCCCTCCCGCGCCCAATTTCTAGGGCG | 4980 | QY | 6049 | ATCAATGCACTGAGCAACTCTTTGCTCCGTACCACTTGGTCTATGCTACCAATCT | 6108 |
| QY | 4969 | CTGTGCGGGTGGCTGCTGAGGAGTACGTGGAGTTACCGGGTGGGGATTTCCACTAC | 5028 | Db | 6061 | ATCAATGCACTGAGCAACTCTTTGCTCCGTACCACTTGGTCTATGCTACCAATCT | 6120 |
| Db | 4981 | CTGTGCGGGTGGCTGCTGAGGAGTACGTGGAGTTACCGGGTGGGGATTTCCACTAC | 5040 | QY | 6109 | CGCAGCGAAGCTCGCGCAGAGAGGTACCTTTGACAGACTGCAAGTCTCTGGACGAC | 6168 |
| QY | 5029 | GTGACGGGATGACCACTGACAAACGTAAGTCCCGTGTGAGTTCCGGCCCCCGAATTC | 5088 | Db | 6121 | CGCAGCGAAGCTCGCGCAGAGAGGTACCTTTGACAGACTGCAAGTCTCTGGACGAC | 6180 |
| Db | 5041 | GTGACGGGATGACCACTGACAAACGTAAGTCCCGTGTGAGTTCCGGCCCCCGAATTC | 5100 | QY | 6169 | CACCTACCGGAGCTGCTCAAGGAGATGAAGCGGAGCGCTCCACAGTTAAGGCTAACTT | 6228 |
| QY | 5089 | TTTACAGAGTGTAGTGGGTGCGGTGTGACAGGTACGCTCCAGCGTGCAACCCCTCCTA | 5148 | Db | 6181 | CACCTACCGGAGCTGCTCAAGGAGATGAAGCGGAGCGCTCCACAGTTAAGGCTAACTT | 6240 |
| Db | 5101 | TTTACAGAGTGTAGTGGGTGCGGTGTGACAGGTACGCTCCAGCGTGCAACCCCTCCTA | 5160 | QY | 6229 | CTATCCGTGGAGAAAGCTTGAAGTGTAGCTGAGCCCCCACTTGGCCAGATCTAAATTTGGC | 6288 |
| QY | 5149 | CGGAGGAGTCACTTCTGCTGGGCTCAATCAATACCTGTTGGTGGGTCACAGCTCCCA | 5208 | Db | 6241 | CTATCCGTGGAGAAAGCTTGAAGTGTAGCTGAGCCCCCACTTGGCCAGATCTAAATTTGGC | 6300 |
| Db | 5161 | CGGAGGAGTCACTTCTGCTGGGCTCAATCAATACCTGTTGGTGGGTCACAGCTCCCA | 5220 | QY | 6289 | TATGGGCAAGAGCTCGGAGACCTATCCAGCAAGCGCTTAAACACATCCCGTCCGTG | 6348 |
| QY | 5209 | TGCGAGCCCGAACCGGACGTAGAGTGTCTCACTTCCATGTCTACCGACCCCTCCCAT | 5268 | Db | 6301 | TATGGGCAAGAGCTCGGAGACCTATCCAGCAAGCGCTTAAACACATCCCGTCCGTG | 6360 |
| Db | 5221 | TGCGAGCCCGAACCGGACGTAGAGTGTCTCACTTCCATGTCTACCGACCCCTCCCAT | 5280 | QY | 6349 | TGGAAGGACTTGTGGAAGACACTGAGACACCAATTTGACACCACTATCTGGAACAAAAT | 6408 |
| QY | 5269 | ACGGCGAGAGCTTACGCTAGGCTGGCCAGGGGATCTCCCTCTCTTGGCCAGCTCA | 5328 | Db | 6361 | TGGAAGGACTTGTGGAAGACACTGAGACACCAATTTGACACCACTATCTGGAACAAAAT | 6420 |
| Db | 5281 | ACGGCGAGAGCTTACGCTAGGCTGGCCAGGGGATCTCCCTCTCTTGGCCAGCTCA | 5340 | | | | |

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QY 6409 GAGGTTTCTGCGTCCAAACAGAGAAAGGGGCGCGCAAGCCAGCTCGCTTATCGTAATTC 6468
DB 6421 GAGGTTTCTGCGTCCAAACAGAGAAAGGGGCGCGCAAGCCAGCTCGCTTATCGTAATTC 6480
QY 6469 CCAGATTGGGGGTTGCGTGTGCGAGAAATAGGCGCTTTAGCATGTGCTTCCACCCCTC 6528
DB 6481 CCAGATTGGGGGTTGCGTGTGCGAGAAATAGGCGCTTTAGCATGTGCTTCCACCCCTC 6540
QY 6529 CCTCAGGCGGTGATGGGCTCTTATACGGATTCCAAATACTCTCTCTGGACAGCGGCTCGAG 6588
DB 6541 CCTCAGGCGGTGATGGGCTCTTATACGGATTCCAAATACTCTCTCTGGACAGCGGCTCGAG 6600
QY 6589 TTCCTGTGTAATGCTCGGAAGCGAAGAAATGCCCTATAGGGCTTCCGATATGACACCCGC 6648
DB 6601 TTCCTGTGTAATGCTCGGAAGCGAAGAAATGCCCTATAGGGCTTCCGATATGACACCCGC 6660
QY 6649 TGTTTGACTCAAGCGTCACGTGAGATGACATCCGCTGTGAGAGTCAATCTACCAATGT 6708
DB 6661 TGTTTGACTCAAGCGTCACGTGAGATGACATCCGCTGTGAGAGTCAATCTACCAATGT 6720
QY 6709 TGTGACTTGGCCCCCGAAGCCAGACAGGCCATAAGTCTGCTCACAGAGCGGCTTTACATC 6768
DB 6721 TGTGACTTGGCCCCCGAAGCCAGACAGGCCATAAGTCTGCTCACAGAGCGGCTTTACATC 6780
QY 6769 GGGGCCCCCTGACTAATTTCTAAGGCGAGAACTGCGGCTATGCGCGGTGCGCGCGAGC 6828
DB 6781 GGGGCCCCCTGACTAATTTCTAAGGCGAGAACTGCGGCTATGCGCGGTGCGCGCGAGC 6840
QY 6829 GGTGTACTGACGACGAGCTGGGTAAATACCTTCACATGTTACTTGAAGCGGCTCGGCG 6888
DB 6841 GGTGTACTGACGACGAGCTGGGTAAATACCTTCACATGTTACTTGAAGCGGCTCGGCGC 6900
QY 6889 TGTGAGCTGCGAAGCTCCAGGACTGCAAGTGTCTGATGCGGAGACGACCTTGTGCTT 6948
DB 6901 TGTGAGCTGCGAAGCTCCAGGACTGCAAGTGTCTGATGCGGAGACGACCTTGTGCTT 6960
QY 6949 ATCTGTGAAGCGGGGACCCAGAGAGAGCGAGCGCTTACGGGCTTCCAGGAGCT 7008
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LOCUS AX036254 8001 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 3 from Patent EPI043399.
ACCESSION AX036254
VERSION AX036254.1 GI:11225870
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1
AUTHORS Bartenschlager R.D.
TITLE Hepatitis c virus cell culture system
JOURNAL Patent: Ep 1043399-A 3 11-OCT-2000;
BARTENSCHLAGER RALF DR (DE)
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ORIGIN
Query Match 99.7%; Score 7967; DB 6; Length 8001;
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Matches 7989; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

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DB 61 TCTTCAGCGAAGAGCGTCTAGCCATGGCGCTAGTAGTGTGCTGAGCGCTCCAGGAC 120
QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAAATGGCAG 180
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| QY | 3229 | GTGACTCCAGAGAACGCGCTCCGGCAT | TGTTTCAATTCCTCGGTTCGTGCGAGTGTAT | 3288 | Db | 4321 | GCGCTCGTGGCTTTTAAAGTTCATGAG | CGCGAGATGCCCTCCACCGAGGACCTGCTTAAAC | 4380 |
| Db | 3241 | GTGACTCCAGAGAACGCGCTCCGGCAT | TGTTTCAATTCCTCGGTTCGTGCGAGTGTAT | 3300 | QY | 4369 | CTACTCCTCTGCTATCTCTCCCTGGCG | CCCTAGTCTGCTGGGTCGTGTGCGCAGCGATA | 4428 |
| QY | 3289 | GACCGGGCTGTGCTTGTGTAGAGTCA | CGCCCGCGAGCCTCAGTTAGTTTGGGGCT | 3348 | Db | 4381 | CTACTCCTCTGCTATCTCTCCCTGGCG | CCCTAGTCTGCTGGGTCGTGTGCGCAGCGATA | 4440 |
| Db | 3301 | GACCGGGCTGTGCTTGTGTAGAGTCA | CGCCCGCGAGCCTCAGTTAGTTTGGGGCT | 3360 | QY | 4429 | CTGGTTCGGCACGTGGGCCCGGAGGGG | CGCTGTGCAATGGAACCGGCTGATAGC | 4488 |
| QY | 3349 | TACCTAAACACACCGAGGTTGCCCGT | CTGCGAGGACCATCTGGAGTTCTGGAGAGGCTC | 3408 | Db | 4441 | CTGGTTCGGCACGTGGGCCCGGAGGGG | CGCTGTGCAATGGAACCGGCTGATAGC | 4500 |
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| QY | 3409 | TTTACAGGCTCACCCACATAGACGCC | CAATTTCTTGTCCAGACTAAGCAGGAGAGAC | 3468 | | | | | |

| | | | | | | | |
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| Db | 4501 | TTCTGCTTCGGGGTAAACCAAGTCTCTCCCAACGCACTATGTGCTGAGAGCAAGCTGCA | 4560 | Qy | 5629 | AAGGACCCGAGTACGTCTCCCTCCAGTGGTACACGGGTGTCCATTGCGGCTGCCAAGGC | 5688 |
| Qy | 4549 | GCACTGTCACTCAGATCTCTCTAGTCTTACATCACTCAGTCTGAAGAGGCTTAC | 4608 | Db | 5641 | AAGGACCCGAGTACGTCTCCCTCCAGTGGTACACGGGTGTCCATTGCGGCTGCCAAGGC | 5700 |
| Db | 4561 | GCACTGTCACTCAGATCTCTCTAGTCTTACATCACTCAGTCTGAAGAGGCTTAC | 4620 | Qy | 5689 | CCTCCGATACCACTTCCACGGAGGAGAGGAGCGTGTCTCTCAGAACTACCGGTCT | 5748 |
| Qy | 4609 | CAGTGGATCAACGAGGAGTCTCCACGCCATGCTCCGGTCTGGTGAAGAGATGTTGG | 4668 | Db | 5701 | CCTCCGATACCACTTCCACGGAGGAGAGGAGCGTGTCTCTCAGAACTACCGGTCT | 5760 |
| Db | 4621 | CAGTGGATCAACGAGGAGTCTCCACGCCATGCTCCGGTCTGGTGAAGAGATGTTGG | 4680 | Qy | 5749 | TCCTGCTTCGGGAGTCTGCCCAAAAGACTTTCGGCAGCTCCGAATCTGTCGGCCGCTGAC | 5808 |
| Qy | 4669 | GATTGGATATGACCGGTGTGATGATTTCAAGACCTGCTCCAGTCCAAGTCTTCGCG | 4728 | Db | 5761 | TCCTGCTTCGGGAGTCTGCCCAAAAGACTTTCGGCAGCTCCGAATCTGTCGGCCGCTGAC | 5820 |
| Db | 4681 | GATTGGATATGACCGGTGTGATGATTTCAAGACCTGCTCCAGTCCAAGTCTTCGCG | 4740 | Qy | 5809 | AGCGGACCGGCAACCGGCTCTCTGACACGCTCTCCGAAGACCGGAGGAGATCCGAC | 5868 |
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| Db | 4801 | GACGGCATCATGCAAAACCACTTCCATGCTGGAGCAAGATCACCGGACATGTGAAAAAC | 4860 | Qy | 5929 | GACGGTCTTGGTCTTACCGTAAGCGAGGAGGCTAGTGAGGACGTCGTCTGCTCTCGATG | 5988 |
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| Qy | 4969 | CTGTGGCGGTGCTGCTGAGGAGTACGTGAGGTACCGGGTGGGGATTTCCACTAC | 5028 | Db | 6061 | ATCAATGCTAGGAACTCTTTCCTCCGCTGACCAACACTTGTCTATGCTCAACAATCT | 6120 |
| Db | 4981 | CTGTGGCGGTGCTGCTGAGGAGTACGTGAGGTACCGGGTGGGGATTTCCACTAC | 5040 | Qy | 6109 | CGCAGCGCAAGCTCGGGCAGAAAGAGTCACTTTTGACAGACTGCAAGTCTCTGGACAC | 6168 |
| Qy | 5029 | GTCAACGGCATGACCACTGACAAAGTAAAGTGCCGTGTCAAGTTCGCGCCCGCAATTC | 5088 | Db | 6121 | CGCAGCGCAAGCTCGGGCAGAAAGAGTCACTTTTGACAGACTGCAAGTCTCTGGACAC | 6180 |
| Db | 5041 | GTCAACGGCATGACCACTGACAAAGTAAAGTGCCGTGTCAAGTTCGCGCCCGCAATTC | 5100 | Qy | 6169 | CACCTACCGGACGTGCTCAAGGAGATGAAGGAGGCGCTCCACAGTTAAGGCTAAACTT | 6228 |
| Qy | 5089 | TTCAAGAGTGGATGGGTGCGGTTCGACAGGTACGCTCCAGGTTCGAACCCCTCTTA | 5148 | Db | 6181 | CACCTACCGGACGTGCTCAAGGAGATGAAGGAGGCGCTCCACAGTTAAGGCTAAACTT | 6240 |
| Db | 5101 | TTCAAGAGTGGATGGGTGCGGTTCGACAGGTACGCTCCAGGTTCGAACCCCTCTTA | 5160 | Qy | 6229 | CTATTCGTGAGGAGGCTGTAGCTGACGCCCCCACTTCGGCCAGACTTAATAATTTGGC | 6288 |
| Qy | 5149 | CGGAGAGGTACATTCCTGCTCGGCTCAATCAATACCTGCTGGGTGCTCAGCTCCCA | 5208 | Db | 6241 | CTATTCGTGAGGAGGCTGTAGCTGACGCCCCCACTTCGGCCAGACTTAATAATTTGGC | 6300 |
| Db | 5161 | CGGAGAGGTACATTCCTGCTCGGCTCAATCAATACCTGCTGGGTGCTCAGCTCCCA | 5220 | Qy | 6289 | TATGGGCAAGAGAGCTCCGGAACCTATCCAGCAAGGCGCTTAACCACTCCGCTCCGTG | 6348 |
| Qy | 5209 | TGCAGGCGCGAACCGGACGTAGTGTCTCATTTCCATGTCTACCGACCCCTCCCAAT | 5268 | Db | 6301 | TATGGGCAAGAGAGCTCCGGAACCTATCCAGCAAGGCGCTTAACCACTCCGCTCCGTG | 6360 |
| Db | 5221 | TGCAGGCGCGAACCGGACGTAGTGTCTCATTTCCATGTCTACCGACCCCTCCCAAT | 5280 | Qy | 6349 | TGGAAGGACTTGTCTGGAAGACACTGAGACACCAATTGACACCACTCATGGGCAAAAT | 6408 |
| Qy | 5269 | ACGCGGAGACGGCTAAGCTAGCTGGCGGAGGATCTCCCTCTCTTGGCCAGCTCA | 5328 | Db | 6361 | TGGAAGGACTTGTCTGGAAGACACTGAGACACCAATTGACACCACTCATGGGCAAAAT | 6420 |
| Db | 5281 | ACGCGGAGACGGCTAAGCTAGCTGGCGGAGGATCTCCCTCTCTTGGCCAGCTCA | 5340 | Qy | 6409 | GAGTTCCTGCTGCTCCAAACAGAGAGGCGGCGCAAGCCAGCTCGCTTATCGTATTC | 6468 |
| Qy | 5329 | TCAGTACCGAGCTGCTGCGCTTCTTGAAGGCAACATGCACTACCGCTCATGCTCC | 5388 | Db | 6421 | GAGTTCCTGCTGCTCCAAACAGAGAGGCGGCGCAAGCCAGCTCGCTTATCGTATTC | 6480 |
| Db | 5341 | TCAGTACCGAGCTGCTGCGCTTCTTGAAGGCAACATGCACTACCGCTCATGCTCC | 5400 | Qy | 6469 | CCAGATTGGGGTTCGTGTGTGCGAGAAATGCGCCCTTTACGATGTGCTTCCACCCCTC | 6528 |
| Qy | 5389 | CCGACCGTGTACCTCATCGAGGCCAACCTCTGTGGCGGAGAGATGGGCGGGAATC | 5448 | Db | 6481 | CCAGATTGGGGTTCGTGTGTGCGAGAAATGCGCCCTTTACGATGTGCTTCCACCCCTC | 6540 |
| Db | 5401 | CCGACCGTGTACCTCATCGAGGCCAACCTCTGTGGCGGAGAGATGGGCGGGAATC | 5460 | Qy | 6529 | CCTCAGGCGGTGATGGGCTCTTCAATGGAATTAATCTCTCTGGAACGCGGTCCAG | 6588 |
| Qy | 5449 | ACCGCGTGGATCAGAAATAGGTAGTAAATTTGGAATTTTGGACTCTTTCGAGCCGCTCAAGC | 5508 | Db | 6541 | CCTCAGGCGGTGATGGGCTCTTCAATGGAATTAATCTCTCTGGAACGCGGTCCAG | 6600 |
| Db | 5461 | ACCGCGTGGATCAGAAATAGGTAGTAAATTTGGAATTTTGGACTCTTTCGAGCCGCTCAAGC | 5520 | Qy | 6589 | TTCTCTGCTGATGCTGGAGAGGAGAAATGCGCTATGGGCTTCGCATATGACACCCGC | 6648 |
| Qy | 5509 | GAGGAGATGAGAGGAGATATCCGTTCCGGCGGAGATCCCTCGGAGTCCAGGAAATTC | 5568 | Db | 6601 | TTCTCTGCTGATGCTGGAGAGGAGAAATGCGCTATGGGCTTCGCATATGACACCCGC | 6660 |
| Db | 5521 | GAGGAGATGAGAGGAGATATCCGTTCCGGCGGAGATCCCTCGGAGTCCAGGAAATTC | 5580 | Qy | 6649 | TGTTTTGACTCAACCGTCACTGAGATGACATCCGTTGTGAGGAGTCAATCTTACCAATGT | 6708 |
| Qy | 5569 | CCTCGAGCGATGCCCATATGGGACACCGCGGATTAACACCCCTCCACTGTTAGTCTGG | 5628 | Db | 6661 | TGTTTTGACTCAACCGTCACTGAGATGACATCCGTTGTGAGGAGTCAATCTTACCAATGT | 6720 |
| Db | 5581 | CCTCGAGCGATGCCCATATGGGACACCGCGGATTAACACCCCTCCACTGTTAGTCTGG | 5640 | | | | |

| | | | |
|----|------|---|------|
| QY | 6709 | TGTGACTTTGGCCCCCGAAGCAGACAGGCCATAAGTTCGCTCA CAGAGCGGCTTTTACATC | 6768 |
| DB | 6721 | TGTGACTTTGGCCCCCGAAGCAGACAGGCCATAAGTTCGCTCA CAGAGCGGCTTTTACATC | 6780 |
| QY | 6769 | GGGGSCCCCTTGACTTAATTCTAAAGGCAGAACCTCGCGCTAT CGCGGTGCGCGCGAGC | 6828 |
| DB | 6781 | GGGGSCCCCTTGACTTAATTCTAAAGGCAGAACCTCGCGCTAT CGCGGTGCGCGCGAGC | 6840 |
| QY | 6829 | GGTGTA CTGACGACAGCTGCGGTAATAACCTCACATGTTACT TGAAGGCGCTTCACGAGGCT | 6888 |
| DB | 6841 | GGTGTA CTGACGACAGCTGCGGTAATAACCTCACATGTTACT TGAAGGCGCTTCACGAGGCT | 6900 |
| QY | 6889 | TGTCGAGCTGCGAAGCTCCAGACTGCGACAGTGTCTGTATGCG GAGACGACTTGTGCTTT | 6948 |
| DB | 6901 | TGTCGAGCTGCGAAGCTCCAGACTGCGACAGTGTCTGTATGCG GAGACGACTTGTGCTTT | 6960 |
| QY | 6949 | ATCTGTGAAGCGGGGACCACAAGAGGACGAGCGAGCCTTACG GSGCTTTCACGAGGCT | 7008 |
| DB | 6961 | ATCTGTGAAGCGGGGACCACAAGAGGACGAGCGAGCCTTACG GSGCTTTCACGAGGCT | 7020 |
| QY | 7009 | ATGACTAGATACTCTGCCCCCCCCTGGGGACCGGCCCAAAC CAGAATACGACTTGGAGTTG | 7068 |
| DB | 7021 | ATGACTAGATACTCTGCCCCCCCCTGGGGACCGGCCCAAAC CAGAATACGACTTGGAGTTG | 7080 |
| QY | 7069 | ATAACATCATGCTCCTCCAATGTCTAGTGTGCGCACGATGOA TCTGCAAAAGGTTGTAC | 7128 |
| DB | 7081 | ATAACATCATGCTCCTCCAATGTCTAGTGTGCGCACGATGOA TCTGCAAAAGGTTGTAC | 7140 |
| QY | 7129 | TATCTCACCGTGACCCACACACCCCTTTGCGGGGCTGCTGG GAGACAGCTAGACAC | 7188 |
| DB | 7141 | TATCTCACCGTGACCCACACACCCCTTTGCGGGGCTGCTGG GAGACAGCTAGACAC | 7200 |
| QY | 7189 | ACTCCAGTCAATTCTTGCTAGGCAACATCATCATGTATGCGC CCACCTTGTGGGCAAGG | 7248 |
| DB | 7201 | ACTCCAGTCAATTCTTGCTAGGCAACATCATCATGTATGCGC CCACCTTGTGGGCAAGG | 7260 |
| QY | 7249 | ATGATTCCTGATGACTCAATTTCTTCCTCATCCTTCTAGCT CAGGAACAACCTTGAAAAGCC | 7308 |
| DB | 7261 | ATGATTCCTGATGACTCAATTTCTTCCTCATCCTTCTAGCT CAGGAACAACCTTGAAAAGCC | 7320 |
| QY | 7309 | CTGATTTGT CAGATCTAGGGGCTGTTACTCCATTGAGCCTT GACCTTACCTCAGATC | 7368 |
| DB | 7321 | CTGATTTGT CAGATCTAGGGGCTGTTACTCCATTGAGCCTT GACCTTACCTCAGATC | 7380 |
| QY | 7369 | ATTCAACGACTCCATGAGCTTTAGCGCAATTTTCACTCCAT AGTTACTCTCCAGTGAGATC | 7428 |
| DB | 7381 | ATTCAACGACTCCATGAGCTTTAGCGCAATTTTCACTCCAT AGTTACTCTCCAGTGAGATC | 7440 |
| QY | 7429 | AATAGGTTGGCTTCATGCTTCAGAAACTTTGGGTTACCGCT TCGAGTCTCGAGACAT | 7488 |
| DB | 7441 | AATAGGTTGGCTTCATGCTTCAGAAACTTTGGGTTACCGCT TCGAGTCTCGAGACAT | 7500 |
| QY | 7489 | CGGGCCAGAGTGTGCGGCTAGGCTACTGTCAGGGGGGAGG GTGCCACTTGTGGC | 7548 |
| DB | 7501 | CGGGCCAGAGTGTGCGGCTAGGCTACTGTCAGGGGGGAGG GTGCCACTTGTGGC | 7560 |
| QY | 7549 | AAGTACCTCTTCAACTGGGAGTAAGGACCAAGCTCAAACT CAACTCTCAATCCCGGCTGG | 7608 |
| DB | 7561 | AAGTACCTCTTCAACTGGGAGTAAGGACCAAGCTCAAACT CAACTCTCAATCCCGGCTGG | 7620 |
| QY | 7609 | TCCAGTTGGAATTA TCACGCTGGTTGCTTGTGTTACAGCG GGAGACATATATCAC | 7668 |
| DB | 7621 | TCCAGTTGGAATTA TCACGCTGGTTGCTTGTGTTACAGCG GGAGACATATATCAC | 7680 |
| QY | 7669 | AGCCTGTCTGTGCCGACCCGCTGGTTCA TGTGTGCTCTA CTCCTACTTTCTGTAGGG | 7728 |
| DB | 7681 | AGCCTGTCTGTGCCGACCCGCTGGTTCA TGTGTGCTCTA CTCCTACTTTCTGTAGGG | 7740 |
| QY | 7729 | GTAGGCATCTACTACTCCCAACCGATGAACGGGAGCTAAAC ACTCCAGGCCAATAGG | 7788 |
| DB | 7741 | GTAGGCATCTACTACTCCCAACCGATGAACGGGAGCTAAAC ACTCCAGGCCAATAGG | 7800 |
| QY | 7789 | CCATCTCTGTTTTTTTCCCTTTTTTTTTTTTTTTTTTTTTTT TTTTTTTTTTTTTTTTTTTTTTTT | 7848 |

[illegible]

Db 961 ATGGCGATCCCTGCTTGGCGAATATCATGTTGAAATGGCGCTTTCTGGATTATCG 1020
QY 1009 ACTGTGGCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCTGGCTACCGTGATA 1068
Db 1021 ACTGTGGCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCTGGCTACCGTGATA 1080
QY 1069 TTGCTGAAGAGCTTGGCGCGGAATGGCTTGACCGCTTCTCGTGTCTTACGGTATCGCG 1128
Db 1081 TTGCTGAAGAGCTTGGCGCGGAATGGCTTGACCGCTTCTCGTGTCTTACGGTATCGCG 1140
QY 1129 CTCGGATTCGAGCGCATCGCTTCTATCGCGCTTCTTACGAGTCTTCTGAGTTAAA 1188
Db 1141 CTCGGATTCGAGCGCATCGCTTCTATCGCGCTTCTTACGAGTCTTCTGAGTTAAA 1200
QY 1189 CAGACCAACAACGGTTTCCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCT 1248
Db 1201 CAGACCAACAACGGTTTCCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCT 1260
QY 1249 AACGTTACTGGCGGAAGCGCTTGAATAAGCGCGGTGTGCGTTTGTCTATATGTTAT 1308
Db 1261 AACGTTACTGGCGGAAGCGCTTGAATAAGCGCGGTGTGCGTTTGTCTATATGTTAT 1320
QY 1309 TCCACCATATTGCGCTTCTTTGGCAATGTGAGGCGCGGAACCTGGCCCTGTCTTCTG 1368
Db 1321 TCCACCATATTGCGCTTCTTTGGCAATGTGAGGCGCGGAACCTGGCCCTGTCTTCTG 1380
QY 1369 ACGAGCATTCCTAGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCGTGTGAATGC 1428
Db 1381 ACGAGCATTCCTAGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCGTGTGAATGC 1440
QY 1429 GTGAAGNAGAGTCTCTGGAAGCTTCTTGAAGCAAAACAAGCTGTGTAGCAACCTT 1488
Db 1441 GTGAAGNAGAGTCTCTGGAAGCTTCTTGAAGCAAAACAAGCTGTGTAGCAACCTT 1500
QY 1489 TGCAGGAGCGGAAACCCCACTGGCGACAGGTGCCTCTCGGGCAAAAGCGTGTGA 1548
Db 1501 TGCAGGAGCGGAAACCCCACTGGCGACAGGTGCCTCTCGGGCAAAAGCGTGTGA 1560
QY 1549 TAAGATACACCTGCAAAAGCGGCAAAACCCAGTGCACAGTGTGAGTGGATAGTTGTG 1608
Db 1561 TAAGATACACCTGCAAAAGCGGCAAAACCCAGTGCACAGTGTGAGTGGATAGTTGTG 1620
QY 1609 GAAAGAGTCAAAATGGCTCTCTCAAGCGTATTCACAAAGGCGCTGAAGGATGCCAAG 1668
Db 1621 GAAAGAGTCAAAATGGCTCTCTCAAGCGTATTCACAAAGGCGCTGAAGGATGCCAAG 1680
QY 1669 GTACCCCATTTGATGGATCTGATCTGGGCTCGGTGCAATGCTTTACATGTTTAG 1728
Db 1681 GTACCCCATTTGATGGATCTGATCTGGGCTCGGTGCAATGCTTTACATGTTTAG 1740
QY 1729 TCGAGGTTAAAAACGTTCTAGGCGCCCGCAACCAAGGCGCTGAAGGATGCCAAG 1788
Db 1741 TCGAGGTTAAAAACGTTCTAGGCGCCCGCAACCAAGGCGCTGAAGGATGCCAAG 1800
QY 1789 CAGGATAATACCATGGCGCTTATAGCGCTTCTCCCAAGAGCGGAGGCTTACTTGGC 1848
Db 1801 CAGGATAATACCATGGCGCTTATAGCGCTTCTCCCAAGAGCGGAGGCTTACTTGGC 1860
QY 1849 TGCATCATCACTAGCCTCACAGGCGGGAAGGAAACAGTGTGAGGCGGAGGTCGAAGTG 1908
Db 1861 TGCATCATCACTAGCCTCACAGGCGGGAAGGAAACAGTGTGAGGCGGAGGTCGAAGTG 1920
QY 1909 GTCTCCACCGCAACAATCTTTCTGGCGACCTGTGCTCAATGCGGTGTGAGCTGTC 1968
Db 1921 GTCTCCACCGCAACAATCTTTCTGGCGACCTGTGCTCAATGCGGTGTGAGCTGTC 1980
QY 1969 TATCATGTGCGGCTCAAGACCTTTGCGGCGCCCAAGGCGCCCAATCAACCAATGTAC 2028
Db 1981 TATCATGTGCGGCTCAAGACCTTTGCGGCGCCCAAGGCGCCCAATCAACCAATGTAC 2040
QY 2029 ACCAATGTGACAGACCTCTGCGGTGCGAAGCGCGCCCGCGGCGGCTTCTTTGACA 2088

Db 2041 ACCAATGTGACAGACCTCTGCGCTGGCAAGCGCCCGCGGCGGTTCTCTTGACA 2100
QY 2089 CCATGCACTGCGGAGCTCGGACCTTTACTTTGGTTCAGGAGCATGCCGATGTCATTCCG 2148
Db 2101 CCATGCACTGCGGAGCTCGGACCTTTACTTTGGTTCAGGAGCATGCCGATGTCATTCCG 2160
QY 2149 GTGCGCGCGGCGGAGCAGACAGGCGGAGCTTCTCTCCCGAGGCGGCTCTCTCTACTTG 2208
Db 2161 GTGCGCGCGGCGGAGCAGACAGGCGGAGCTTCTCTCCCGAGGCGGCTCTCTCTACTTG 2220
QY 2209 AAGGCTCTTTCCGGCGGCTCCACTGCTCTGCCCTCGGGGACGCTTCTCTCCCGAGGCGGCTCTCTCTACTTG 2268
Db 2221 AAGGCTCTTTCCGGCGGCTCCACTGCTCTGCCCTCGGGGACGCTGTGGGCACTCTTCCG 2280
QY 2269 GCTGCGGTGTGCA CCGGAGGGGTTCGAGAGGCGTGGACTTTGTACCCCTCGAGTCTATG 2328
Db 2281 GCTGCGGTGTGCA CCGGAGGGGTTCGAGAGGCGTGGACTTTGTACCCCTCGAGTCTATG 2340
QY 2329 GAAACCACTATCGGTGCCCGTCTTCAAGGAGCTTCTCAAGGAGCTTCTGAGTCTATG 2388
Db 2341 GAAACCACTATCGGTGCCCGTCTTCAAGGAGCTTCTCAAGGAGCTTCTGAGTCTATG 2400
QY 2389 ACATTCAGGTGGCCATCTACACGCCCTTACTGTAGCGGCAAGGAGCTAAGGTGCG 2448
Db 2401 ACATTCAGGTGGCCATCTACACGCCCTTACTGTAGCGGCAAGGAGCTAAGGTGCG 2460
QY 2449 GCTGGTATGAGGCCAAGGTATAAGGTGTCTCTGAAACCCCTCGCTCGGCCAC 2508
Db 2461 GCTGGTATGAGGCCAAGGTATAAGGTGTCTCTGAAACCCCTCGCTCGGCCAC 2520
QY 2509 CTAGGTTTGGGGGTATATGCTTAAAGGACATGGTATCGACCTTAACATCAGAACCGG 2568
Db 2521 CTAGGTTTGGGGGTATATGCTTAAAGGACATGGTATCGACCTTAACATCAGAACCGG 2580
QY 2569 GTAAAGACCATCACACCGGTGCCCATCACGTACTCCACTATGCAAGTTCCTGTC 2628
Db 2581 GTAAAGACCATCACACCGGTGCCCATCACGTACTCCACTATGCAAGTTCCTGTC 2640
QY 2629 GACGGTGGTGTCTCTGGGGCGCTATGACATCAATAATATGTATGATGCACTCACT 2688
Db 2641 GACGGTGGTGTCTCTGGGGCGCTATGACATCAATAATATGTATGATGCACTCACT 2700
QY 2689 GACTCGACCACTATCTCTGGGATCGGACAGTCTCTGACCAAGCGGAGAGCGGTGGAG 2748
Db 2701 GACTCGACCACTATCTCTGGGATCGGACAGTCTCTGACCAAGCGGAGAGCGGTGGAG 2760
QY 2749 CGACTCTGCTGTCTCGCACCGCTTACGCTTCCGGATCGGTCAACGCTGCAATCAAT 2808
Db 2761 CGACTCTGCTGTCTCGCACCGCTTACGCTTCCGGATCGGTCAACGCTGCAATCAAT 2820
QY 2809 ATCGAGAGGTGCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCC 2868
Db 2821 ATCGAGAGGTGCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCC 2880
QY 2869 ATCGAGACCATCAAGGGGGGAGGACCTCATTTTCTGCCATTCGAAGAAATGTAT 2928
Db 2881 ATCGAGACCATCAAGGGGGGAGGACCTCATTTTCTGCCATTCGAAGAAATGTAT 2940
QY 2929 GAGCTCGCGCGAAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTACCGGGGCTT 2988
Db 2941 GAGCTCGCGCGAAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTACCGGGGCTT 3000
QY 2989 GATGTAATCGTCAATCAAACTAGCGGAGAGCTCATTTGCTAGCAACGAGCTCTAATG 3048
Db 3001 GATGTAATCGTCAATCAAACTAGCGGAGAGCTCATTTGCTAGCAACGAGCTCTAATG 3060
QY 3049 ACGGGCTTTACCGGCGATTTGACTCAGTGTGCTGCAATACATGTGTCAACCCAGACA 3108
Db 3061 ACGGGCTTTACCGGCGATTTGACTCAGTGTGCTGCAATACATGTGTCAACCCAGACA 3120
QY 3109 GTGCACTTCAGCTGAGCCGACCTTCAACATTTGAGACGACCGGTGCAAGACGG 3168
Db 3121 GTGCACTTCAGCTGAGCCGACCTTCAACATTTGAGACGACCGGTGCAAGACGG 3180

| | | | | | | | |
|----|------|--|------|----|------|---|------|
| QY | 3169 | GTGTCACTCGCAGCGGAGGAGGAGTGTGTAGGGGACAGATGGGCAATTTACAGGTTT | 3228 | QY | 4249 | ATAGCCCTTGGAGAGTGTGTGTGATATTTTGGCAGGTATGAGCAGGGTGGCAGGC | 4308 |
| Db | 3181 | GTGTACACCTCGCAGCGGAGGAGGAGTGTGTAGGGGACAGATGGGCAATTTACAGGTTT | 3240 | Db | 4261 | ATAGCCCTTGGAGAGTGTGTGTGATATTTTGGCAGGTATGAGCAGGGTGGCAGGC | 4320 |
| QY | 3229 | GTGACTCCAGAGAAAGCGCCCTCGGGCATGTTCGATTCCTCGGTTCTGTGCGAGTGCTAT | 3288 | QY | 4309 | CGCTCTGTGGCTTTAAGGTCAATGAGCGGCGAGATGCCCTCCACGAGGACCTGTGTTAAC | 4368 |
| Db | 3241 | GTGACTCCAGAGAAAGCGCCCTCGGGCATGTTCGATTCCTCGGTTCTGTGCGAGTGCTAT | 3300 | Db | 4321 | CGCTCTGTGGCTTTAAGGTCAATGAGCGGCGAGATGCCCTCCACGAGGACCTGTGTTAAC | 4380 |
| QY | 3289 | GACCGGGCTGTGCTTTGTGTACGAGCTACGCGCCGCGAGACCTCAGTTAGTTGTGGGCT | 3348 | QY | 4369 | CTACTCCCTGTATCTCTCTCCCTGGCGCCCTGTGCTCGGGTCTGTGCGCAGGATA | 4428 |
| Db | 3301 | GACCGGGCTGTGCTTTGTGTACGAGCTACGCGCCGCGAGACCTCAGTTAGTTGTGGGCT | 3360 | Db | 4381 | CTACTCCCTGTATCTCTCTCCCTGGCGCCCTGTGCTCGGGTCTGTGCGCAGGATA | 4440 |
| QY | 3349 | TACTTAACACACAGGTTGCCCTCTGCGAGGACCATCTGAGTTCTGGAGAGCGTC | 3408 | QY | 4429 | CTGCGTCCGACAGTGGGCGGAGGAGGCGGTGTGCACTGATGAACCGGCTGATAGCG | 4488 |
| Db | 3361 | TACTTAACACACAGGTTGCCCTCTGCGAGGACCATCTGAGTTCTGGAGAGCGTC | 3420 | Db | 4441 | CTGCGTCCGACAGTGGGCGGAGGAGGCGGTGTGCACTGATGAACCGGCTGATAGCG | 4500 |
| QY | 3409 | TTTACAGGCTCACCACATAGACGCCCATTTCTTGTCACAGCTAAGCAGGACGAGAC | 3468 | QY | 4489 | TTTCGTTCCGCGGGTAAACACAGTCTCCCGCCACGCACTATGTCTGAGAGCAAGCTGCA | 4548 |
| Db | 3421 | TTTACAGGCTCACCACATAGACGCCCATTTCTTGTCACAGCTAAGCAGGACGAGAC | 3480 | Db | 4501 | TTTCGTTCCGCGGGTAAACACAGTCTCCCGCCACGCACTATGTCTGAGAGCAAGCTGCA | 4560 |
| QY | 3469 | AACTTCCCTACTCTGTAGCATACAGGCTACGGTGTGCGCAGGCTCAGGCTCCACCT | 3528 | QY | 4549 | GCACTGTCACTCAGATCCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTAC | 4608 |
| Db | 3481 | AACTTCCCTACTCTGTAGCATACAGGCTACGGTGTGCGCAGGCTCAGGCTCCACCT | 3540 | Db | 4561 | GCACTGTCACTCAGATCCTCTCTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTAC | 4620 |
| QY | 3529 | CCATCGTGGACCAATGTGAAGTGTCTCATACGGCTAAAGCCTACGCTGACCGGCCA | 3588 | QY | 4609 | CAGTGGATCAACAGGAGTGTCTCCAGCCATGCTCCGGCTCGTGGCTAAGAGATGTTGG | 4668 |
| Db | 3541 | CCATCGTGGACCAATGTGAAGTGTCTCATACGGCTAAAGCCTACGCTGACCGGCCA | 3600 | Db | 4621 | CAGTGGATCAACAGGAGTGTCTCCAGCCATGCTCCGGCTCGTGGCTAAGAGATGTTGG | 4680 |
| QY | 3589 | AGCCCTCTGTGTATAGGCTGGAGCGGTTTCAAAACGAGGTTACTACCAACACACCCCAT | 3660 | QY | 4669 | GATTGGATATGACCGGTGTGACTGATTTCAAGACCTGGCTCAGTCCAAGCTCTGCCG | 4740 |
| Db | 3601 | AGCCCTCTGTGTATAGGCTGGAGCGGTTTCAAAACGAGGTTACTACCAACACACCCCAT | 3680 | Db | 4681 | GATTGGATATGACCGGTGTGACTGATTTCAAGACCTGGCTCAGTCCAAGCTCTGCCG | 4740 |
| QY | 3649 | ACCAATAATCATATGCGATGCTGCGGTGACCTCGAGTGTCTACGAGCACTCGGTG | 3708 | QY | 4729 | CGATTCCCGGAGTCCCTTTCTCTCATGTCAACGTGGGTACNAGGAGTCTCGCGGGC | 4788 |
| Db | 3661 | ACCAATAATCATATGCGATGCTGCGGTGACCTCGAGTGTCTACGAGCACTCGGTG | 3720 | Db | 4741 | CGATTCCCGGAGTCCCTTTCTCTCATGTCAACGTGGGTACNAGGAGTCTCGCGGGC | 4800 |
| QY | 3709 | CTGTAGGCGGAGTCTAGCAGTCTGGCGCGTATTTGCTGTGACAAAGCAGCGTGGTC | 3768 | QY | 4789 | GACCGCATCATGAAACACCTGCCATGTGGAGCACAGATCAACCGGACATGTGAAAAAC | 4848 |
| Db | 3721 | CTGTAGGCGGAGTCTAGCAGTCTGGCGCGTATTTGCTGTGACAAAGCAGCGTGGTC | 3780 | Db | 4801 | GACCGCATCATGAAACACCTGCCATGTGGAGCACAGATCAACCGGACATGTGAAAAAC | 4860 |
| QY | 3769 | ATTGTGGGAGGATCATCTTGTCCGAAAGCCCGCCATCATTTCCGACAGGGAAGTCTT | 3828 | QY | 4849 | GGTTCCATGAGGATCGTGGGGCTTAGACCTGTAGTAAACAGTGGCATGGAACATTTCCC | 4908 |
| Db | 3781 | ATTGTGGGAGGATCATCTTGTCCGAAAGCCCGCCATCATTTCCGACAGGGAAGTCTT | 3840 | Db | 4861 | GGTTCCATGAGGATCGTGGGGCTTAGACCTGTAGTAAACAGTGGCATGGAACATTTCCC | 4920 |
| QY | 3829 | TACCGGAGTTGATGAGTGAAGTGGCGCTCACACCTCCCTTACATCGAACAGGA | 3888 | QY | 4909 | ATTAAACGCTPACACACCGGCGCTGACCGCTTCCCGCGCGCAATTTCTAGGGCG | 4968 |
| Db | 3841 | TACCGGAGTTGATGAGTGAAGTGGCGCTCACACCTCCCTTACATCGAACAGGA | 3900 | Db | 4921 | ATTAAACGCTPACACACCGGCGCTGACCGCTTCCCGCGCGCAATTTCTAGGGCG | 4980 |
| QY | 3889 | ATCAGCTCCCGAAACAAATTCAAACAGAGGCAATCGGTTGCTGCAAAACAGCCACCAAG | 3948 | QY | 4969 | CTGTGCGGGTGGCTGCTGAGGAGTACGTGGAGTACGCGGGTGGGGGATTTCCACTAC | 5028 |
| Db | 3901 | ATCAGCTCCCGAAACAAATTCAAACAGAGGCAATCGGTTGCTGCAAAACAGCCACCAAG | 3960 | Db | 4981 | CTGTGCGGGTGGCTGCTGAGGAGTACGTGGAGTACGCGGGTGGGGGATTTCCACTAC | 5040 |
| QY | 3949 | CAAGCGAGGCTGTCTGCTCCCGTGGTGAATPCCAAAGTGGGAGCCCTCGAAGCTTCTG | 4008 | QY | 5029 | GTGACGGGATGACCACTGACAAAGTAAAGTGGCGGTGTAGTTCAGGTTCCGGCCCCCGGAATTC | 5088 |
| Db | 3961 | CAAGCGAGGCTGTCTGCTCCCGTGGTGAATPCCAAAGTGGGAGCCCTCGAAGCTTCTG | 4020 | Db | 5041 | GTGACGGGATGACCACTGACAAAGTAAAGTGGCGGTGTAGTTCAGGTTCCGGCCCCCGGAATTC | 5100 |
| QY | 4009 | GCGAGCATATGTGAATTTTATCAGCGGGATACAATATTTAGCAGGCTTGTCCACTCTG | 4068 | QY | 5089 | TTACAGAAAGTGAATGGGGTGGGTGCAAGTGTGCGGTGTAGTTCAGGTTCCGGCCCCCGGAATTC | 5148 |
| Db | 4021 | GCGAGCATATGTGAATTTTATCAGCGGGATACAATATTTAGCAGGCTTGTCCACTCTG | 4080 | Db | 5101 | TTACAGAAAGTGAATGGGGTGGGTGCAAGTGTGCGGTGTAGTTCAGGTTCCGGCCCCCGGAATTC | 5160 |
| QY | 4069 | CCTGGCAACCCCGATAGCATCACTGATGGCAATTCAGCCTCTATCACAGCCCGCTC | 4128 | QY | 5149 | CGGAGGAGGTCAATTTCTGCTGGGTCAATCAATACCTGTTGGTGGGTGACAGCTCCCA | 5208 |
| Db | 4081 | CCTGGCAACCCCGATAGCATCACTGATGGCAATTCAGCCTCTATCACAGCCCGCTC | 4140 | Db | 5161 | CGGAGGAGGTCAATTTCTGCTGGGTCAATCAATACCTGTTGGTGGGTGACAGCTCCCA | 5220 |
| QY | 4129 | ACCAACCAACATACCTCTGTTTAAATCTCTGGGGGATGGGTGGCGCCCACTTGTCT | 4188 | QY | 5209 | TGCGAGCCCGAACCGGACGTAGAGTGTCTCATTTCCATGTCTACCGACCCCTCCCACTT | 5268 |
| Db | 4141 | ACCAACCAACATACCTCTGTTTAAATCTCTGGGGGATGGGTGGCGCCCACTTGTCT | 4200 | Db | 5221 | TGCGAGCCCGAACCGGACGTAGAGTGTCTCATTTCCATGTCTACCGACCCCTCCCACTT | 5280 |
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ORGANISM Unknown.
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AUTHORS Bartenschlager,R.
TITLE Hepatitis C virus culture system
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| QY | 1369 | ACGAGCATTTCTAGGGTCTTTTCCCTCTCGCCAAAGGATCAAGGTCTGTTGAATGTC | 1428 | Db | 2461 | GCTGCGTATGACAGCCCAAGGGTATAAGGTGCTTGTCTGAAACCCCGTCCGTCGCCACCC | 2520 |
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3889 ATGACCTGCCGAACATTCAAACAGAGGCAATCGGTTGCTGCAACAGCCACCAAG 3948
3901 ATGACCTGCCGAACATTCAAACAGAGGCAATCGGTTGCTGCAACAGCCACCAAG 3960
3949 CAAGCGAGGCTCTGCTCCCGTGGTGAATCAAGTGGCGGACCCCTCGAAGCCTTCTGG 4008
3961 CAAGCGAGGCTCTGCTCCCGTGGTGAATCAAGTGGCGGACCCCTCGAAGCCTTCTGG 4020
4009 GCGAAGCATATGGAATTTCAATGAGCGGATACAAATATTAGAGGCTTGTCCACTCTG 4068
4021 GCGAAGCATATGGAATTTCAATGAGCGGATACAAATATTAGAGGCTTGTCCACTCTG 4080
4069 CTTGGCAACCCCGGATAGCATCACTGATGGATTCACAGCTCTATACACCGCCGCTC 4128
4081 CTTGGCAACCCCGGATAGCATCACTGATGGATTCACAGCTCTATACACCGCCGCTC 4140
4129 ACCACCAACATACCTCTCTGTTTAAATCCTCGGGGGATGGTGGCGGCCCACTTGTCT 4188
4141 ACCACCAACATACCTCTCTGTTTAAATCCTCGGGGGATGGTGGCGGCCCACTTGTCT 4200
4189 CTTCCAGAGCTCTCTGCTTTCTGATAGGCGCGGATCGCTGAGCGGCTGTTGGAGC 4248
4201 CTTCCAGAGCTCTCTGCTTTCTGATAGGCGCGGATCGCTGAGCGGCTGTTGGAGC 4260
4249 ATAGGCTTTGGGAGGTGCTTGGATATTTTGGCAGTTATGGAGCGGCTGGCAGGC 4308
4261 ATAGGCTTTGGGAGGTGCTTGGATATTTTGGCAGTTATGGAGCGGCTGGCAGGC 4320
4309 GCCTCGTGCCCTTTAAGGTCATGAGCGGAGATGCCCTCCACCGAGGACCTGGTTAAC 4368
4321 GCCTCGTGCCCTTTAAGGTCATGAGCGGAGATGCCCTCCACCGAGGACCTGGTTAAC 4380
4369 CTACTCCCTGCTATCTCTCCCTGGCGCCCTAGTCTGGGGTGTGTGGCAGCGATA 4428
4381 CTACTCCCTGCTATCTCTCCCTGGCGCCCTAGTCTGGGGTGTGTGGCAGCGATA 4440
4429 CTGGTCGGCAGCTGGGCGCCAGGGGAGGGGCTGTGAGTGGATGAACCGGCTGATAGCG 4488
4441 CTGGTCGGCAGCTGGGCGCCAGGGGAGGGGCTGTGAGTGGATGAACCGGCTGATAGCG 4500
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4501 TTGCTTTCCGGGGTAAACAGCTCTCCCAACGACTATGTGCTGAGAGCGCTGCA 4560
4549 GCAGTGTCACTAGATCTCTCTAGTCTTACCATCACTAGCTGCTGAGAGGCTTCA 4608
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4621 CAGTGGATCAACGAGGACTGCTCCAGCCATGCTCGGCTCGTGGCTAGAGATGTTGG 4680
4669 GATTGGATATGCAACGGTGTGATGATTTCAAGACCTGGCTCAGTCAAGCTCTCTGGCG 4728
4681 GATTGGATATGCAACGGTGTGATGATTTCAAGACCTGGCTCAGTCAAGCTCTCTGGCG 4740
4729 CATTTCGGGGAGTCCCTTCTTCATGTCAACGTGGGTCAAGGAGTCTTGGCGGGC 4788
4741 CATTTCGGGGAGTCCCTTCTTCATGTCAACGTGGGTCAAGGAGTCTTGGCGGGC 4800
4789 GACGGCATCATGCAAAACCACTGCCCATGTGGAGCAAGATCAACGGACATGTGAAAAAC 4848
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4849 GGTTCATGAGGATCGTGGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTTCCC 4908
4861 GGTTCATGAGGATCGTGGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTTCCC 4920
4909 ATTAACGGCTACACACGCGCCCTCGACGCCCTCCCGCGCCAAATATTCTAGGGCG 4968
4921 ATTAACGGCTACACACGCGCCCTCGACGCCCTCCCGCGCCAAATATTCTAGGGCG 4980
4969 CTGTGGCGGTGGCTCTGAGGAGTACGTGGAGTTACGCGGTGGGGATTTCCACTAC 5028
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5101 TTACAGAGAGTGAATGGGTGGCTGACAGTACGCTCCAGCGTGAACCCCTCCTA 5160
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5281 ACCGCGGAGACGCTAAGCTAGGCTGGCGAGGAGTCTCTCTCCCGCTTTGGCCAGCTCA 5340
5329 TCAGCTAGCCAGCTGTCTGGCCTTCCTTGAAGGCAACATGCACTACCGCTCATGCTCC 5388
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5461 ACCCGGTGGAGTCAGAAAAAAGTAGTAATTTTGGACTCTTTCCAGCGCTCCAAAGC 5520
5509 GAGGAGATGAGAGGAGTATCGTTCGGCGGAGATTCCTGGGAGGTCCAGGAAATTC 5568
5521 GAGGAGATGAGAGGAGTATCGTTCGGCGGAGATTCCTGGGAGGTCCAGGAAATTC 5580
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5581 CTTGACGATGCCATATGGGACGCCCGGATTTACAACTCCCTCAGCTGTTAGCTCTCTGG 5640
5629 AAGGACCCGAGTACGCTCCCTCCAGTGTACAGGGGTGTCATTTGCGCGCTGCCAAGGCC 5688
5641 AAGGACCCGAGTACGCTCCCTCCAGTGTACAGGGGTGTCATTTGCGCGCTGCCAAGGCC 5700

| | | | | | | | |
|----|------|--|------|----|------|--|------|
| QY | 5689 | CCTCCGATACCACTCTCCACGGAGGAAGAGACGGTTGTCTCTGCAATCTACCGTGTCT | 5748 | Db | 6781 | GGGGGCCCCCTGACTTAATTTCTAAAGGCGAGAACTGCGGTATCGCGGTGCGCGCGAGC | 6840 |
| Db | 5701 | CCTCCGATACCACTCTACGGAGGAAGAGACGGTTGTCTCTGCAATCTACCGTGTCT | 5760 | QY | 6829 | GGTGTACTGACACAGCTGCGGTAAATACCTTCACATGTTACTTGAAGCCCGCTGCGGC | 6888 |
| QY | 5749 | TCGTGCTTGGCGAGCTCGCACAAGACCTTTCGGCAGCTCCGAATCGTGGCGCGTGCAG | 5808 | Db | 6841 | GGTGTACTGACACAGCTGCGGTAAATACCTTCACATGTTACTTGAAGCCCGCTGCGGC | 6900 |
| Db | 5761 | TCGTGCTTGGCGAGCTCGCACAAGACCTTTCGGCAGCTCCGAATCGTGGCGCGTGCAG | 5820 | QY | 6889 | TGTCCAGCTGCGAAGCTTCAGSACTGACAGTGTCTGATGCGGAGACGACCTTGTGCTT | 6948 |
| QY | 5809 | AGCGCACGGCAACGGCTCTCTGACACAGCCCTTCGACAGCGGAGCGCGGATCCCGAC | 5868 | Db | 6901 | TGTCCAGCTGCGAAGCTTCAGSACTGACAGTGTCTGATGCGGAGACGACCTTGTGCTT | 6960 |
| Db | 5821 | AGCGCACGGCAACGGCTCTCTGACACAGCCCTTCGACAGCGGAGCGCGGATCCCGAC | 5880 | QY | 6949 | ATCTCTGAAAGCGCGGGACCCCAAGAGACGAGCGAGCTACGGGCTTTCAGGAGGCT | 7008 |
| QY | 5869 | GTTGAGTGTACTCTCTGACAGCCCTTCGACAGCGGAGCGCGGATCCCGAC | 5928 | Db | 6961 | ATCTCTGAAAGCGCGGGACCCCAAGAGACGAGCGAGCTACGGGCTTTCAGGAGGCT | 7020 |
| Db | 5881 | GTTGAGTGTACTCTCTGACAGCCCTTCGACAGCGGAGCGCGGATCCCGAC | 5940 | QY | 7009 | ATGACTAGATATCTGTGCCCCCTTCGGGACCCCGCCAAACACAGAAATAGACTTTCAGGTTG | 7068 |
| QY | 5929 | GACGGTCTTGTCTACCGTAGCCGAGGAGCTAGTGGAGAGCTGTCTGTCTGTCTGATG | 5988 | Db | 7021 | ATGACTAGATATCTGTGCCCCCTTCGGGACCCCGCCAAACACAGAAATAGACTTTCAGGTTG | 7080 |
| Db | 5941 | GACGGTCTTGTCTACCGTAGCCGAGGAGCTAGTGGAGAGCTGTCTGTCTGTCTGATG | 6000 | QY | 7069 | ATAACATCATGCTCTCTCAATGTGTCACTGCGGACAGATGATCTGGGCAAAAGGTTGAC | 7128 |
| QY | 5989 | TCCTACATGACAGCGGCGCTCTGATCAGCCCATGCGCTGCGGAGGAAACCAAGCTGCC | 6048 | Db | 7081 | ATAACATCATGCTCTCTCAATGTGTCACTGCGGACAGATGATCTGGGCAAAAGGTTGAC | 7140 |
| Db | 6001 | TCCTACATGACAGCGGCGCTCTGATCAGCCCATGCGCTGCGGAGGAAACCAAGCTGCC | 6060 | QY | 7129 | TATCTCACCCGCTGACCCCAACCCCTTCGCGGGCTGCGTGGGAGCAGCTAGACAC | 7188 |
| QY | 6049 | ATCAATGCACTGAGCAATCTTTGTCTCGTCAACAACCTTGGTCTATGCTACAACTCT | 6108 | Db | 7141 | TATCTCACCCGCTGACCCCAACCCCTTCGCGGGCTGCGTGGGAGCAGCTAGACAC | 7200 |
| Db | 6061 | ATCAATGCACTGAGCAATCTTTGTCTCGTCAACAACCTTGGTCTATGCTACAACTCT | 6120 | QY | 7189 | ACTCCAGTCAATCTCTGGCTAGGCAACATCATGTATGCGGCCACCTTGTGGGCAAGG | 7248 |
| QY | 6109 | CGCAGCGAAGCTTCGCGCAAGAGGCTCACTTTGACAGACTGACAGTCTGAGACAC | 6168 | Db | 7201 | ACTCCAGTCAATCTCTGGCTAGGCAACATCATGTATGCGGCCACCTTGTGGGCAAGG | 7260 |
| Db | 6121 | CGCAGCGAAGCTTCGCGCAAGAGGCTCACTTTGACAGACTGACAGTCTGAGACAC | 6180 | QY | 7249 | ATGATCCTGTAGTCACTTTCTTCCATCTCTAGCTCAGGAAACAATCTTGAAAGAGC | 7308 |
| QY | 6169 | CATACCGGAGCTGCTCAAGAGATGAAGCGAGGCTCCACAGTTTAAAGCTTAACTT | 6228 | Db | 7261 | ATGATCCTGTAGTCACTTTCTTCCATCTCTAGCTCAGGAAACAATCTTGAAAGAGC | 7320 |
| Db | 6181 | CATACCGGAGCTGCTCAAGAGATGAAGCGAGGCTCCACAGTTTAAAGCTTAACTT | 6240 | QY | 7309 | CTAGATTGTCAAGTCTACGGGCTGTCTTCTCCATGAGCCACTTGAAGCCACTCAGATC | 7368 |
| QY | 6229 | CTATCCGTGGAGAGCTGTAAAGTGAAGCGGCGGCAATTCGGGAGATCTAAATTTGGC | 6288 | Db | 7321 | CTAGATTGTCAAGTCTACGGGCTGTCTTCTCCATGAGCCACTTGAAGCCACTCAGATC | 7380 |
| Db | 6241 | CTATCCGTGGAGAGCTGTAAAGTGAAGCGGCGGCAATTCGGGAGATCTAAATTTGGC | 6300 | QY | 7369 | ATTCAGAGCTCCATGAGCTTACGGCAATTTCACTCCATAGTTACTCTCCAGGTGAGATC | 7428 |
| QY | 6289 | TATGGGCAAGAGCTTCGGAAGCTTACAGCAAGCGGTTAACCATCCGCTCCGCTG | 6348 | Db | 7381 | ATTCAGAGCTCCATGAGCTTACGGCAATTTCACTCCATAGTTACTCTCCAGGTGAGATC | 7440 |
| Db | 6301 | TATGGGCAAGAGCTTCGGAAGCTTACAGCAAGCGGTTAACCATCCGCTCCGCTG | 6360 | QY | 7429 | AATAGGCTGCTTCATGCTCAGAAACTTGGGGTACCGGCTTGGAGTCTGGAGACAT | 7488 |
| QY | 6349 | TGAAGGACTTGTGGAAGACACTGAGACACCAATTCACACCAATTCAGCAACCAAT | 6408 | Db | 7441 | AATAGGCTGCTTCATGCTCAGAAACTTGGGGTACCGGCTTGGAGTCTGGAGACAT | 7500 |
| Db | 6361 | TGAAGGACTTGTGGAAGACACTGAGACACCAATTCACACCAATTCAGCAACCAAT | 6420 | QY | 7489 | CGGSCCAAGAGTGTCCCGCTAGGCTACTGTCCAGGGGGGAGGGCTGCCACTTGTGGC | 7548 |
| QY | 6409 | GAGGTTTCTGCTCCACAGAGAGAGGGGGCGGAGAGCGCTTATCGTATTC | 6468 | Db | 7501 | CGGSCCAAGAGTGTCCCGCTAGGCTACTGTCCAGGGGGGAGGGCTGCCACTTGTGGC | 7560 |
| Db | 6421 | GAGGTTTCTGCTCCACAGAGAGAGGGGGCGGAGAGCGCTTATCGTATTC | 6480 | QY | 7549 | AGTACCTCTTCACTGGGCGAGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGG | 7608 |
| QY | 6469 | CCAGATTGGGGGTTCTGTGTGCGAGAAATGSCCTTTACGATGTGTCTCCACCTC | 6528 | Db | 7561 | AGTACCTCTTCACTGGGCGAGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGG | 7620 |
| Db | 6481 | CCAGATTGGGGGTTCTGTGTGCGAGAAATGSCCTTTACGATGTGTCTCCACCTC | 6540 | QY | 7609 | TCCAGTTGGAATTTATCCAGCTGGTGTCTGTGTTAGCGGGGGGAGACATATATCAC | 7668 |
| QY | 6529 | CCTCAGCCCGTGTGGGCTCTTCATACGGAATTCATATCTCTCTGAGAGCGGGTCGAG | 6588 | Db | 7621 | TCCAGTTGGAATTTATCCAGCTGGTGTCTGTGTTAGCGGGGGGAGACATATATCAC | 7680 |
| Db | 6541 | CCTCAGCCCGTGTGGGCTCTTCATACGGAATTCATATCTCTCTGAGAGCGGGTCGAG | 6600 | QY | 7669 | AGGCTGTCTCGTCCCGACCCCGCTGTTTCATGTGTGGCTACTCTCTCTCTGTAGGG | 7728 |
| QY | 6589 | TTCTGTGTGAATGCTGGAAGCGGAGAAATGSCCTATGSGGCTTCGATATGACACCCG | 6648 | Db | 7681 | AGGCTGTCTCGTCCCGACCCCGCTGTTTCATGTGTGGCTACTCTCTCTCTGTAGGG | 7740 |
| Db | 6601 | TTCTGTGTGAATGCTGGAAGCGGAGAAATGSCCTATGSGGCTTCGATATGACACCCG | 6660 | QY | 7729 | GTAGGATCTATCTACTCCCAACCGGAGCTTAAACACTTCCAGGCGCAATAGG | 7788 |
| QY | 6649 | TGTTTCTCACTCAAGCTGAGTACATCGTGTGAGAGTCAATCTACCAATGT | 6708 | Db | 7741 | GTAGGATCTATCTACTCCCAACCGGAGCTTAAACACTTCCAGGCGCAATAGG | 7800 |
| Db | 6661 | TGTTTCTCACTCAAGCTGAGTACATCGTGTGAGAGTCAATCTACCAATGT | 6720 | QY | 7789 | CCATCTGTGTTTTTTCCTTT | 7848 |
| QY | 6709 | TGTGACTTGGCCCCCGAAGCGAGACAGGCGCATAGGTCGCTCAGAGCGGCTTTTACATC | 6768 | Db | 7801 | CCATCTGTGTTTTTTCCTTT | 7860 |
| Db | 6721 | TGTGACTTGGCCCCCGAAGCGAGACAGGCGCATAGGTCGCTCAGAGCGGCTTTTACATC | 6780 | QY | 7849 | TTTTTCTCTTTTTTTTTTCTTT | 7908 |
| QY | 6769 | GGGGGCCCCCTGACTTAATTTCTAAAGGCGAGAACTGCGGGCTATCGCGGTGCGCGGAGC | 6828 | | | | |

QY 1609 GAAAGAGTCAATGGCTCTCTCAAGCGTATTCAACAAGGGGCTGAAGATGCCAGAG 1668
DB 1621 GAAAGAGTCAATGGCTCTCTCAAGCGTATTCAACAAGGGGCTGAAGATGCCAGAG 1680
QY 1669 GTACCCCATTTGATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTTGTTAG 1728
DB 1681 GTACCCCATTTGATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTTGTTAG 1740
QY 1729 TCGAGGTTAAAAAAGCTCTAGGCCCCCGAAACACAGGGGACGTGGTTTTCTTTCAAAAA 1788
DB 1741 TCGAGGTTAAAAAAGCTCTAGGCCCCCGAAACACAGGGGACGTGGTTTTCTTTCAAAAA 1800
QY 1789 CACGATATACATGGCGCTATTACGGCTTACTCCCAACAGACCGAGGCGCTACTTGCC 1848
DB 1801 CACGATATACATGGCGCTATTACGGCTTACTCCCAACAGACCGAGGCGCTACTTGCC 1860
QY 1849 TGCATCATCACTAGCTCACAGCGCGGACAGACAGGACAGGACAGGACAGGACAGGACAGG 1908
DB 1861 TGCATCATCACTAGCTCACAGCGCGGACAGACAGGACAGGACAGGACAGGACAGGACAGG 1920
QY 1909 GTCTCCACCGCAACAATCTTTCTGCGACCTTGCTCAATGGCGTGTGTTGGACTGTC 1968
DB 1921 GTCTCCACCGCAACAATCTTTCTGCGACCTTGCTCAATGGCGTGTGTTGGACTGTC 1980
QY 1969 TATCATGTGCGGCTTAAGACCTTTCGCGGCCCAAGGGGCCAATCACCCAAATGTAC 2028
DB 1981 TATCATGTGCGGCTTAAGACCTTTCGCGGCCCAAGGGGCCAATCACCCAAATGTAC 2040
QY 2029 ACCAATGTGACCAAGGACCTCGTGGCTGGCAAGCGCCCCCGGGCGGCTTCTTGACA 2088
DB 2041 ACCAATGTGACCAAGGACCTCGTGGCTGGCAAGCGCCCCCGGGCGGCTTCTTGACA 2100
QY 2089 CCATGCACCTCGGCGAGCTCGGACCTTTTACTTGGTCAAGAGCATGCCGATGTCAATCCG 2148
DB 2101 CCATGCACCTCGGCGAGCTCGGACCTTTTACTTGGTCAAGAGCATGCCGATGTCAATCCG 2160
QY 2149 GTGGCGCGCGGGGAGCAGCAGGGGGAGCTTACTCTCCCGACAGCCCGCTCTCTACTTG 2208
DB 2161 GTGGCGCGCGGGGAGCAGCAGGGGGAGCTTACTCTCCCGACAGCCCGCTCTCTACTTG 2220
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DB 2221 AAGGGCTCTTCGGGGGTCACATGCTCTGCCCCCTCGGGGACGCTGTGGGACATCTTTCGG 2280
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DB 2281 GCTGCCGTGTGCACCCAGGGGTTGCCAAGCGGTGGACTTTGTACCCGCTCGAGTCTATG 2340
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DB 2461 GCTCGGTATGACGCCCAAGGGTATAAGGTGCTTGTCTCTGAACCCGCTCGCTCGCGCCACC 2520
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DB 2581 GTAAGGACCACTACAGGGGTGCCCCCATCACGTTACTCCACCTATGCAAGTTTCTTGCC 2640
QY 2629 GACGGTGTGCTCTGGGGGCGCCTATGACATCATATATGATGATGATGCTCACTCAACT 2688
DB 2641 GACGGTGTGCTCTGGGGGCGCCTATGACATCATATATGATGATGATGCTCACTCAACT 2700
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DB 2701 GACTCGACCACTATCTCTGGGCACTCGGCACAGTCTCGGACCAAGCGGAGCGCTGGAGCG 2760
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DB 3061 ACGGGCTTTTACCGGCGATTTCCGACTCAGTGTATCGACTGCAATACATGTGTCAACCAGACA 3120
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DB 3481 AACTTCCTCTACTGTGTAGCATACAGGCTACGGTGTGCGCCAGGCTCAGGCTCCACCT 3540
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DB 3601 ACGCCCCCTGTGTATAGGCTGGGAGCGGTTCAAAACGAGGTTACTACACACACCCCATTA 3660
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RESULT 10
AR406045
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AR406045
Sequence 16 from patent US 6630343.
AR406045
AR406045.1 GI:40155172
Unknown.
Unknown.

linear

PAT 18-DEC-2003

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| QY | 1969 | TATCATGGTCCGGCTCAAGAACCTTTGCCGGGCCAAAGGGCCCAATCACCCAAATGTAC | 2028 |
| Db | 1981 | TATCATGGTCCGGCTCAAGAACCTTTGCCGGGCCAAAGGGCCCAATCACCCAAATGTAC | 2040 |
| QY | 2029 | ACCAATGTGACACAGACCTCGTCGGCTGCGAAGCGCCCGGGGGCGGTTCTCTTGACA | 2088 |
| Db | 2041 | ACCAATGTGACACAGACCTCGTCGGCTGCGAAGCGCCCGGGGGCGGTTCTCTTGACA | 2100 |
| QY | 2089 | CCATGCACTTCGGCGAGCTCGGACCTTTTACTTGGTCACGAGGCGATGCGGATGTCATTCGG | 2148 |
| Db | 2101 | CCATGCACTTCGGCGAGCTCGGACCTTTTACTTGGTCACGAGGCGATGCGGATGTCATTCGG | 2160 |
| QY | 2149 | GTCCGCGGGGGCGACAGAGGGGAGCTTACTCTCCGCCAGGCCCGTCTCTACTTTG | 2208 |
| Db | 2161 | GTCCGCGGGGGCGACAGAGGGGAGCTTACTCTCCGCCAGGCCCGTCTCTACTTTG | 2220 |
| QY | 2209 | AAGGGCTCTTCGGGGGCTCACTGCTGCTGCCCTCGGGGCGATGCTGTGGGCACTTTTCGG | 2268 |
| Db | 2221 | AAGGGCTCTTCGGGGGCTCACTGCTGCTGCCCTCGGGGCGATGCTGTGGGCACTTTTCGG | 2280 |
| QY | 2269 | GCTGCCGTGTGACCCGAGGGGTTCGAAGGGGCTGGAATTTGTACCCCGTTCGAGTCTATG | 2328 |
| Db | 2281 | GCTGCCGTGTGACCCGAGGGGTTCGAAGGGGCTGGAATTTGTACCCCGTTCGAGTCTATG | 2340 |
| QY | 2329 | GAAACCACTATCGGTCCTCCCGTCTTTCACGGCAACTCGTTCCTCCCGGCTACCGGAG | 2388 |
| Db | 2341 | GAAACCACTATCGGTCCTCCCGTCTTTCACGGCAACTCGTTCCTCCCGGCTACCGGAG | 2400 |
| QY | 2389 | ACATTTCCAGTGGCCCATCTACACGCCCTTACTGTTAGTGGGCAAGAGCACTAAGTGCGG | 2448 |
| Db | 2401 | ACATTTCCAGTGGCCCATCTACACGCCCTTACTGTTAGTGGGCAAGAGCACTAAGTGCGG | 2460 |
| QY | 2449 | GCTGCTATGACGCCCAAGGGTATTAAGTGCTTTGCTGAAACCGGTCGGTCCGCCACCC | 2508 |
| Db | 2461 | GCTGCTATGACGCCCAAGGGTATTAAGTGCTTTGCTGAAACCGGTCGGTCCGCCACCC | 2520 |
| QY | 2509 | CTAGGTTTCGGGGCTATATGTCTAAGGCAATGATGATCGACCTTAACATCAGAACCGGG | 2568 |
| Db | 2521 | CTAGGTTTCGGGGCTATATGTCTAAGGCAATGATGATCGACCTTAACATCAGAACCGGG | 2580 |
| QY | 2569 | GTAAGGACCATCACACGGGTGCCCCCATCAGTACTCAGTACTCAGTACTCAGTACTCAGT | 2628 |
| Db | 2581 | GTAAGGACCATCACACGGGTGCCCCCATCAGTACTCAGTACTCAGTACTCAGTACTCAGT | 2640 |
| QY | 2629 | GACGTTGTTGCTCTGGGGGCGCTTATGACATCAATAATGATGATGATGATGATGATGATGAT | 2688 |
| Db | 2641 | GACGTTGTTGCTCTGGGGGCGCTTATGACATCAATAATGATGATGATGATGATGATGATGAT | 2700 |
| QY | 2689 | GACTCGACCATCTCTGGGATCGGCAAGTCTCGGACCAAGCGGAGACGCTGGAGCG | 2748 |
| Db | 2701 | GACTCGACCATCTCTGGGATCGGCAAGTCTCGGACCAAGCGGAGACGCTGGAGCG | 2760 |
| QY | 2749 | CGACTCGTCTGCTCGCCACCGTACGCTCCGGGATCGGTCAGTCTCGGACCAAGCGGAG | 2808 |
| Db | 2761 | CGACTCGTCTGCTCGCCACCGTACGCTCCGGGATCGGTCAGTCTCGGACCAAGCGGAG | 2820 |
| QY | 2809 | ATCAGGAGGTGGTCTGTCCAGACCTGGAGAAATCCCTTTTATGGCAAGGCCATCCCC | 2868 |
| Db | 2821 | ATCAGGAGGTGGTCTGTCCAGACCTGGAGAAATCCCTTTTATGGCAAGGCCATCCCC | 2880 |
| QY | 2869 | ATCAGACCATCAAGGGGGGAGGCACTCATTTTCTGGCATTCGAAGAAATGTGAT | 2928 |
| Db | 2881 | ATCAGACCATCAAGGGGGGAGGCACTCATTTTCTGGCATTCGAAGAAATGTGAT | 2940 |
| QY | 2929 | GAGTCTCCCGGAAGCTGTCCGGCTCGGACTCAATGCTAGCATATTTACCGGGGCTT | 2988 |
| Db | 2941 | GAGTCTCCCGGAAGCTGTCCGGCTCGGACTCAATGCTAGCATATTTACCGGGGCTT | 3000 |
| QY | 2989 | GATGTATCCGTATPACCACTAGCGGAGACGCTATTTGCTGAGCAACGGAGCTCTAATG | 3048 |
| Db | 3001 | GATGTATCCGTATPACCACTAGCGGAGACGCTATTTGCTGAGCAACGGAGCTCTAATG | 3060 |

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| QY | 3049 | ACGGGCTTTACCGCGGATTTTCGACTCAGTGCATCGACTGCATATACATGTGTCAACCGACA | 3108 |
| Db | 3061 | ACGGGCTTTACCGCGGATTTTCGACTCAGTGCATCGACTGCATATACATGTGTCAACCGACA | 3120 |
| QY | 3109 | GTGCACTTCAGCTCGGACCGGACCTTTCAACATTTGAGACGACCGGTCGCACAGAGCGG | 3168 |
| Db | 3121 | GTGCACTTCAGCTCGGACCGGACCTTTCAACATTTGAGACGACCGGTCGCACAGAGCGG | 3180 |
| QY | 3169 | GTGTACGCTCGGACGGGGAGGAGCTGTGTAGGGGAGGATGGGCAATTTACAGGTTT | 3228 |
| Db | 3181 | GTGTACGCTCGGACGGGGAGGAGCTGTGTAGGGGAGGATGGGCAATTTACAGGTTT | 3240 |
| QY | 3229 | GTGACTTCCAGGAGAAAGCGCCCTCGGACATGTTTCGATTTCTCGGTTCTGTGCGAGTGCTAT | 3288 |
| Db | 3241 | GTGACTTCCAGGAGAAAGCGCCCTCGGACATGTTTCGATTTCTCGGTTCTGTGCGAGTGCTAT | 3300 |
| QY | 3289 | GACGGGGCTGTGCTTTGTTGTAACGAGCTCACGCCCGCGGACCTTCAGTTCAGTTCAGGCT | 3348 |
| Db | 3301 | GACGGGGCTGTGCTTTGTTGTAACGAGCTCACGCCCGCGGACCTTCAGTTCAGTTCAGGCT | 3360 |
| QY | 3349 | TACCTTAAACACACAGGAGGTTGCCGCTGTGCCAGGACCACTCTGGAGTTCTGGGAGAGCTC | 3408 |
| Db | 3361 | TACCTTAAACACACAGGAGGTTGCCGCTGTGCCAGGACCACTCTGGAGTTCTGGGAGAGCTC | 3420 |
| QY | 3409 | TTTACAGGCTCACCCACATAGACGCCCATTTTCTTGTCCAGACTAGGAGGAGGAGAC | 3468 |
| Db | 3421 | TTTACAGGCTCACCCACATAGACGCCCATTTTCTTGTCCAGACTAGGAGGAGGAGAC | 3480 |
| QY | 3469 | AACTTTCCCTTACTTGGTAGCATACAGGCTACGGTGTGCGCCAGGCTCAGGCTCCACCT | 3528 |
| Db | 3481 | AACTTTCCCTTACTTGGTAGCATACAGGCTACGGTGTGCGCCAGGCTCAGGCTCCACCT | 3540 |
| QY | 3529 | CCATCGTGGGACCAATGTGGAAGTGTCTCTACCGCTAAAGCCCTACGCTGCAACGGGCA | 3588 |
| Db | 3541 | CCATCGTGGGACCAATGTGGAAGTGTCTCTACCGCTAAAGCCCTACGCTGCAACGGGCA | 3600 |
| QY | 3589 | ACGCCCTTCTGTATAGGCTGGAGCGCTTCAAAACGAGGTTACTACACACACCCCATTA | 3648 |
| Db | 3601 | ACGCCCTTCTGTATAGGCTGGAGCGCTTCAAAACGAGGTTACTACACACACCCCATTA | 3660 |
| QY | 3649 | ACCAATAATCATGAGCATGTGCGCTGACCTGGAGGTCGTCAACGAGACCTGGGTC | 3708 |
| Db | 3661 | ACCAATAATCATGAGCATGTGCGCTGACCTGGAGGTCGTCAACGAGACCTGGGTC | 3720 |
| QY | 3709 | CTGCTAGCGGAGTCTTAGAGCTCTGGCCGCGTATTCCTGACAAACGAGGAGCTGGTC | 3768 |
| Db | 3721 | CTGCTAGCGGAGTCTTAGAGCTCTGGCCGCGTATTCCTGACAAACGAGGAGCTGGTC | 3780 |
| QY | 3769 | ATTGTGGCAGGATCATCTTGTCCGGAAGCGGCCATCATTTCCGACAGGAAATGCTTT | 3828 |
| Db | 3781 | ATTGTGGCAGGATCATCTTGTCCGGAAGCGGCCATCATTTCCGACAGGAAATGCTTT | 3840 |
| QY | 3829 | TACCGGAGTTTCGATGAGATGGAAGAGTGGCCCTCACACCTCCCTTACATCGAAACAGGA | 3888 |
| Db | 3841 | TACCGGAGTTTCGATGAGATGGAAGAGTGGCCCTCACACCTCCCTTACATCGAAACAGGA | 3900 |
| QY | 3889 | ATGCACTCGCCGAAATTAATTAACAGAGCAATTCGGTTGTGTGCAACAGCACCAAG | 3948 |
| Db | 3901 | ATGCACTCGCCGAAATTAATTAACAGAGCAATTCGGTTGTGTGCAACAGCACCAAG | 3960 |
| QY | 3949 | CAAGCGAGGCTGTGCTCCGTTGGTGAATCCAAAGTGGGAGCCCTCGAAGCCCTTCG | 4008 |
| Db | 3961 | CAAGCGAGGCTGTGCTCCGTTGGTGAATCCAAAGTGGGAGCCCTCGAAGCCCTTCG | 4020 |
| QY | 4009 | GCGAAGCATATGTGAATTTTATCAGCGGATACAAATTTTAGCAGGCTTGTCCACTCTG | 4068 |
| Db | 4021 | GCGAAGCATATGTGAATTTTATCAGCGGATACAAATTTTAGCAGGCTTGTCCACTCTG | 4080 |
| QY | 4069 | CTTGGCAACCCCGGATAGCATCACTGATGGCAATTCACAGCCTTATFACAGCCGCTC | 4128 |
| Db | 4081 | CTTGGCAACCCCGGATAGCATCACTGATGGCAATTCACAGCCTTATFACAGCCGCTC | 4140 |
| QY | 4129 | ACCACCAACATACCTCTGTTTAACTCTGGGGGATGGGTGGCGGCCCACTTGTCT | 4188 |


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RESULT 11
AX036257
LOCUS AX036257 8001 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 6 from Patent EP1043399.
ACCESSION AX036257
VERSION AX036257.1 GI:11225873
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1
AUTHORS Bartenschlager R.D.
TITLE Hepatitis c virus cell culture system
JOURNAL Patent: EP 1043399-A 6 11-OCT-2000;
BARTENSCHLAGER RALF DR (DE)
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| Db | 7381 | ATTCAACGACTCCATGGCCTTAGCGATTTTCACTCCATAGTTACTTCCAGGTGAGATC | 7440 |
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| Db | 7501 | CGGGCCAGAAAGTGTCCGCGCTAGGCTACTGTGCCAGGGGAGAGGCTGCCACTTGTGGC | 7560 |
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| 12; Gaps | | | |
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| Db | 1 | GCAGAGCCCGGATGTTGGGGCGGACACTCCACCATAGATCACTCCCTGTGAGGAACACTCTG | 60 |
| QY | 61 | TCTTTCACGCAGAAAGCGTCTAGCCATGGGTTAGTATGAGTGTCTGTGAGAGCTCCAGAC | 120 |
| Db | 61 | TCTTTCACGCAGAAAGCGTCTAGCCATGGGTTAGTATGAGTGTCTGTGAGAGCTCCAGAC | 120 |
| QY | 121 | CCCCCTCCCGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAG | 180 |
| Db | 121 | CCCCCTCCCGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAG | 180 |
| QY | 181 | GAGACACCGGTCTTCTTCTTGATCAACCGCTCAATGCTCGAGATTGGCGGTGCCCCC | 240 |
| Db | 181 | GAGACACCGGTCTTCTTCTTGATCAACCGCTCAATGCTCGAGATTGGCGGTGCCCCC | 240 |
| QY | 241 | GGGAGACTGCTAGCCGAGTAGTGTGGGTGCGGAAGGCGCTTGGTACTGCTCTGATAGG | 300 |
| Db | 241 | GGGAGACTGCTAGCCGAGTAGTGTGGGTGCGGAAGGCGCTTGGTACTGCTCTGATAGG | 300 |
| QY | 301 | GTGCTTGGAGTGCCCGGGAGGTCTCTGTAGACCGTGCACCATGAGCAGCAATCCTAAAC | 360 |
| Db | 301 | GTGCTTGGAGTGCCCGGGAGGTCTCTGTAGACCGTGCACCATGAGCAGCAATCCTAAAC | 360 |
| QY | 361 | CTCAAGAAAAACCAAA-----GGGCGCGCATGATTGAACAAGATGGATTGC | 408 |
| Db | 361 | CTCAAGAAAAACCAAGCTAACCAACCGGCGCGCATGATTGAACAAGATGGATTGC | 420 |

QY 409 ACGAGGTTCTCCGCGCGTTGGGTGAGAGGCTATTGGCTATTGACTGGGCAACACAGA 468
Db 421 ACGCAGGTTCTCCGCGCGCTTGGGTGAGAGGCTATTGGCTATTGACTGGGCAACACAGA 480
QY 469 CAATCGGCTGCTGATGCGCGCGTGTTCGGGCTGTACGCGAGGGCGCGCGGTTCTTT 528
Db 481 CAATCGGCTGCTGATGCGCGCGTGTTCGGGCTGTACGCGAGGGCGCGCGTCTTT 540
QY 529 TTGTCAAGACCGACCTGTCCGCTGCGCTGAATGAACCTGAGACGAGGAGCGCGCTAT 588
Db 541 TTGTCAAGACCGACCTGTCCGCTGCGCTGAATGAACCTGAGACGAGGAGCGCGCTAT 600
QY 589 CGTGGCTGCGCAGCAGCGGCGTCTTGGCGAGCTGTGCGAGCTGTGCACTGAAGCGG 648
Db 601 CGTGGCTGCGCAGCAGCGGCGTCTTGGCGAGCTGTGCGAGCTGTGCACTGAAGCGG 660
QY 649 GAAGGACTGGCTGTATTGGGCGAAGTCCGCGGAGGATCTCTGTCACTCACTTG 708
Db 661 GAAGGACTGGCTGTATTGGGCGAAGTCCGCGGAGGATCTCTGTCACTCACTTG 720
QY 709 CTCCTCCGAGAAAGTATCATCATGCTGATGCAATGGCGCGCTGCATACGCTTGATC 768
Db 721 CTCCTCCGAGAAAGTATCATCATGCTGATGCAATGGCGCGCTGCATACGCTTGATC 780
QY 769 CGGCTACCTGCCATTCGACACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGA 828
Db 781 CGGCTACCTGCCATTCGACACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGA 840
QY 829 TGAAGCGGCTGTTGTGATCAGGATGATCTGAGCAAGAGCATCAGGGGCTCGCGCAG 888
Db 841 TGAAGCGGCTGTTGTGATCAGGATGATCTGAGCAAGAGCATCAGGGGCTCGCGCAG 900
QY 889 CGAAGCTGTCGAGGCTCAAGCGCGCATGCCGAGCGAGGATCTCGTGTGACCC 948
Db 901 CCGAAGCTGTCGAGGCTCAAGCGCGCATGCCGAGCGAGGATCTCGTGTGACCC 960
QY 949 ATGGGATGCTGCTCCGGAATATCATGTGGAATATGGCGCTTCTTCTGGATTATCG 1008
Db 961 ATGGGATGCTGCTCCGGAATATCATGTGGAATATGGCGCTTCTTCTGGATTATCG 1020
QY 1009 ACTGTGCGCGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCGGTGATA 1068
Db 1021 ACTGTGCGCGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCGGTGATA 1080
QY 1069 TTGCTGAAGAGCTTGGCGCGCAATGGGCTGACCGCTTCTCGTGTACGATCGCG 1128
Db 1081 TTGCTGAAGAGCTTGGCGCGCAATGGGCTGACCGCTTCTCGTGTACGATCGCG 1140
QY 1129 CTCCGATTCGACGCGATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAA 1188
Db 1141 CTCCGATTCGACGCGATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAA 1200
QY 1189 CAGACCAACAGGTTTCCCTCTAGCGGATCAATTCGCGCTTCTCCCTCCGCGCGCT 1248
Db 1201 CAGACCAACAGGTTTCCCTCTAGCGGATCAATTCGCGCTTCTCCCTCCGCGCGCT 1260
QY 1249 AACGTTACTGCGGAGCGCTTGAATAAGGCGGTGTGCTGTATATGTTATTT 1308
Db 1261 AACGTTACTGCGGAGCGCTTGAATAAGGCGGTGTGCTGTATATGTTATTT 1320
QY 1309 TCCACCATATTGCGCTTCTTTGGCAATGTGAGGCGCGGAAACCTGGCGCTGTCTTTG 1368
Db 1321 TCCACCATATTGCGCTTCTTTGGCAATGTGAGGCGCGGAAACCTGGCGCTGTCTTTG 1380
QY 1369 ACGAGCATTCCTAGGGGCTTTTCCCTCTGCGCAAGGAATGCAAGGCTGTGATGTC 1428
Db 1381 ACGAGCATTCCTAGGGGCTTTTCCCTCTGCGCAAGGAATGCAAGGCTGTGATGTC 1440
QY 1429 GTGAAGGAGCAGTTCCTCTGAGAGCTTCTGAAGACAAACAGCTCTGTAGCGACCTT 1488
Db 1441 GTGAAGGAGCAGTTCCTCTGAGAGCTTCTGAAGACAAACAGCTCTGTAGCGACCTT 1500
QY 1489 TGCAGGCGAGGGAACCCGCCACCTGCGGACAGGTGCTCTGCGGCAAAAGCCAGTGTA 1548

1501 TGCAGGCGAGCGAAACCCGCCACCTTGGCGACAGGTGCTCTGCGGCAAAAGCCAGTGTA 1560
QY 1549 TAAAGATACACCTGCAAGAGCGGCAAAACCCAGTGCACAGTTGTGAGTTGATGTTG 1608
Db 1561 TAAAGATACACCTGCAAGAGCGGCAAAACCCAGTGCACAGTTGTGAGTTGATGTTG 1620
QY 1609 GAAAGAGTCAAAATGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGATGCCAGAAG 1668
Db 1621 GAAAGAGTCAAAATGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGATGCCAGAAG 1680
QY 1669 GTACCCCATTTGATGGGATCTGATCTGGGCGCTCGGTGCACATGCTTTACATGTTTAG 1728
Db 1681 GTACCCCATTTGATGGGATCTGATCTGGGCGCTCGGTGCACATGCTTTACATGTTTAG 1740
QY 1729 TCGAGGTTAAAAAAGCTGTAGGCCCCCGAAACACAGGGGACGTGGTTTCTTTGAAAA 1788
Db 1741 TCGAGGTTAAAAAAGCTGTAGGCCCCCGAAACACAGGGGACGTGGTTTCTTTGAAAA 1800
QY 1789 CAGCATTAATACCATGGGCTTATTAGGCGCTACTCCCAACAGACGCGGCTACTTTGGC 1848
Db 1801 CAGCATTAATACCATGGGCTTATTAGGCGCTACTCCCAACAGACGCGGCTACTTTGGC 1860
QY 1849 TGCATCATCACTAGCTCAAGCGCGGACAGAAACAGGTTCGAGGGGAGGTCCAAAGT 1908
Db 1861 TGCATCATCACTAGCTCAAGCGCGGACAGAAACAGGTTCGAGGGGAGGTCCAAAGT 1920
QY 1909 GTCTCCACCGCAACAAATCTTCTTGGGACCTGCTCAATGGCGTGTGTTGACGTGTC 1968
Db 1921 GTCTCCACCGCAACAAATCTTCTTGGGACCTGCTCAATGGCGTGTGTTGACGTGTC 1980
QY 1969 TATCATGGTCCGGCTCAAAAGACCTTTCGCGGCGCAAAAGGGCCCAATCACCRAATGTAC 2028
Db 1981 TATCATGGTCCGGCTCAAAAGACCTTTCGCGGCGCAAAAGGGCCCAATCACCRAATGTAC 2040
QY 2029 ACCAATGTGACACAGACCTCTGCTGGTGGCAAGCGCCCCCGGGGCGCTTCTTTCGACA 2088
Db 2041 ACCAATGTGACACAGACCTCTGCTGGTGGCAAGCGCCCCCGGGGCGCTTCTTTCGACA 2100
QY 2089 CCATGACCTTGGCGAGCTCGGACCTTTACTTGGTTCACAGGCAATGCGATGTCATTCG 2148
Db 2101 CCATGACCTTGGCGAGCTCGGACCTTTACTTGGTTCACAGGCAATGCGATGTCATTCG 2160
QY 2149 GTGCGCGCGGCGGCGACAGAGGGGAGCTTCTCTCCCGGCGGCTCTCTACTTTG 2208
Db 2161 GTGCGCGCGGCGGCGACAGAGGGGAGCTTCTCTCCCGGCGGCTCTCTACTTTG 2220
QY 2209 AAGGCTCTTGGGCGGTCCACTGCTCTGCGGCGGACGCTGTGGGCTATTTTCG 2268
Db 2221 AAGGCTCTTGGGCGGTCCACTGCTCTGCGGCGGACGCTGTGGGCTATTTTCG 2280
QY 2269 GCTGCGGTGTGCAACCGAGGGGTTGCGAAGCGGTGGAATTTGACCGGTGAGTCTATG 2328
Db 2281 GCTGCGGTGTGCAACCGAGGGGTTGCGAAGCGGTGGAATTTGACCGGTGAGTCTATG 2340
QY 2329 GAAACCATATGCGGTTCGCGTCTTCAAGGCACTGCTCCCTCCGCGCTACCGGAG 2388
Db 2341 GAAACCATATGCGGTTCGCGTCTTCAAGGCACTGCTCCCTCCGCGCTACCGGAG 2400
QY 2389 ACATTCAGAGTGGCCATCTACAGCGCTTACTGGTAGCGGACAGACTAAGGTGCG 2448
Db 2401 ACATTCAGAGTGGCCATCTACAGCGCTTACTGGTAGCGGACAGACTAAGGTGCG 2460
QY 2449 GCTGCGTAGCAGCCAAAGGTTAAGGTGTTGCTTGAACCGCTCGTCCGCGGCGAC 2508
Db 2461 GCTGCGTAGCAGCCAAAGGTTAAGGTGTTGCTTGAACCGCTCGTCCGCGGCGAC 2520
QY 2509 CTAGGTTTCGGGCGTATATGCTAAGGCACTGATGTCAGCCCTAAACATCAGAAATCG 2568
Db 2521 CTAGGTTTCGGGCGTATATGCTAAGGCACTGATGTCAGCCCTAAACATCAGAAATCG 2580
QY 2569 GTAAGGACCATCACCACGCGGTGCGGCGCTACGTTACCTCACTATGCGAAGTTTCTTGC 2628

QY 4789 GACGGCATATGCAAAACCACTGCGCCATGTGGAGCACAGATCACCGGACATGTGAAAAAC 4848
DB 4801 GACGGCATATGCAAAACCACTGCGCCATGTGGAGCACAGATCACCGGACATGTGAAAAAC 4860
QY 4849 GGTTCATGAGGATCGTGGGGCTTAGGACCTCTAGTAAACACGTGGCATGAAACATTTCCCC 4908
DB 4861 GGTTCATGAGGATCGTGGGGCTTAGGACCTCTAGTAAACACGTGGCATGAAACATTTCCCC 4920
QY 4909 ATTAAAGCGGTACACCAACCGGCGCCCTGACAGCCCTCCCGGCGGCAAAATTTCTAGGGCG 4968
DB 4921 ATTAAAGCGGTACACCAACCGGCGCCCTGACAGCCCTCCCGGCGGCAAAATTTCTAGGGCG 4980
QY 4969 CTGTGCGGGTGGCTGCTGAGGAGTACGTGGAGTTACCGGCTGGGGGATTTCCACTAC 5028
DB 4981 CTGTGCGGGTGGCTGCTGAGGAGTACGTGGAGTTACCGGCTGGGGGATTTCCACTAC 5040
QY 5029 GTGACGGGATGACCACTGACAACTGAAAGTGGCCCGTGTCAAGTTCCGGGCCCGGAATTC 5088
DB 5041 GTGACGGGATGACCACTGACAACTGAAAGTGGCCCGTGTCAAGTTCCGGGCCCGGAATTC 5100
QY 5089 TTCAAGAGATGATGGGTGGCGGTGGACAGGTACGCTCCAGCGTGCAAAACCCCTCCTA 5148
DB 5101 TTCAAGAGATGATGGGTGGCGGTGGACAGGTACGCTCCAGCGTGCAAAACCCCTCCTA 5160
QY 5149 CGGGAGGATGACATTTCTGTGGTGGGCTCAATCAATACCTGTGGTTCAGAGTCCCA 5208
DB 5161 CGGGAGGATGACATTTCTGTGGTGGGCTCAATCAATACCTGTGGTTCAGAGTCCCA 5220
QY 5209 TGGAGCGCCAAACCGGACGTAGCAGTGTCTCAATTTCAATGTCTACCGGACCCCTCCCAATT 5268
DB 5221 TGGAGCGCTGAAACCGGATGTAGCAGTGTCTCAATTTCAATGTCTACCGGACCCCTCCCAATT 5280
QY 5269 ACGCGGAGACGGGTAAAGGTAGGCTGGCGAGGGGATCTCCCGCTCTTTGGCGGAGCTCA 5328
DB 5281 ACGCGGAGACGGGTAAAGGTAGGCTGGCGAGGGGATCTCCCGCTCTTTGGCGGAGCTCA 5340
QY 5329 TCAGCTAGCAGCTGTCTGCGCTTCTTGAAGCAACATGCACTACCGCTCATGACTCC 5388
DB 5341 TCAGCTAGCAGCTGTCTGCGCTTCTTGAAGCAACATGCACTACCGCTCATGACTCC 5400
QY 5389 CCGGACGCTGACCTCATCGAGGCCAACTCTCTGTGGCGGAGGAGATGGCGGGAAATTC 5448
DB 5401 CCGGACGCTGACCTCATCGAGGCCAACTCTCTGTGGCGGAGGAGATGGCGGGAAATTC 5460
QY 5449 ACCCGGTGGAGTCAGAAAATAAGTAGTAATTTTGGACTCTTTGAGCGCTCCCAAGCG 5508
DB 5461 ACCCGGTGGAGTCAGAAAATAAGTAGTAATTTTGGACTCTTTGAGCGCTCCCAAGCG 5520
QY 5509 GAGGAGATGAGAGGAGTATCCGTTCGCGGAGATCTCTGCGGAGTCCAGGAAATTC 5568
DB 5521 GAGGAGATGAGAGGAGTATCCGTTCGCGGAGATCTCTGCGGAGTCCAGGAAATTC 5580
QY 5569 CCTCGAGCATGCCCATATGGGACAGCGCCGATTAACACCTTCACTGTTAGTCTCTGG 5628
DB 5581 CCTCGAGCATGCCCATATGGGACAGCGCCGATTAACACCTTCACTGTTAGTCTCTGG 5640
QY 5629 AAGGACCGGAGTACGTCTCTCAGTGTACAGGGTGTCCATGCGCGCTGCCAAGGCC 5688
DB 5641 AAGGACCGGAGTACGTCTCTCAGTGTACAGGGTGTCCATGCGCGCTGCCAAGGCC 5700
QY 5689 CCTCCGATACCACTCCAGGAGGAGGAGCGGTGTCTGTGAGAAATCTACCGTGTCT 5748
DB 5701 CCTCCGATACCACTCCAGGAGGAGGAGCGGTGTCTGTGAGAAATCTACCGTGTCT 5760
QY 5749 TCTGCTTTGGCGAGTCCGCCAAAGACCTTTGGAGCTTCGGAATCGTGGCGCTCGAC 5808
DB 5761 TCTGCTTTGGCGAGTCCGCCAAAGACCTTTGGAGCTTCGGAATCGTGGCGCTCGAC 5820
QY 5809 ACGGACCGGAGTCTCTGACAGCGCTTCCGACGCGGAGCGGAGTCCCGAC 5868
DB 5821 ACGGACCGGAGTCTCTGACAGCGCTTCCGACGCGGAGCGGAGTCCCGAC 5880
QY 5869 GTTGAGTCGTACTCTCTCCATGCCCCCTTTGAGGGGAGCGCGGGGATCCCGATCTCAGC 5928

DB 5881 GTTGAGTCGTACTCTCTCCATGCCCTTTGAGGGGAGCGCGGGATCCCGATCTCAGC 5940
QY 5929 GACGGCTTTGTCTTACCGTAAAGCGAGGCTAGTGAGGACGTCTGTCTGTCTCGATG 5988
DB 5941 GACGGCTTTGTCTTACCGTAAAGCGAGGCTAGTGAGGACGTCTGTCTGTCTCGATG 6000
QY 5989 TCTTACATGACAGGAGGCTGATCAGCCATGCGCTGGCGAGGAAACCAAGCTGCC 6048
DB 6001 TCTTACATGACAGGAGGCTGATCAGCCATGCGCTGGCGAGGAAACCAAGCTGCC 6060
QY 6049 ATCAATGCTAGCAACTCTTTTGTCTCGCTACCACTCTGTCTTATCTTATCTCAACATCT 6108
DB 6061 ATCAATGCTAGCAACTCTTTTGTCTCGCTACCACTCTGTCTTATCTTATCTCAACATCT 6120
QY 6109 CGCAGCGCAAGCTGCGGAGAGAGGTCACTTTGACAGACTGCAAGTCTCTGGAGCGAC 6168
DB 6121 CGCAGCGCAAACTGCGGAGAGAGGTCACTTTGACAGACTGCAAGTCTCTGGAGCGAC 6180
QY 6169 CACTACCGGAGCTGTCTAAGGAGATGAAGGCGAGGCTCCACAGTTAAGGCTAAACTT 6228
DB 6181 CACTACCGGAGCTGTCTAAGGAGATGAAGGCGAGGCTCCACAGTTAAGGCTAAACTT 6240
QY 6229 CTATCCGTGGAGAGGCTGTAAAGCTGAGCGCCCACTTCGGCCAGATCTAAATTTGGC 6288
DB 6241 CTATCCGTGGAGAGGCTGTAAAGCTGAGCGCCCACTTCGGCCAGATCTAAATTTGGC 6300
QY 6289 TATGGGCGCAAGGACCTGCGGAACTTATCCAGCAAGCCGTTAAACCACTCCGCTCGGT 6348
DB 6301 TATGGGCGCAAGGACCTGCGGAACTTATCCAGCAAGCCGTTAAACCACTCCGCTCGGT 6360
QY 6349 TGGAGGACTTGTGGAAGACACTGAGACACCAATTTGACACCACTCATGCGCAAAAT 6408
DB 6361 TGGAGGACTTGTGGAAGACACTGAGACACCAATTTGACACCACTCATGCGCAAAAT 6420
QY 6409 GAGTTTCTGCGTCCAAACAGAGAGGCGCGCAAGCCAGCTCGCTCTTATCGTATTC 6468
DB 6421 GAGTTTCTGCGTCCAAACAGAGAGGCGCGCAAGCCAGCTCGCTCTTATCGTATTC 6480
QY 6469 CCAGATTGGGGGTTCTGTGTGCGAGAAATGGCCCTTTACGATGTGTCTCCACCTTC 6528
DB 6481 CCAGATTGGGGGTTCTGTGTGCGAGAAATGGCCCTTTACGATGTGTCTCCACCTTC 6540
QY 6529 CCTCAGCGCTGATGGGCTCTTATACGATTTCAATCTCTCTGAGACGCGGTCTGAG 6588
DB 6541 CCTCAGCGCTGATGGGCTCTTATACGATTTCAATCTCTCTGAGACGCGGTCTGAG 6600
QY 6589 TTTCTGTGTGATGCTGCGGAAAGCAAGAAATGGCCCTTTCGATATGACACCCGCG 6648
DB 6601 TTTCTGTGTGATGCTGCGGAAAGCAAGAAATGGCCCTTTCGATATGACACCCGCG 6660
QY 6649 TGTGTTGACTCAACCGTCACTGAGAAATGACATCCGTTGTGAGGAGTCAATCTACATGT 6708
DB 6661 TGTGTTGACTCAACCGTCACTGAGAAATGACATCCGTTGTGAGGAGTCAATCTACATGT 6720
QY 6709 TGTGATTTGGCCCCCGAAGCGACAGCGGCTTACAGGCTCTGAGAGCGCTTTTACATC 6768
DB 6721 TGTGATTTGGCCCCCGAAGCGACAGCGGCTTACAGGCTCTGAGAGCGCTTTTACATC 6780
QY 6769 GGGGGCCCCCTGACTTAATTTTAAAGGCGAGAACTGCGGCTATCGCGGTGCGCGCGAGC 6828
DB 6781 GGGGGCCCCCTGACTTAATTTTAAAGGCGAGAACTGCGGCTATCGCGGTGCGCGCGAGC 6840
QY 6829 GGTGTACTGAGGACGAGCTGGGTAATACCTTCACTGTTTACTTGAAGCGCTCGGGC 6888
DB 6841 GGTGTACTGAGGACGAGCTGGGTAATACCTTCACTGTTTACTTGAAGCGCTCGGGC 6900
QY 6889 TGTGAGCTGCGAAGCTCCAGGACTGACGATGTCTGATGCGGAGACGACCTTGTCTGTT 6948
DB 6901 TGTGAGCTGCGAAGCTCCAGGACTGACGATGTCTGATGCGGAGACGACCTTGTCTGTT 6960
QY 6949 ATCTGTGAAAGCGCGGGGACCCAGAGGACGAGGCGAGCTTACGGGCTTCCAGGAGGT 7008

| | | | | | | | |
|----|------|--|------|----|------|---|------|
| QY | 709 | CTCCTGCCGAGAAAGTATCCATCATGCTGCTGATGCAATGCGCGCTGCATACGCTTGATC | 768 | Db | 1801 | CACGATAATACCATGCGCCTATTACGGCCTTACTCCCAACAGACGGGAGCCTACTTGGC | 1860 |
| Db | 721 | CTCCTGCCGAGAAAGTATCCATCATGCTGCTGATGCAATGCGCGCTGCATACGCTTGATC | 780 | QY | 1849 | TGCATCATCACTAGTCTCACAGCGCGGACAGAAACAGGTGAGGGGAGGTCCAAAGTG | 1908 |
| QY | 769 | CGGCTACCTGCCCATTTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGA | 828 | Db | 1861 | TGCATCATCACTAGTCTCACAGCGCGGACAGAAACAGGTGAGGGGAGGTCCAAAGTG | 1920 |
| Db | 781 | CGGCTACCTGCCCATTTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGA | 840 | QY | 1909 | GTCTCCACCGCAACAACATCTTTCTCTGGCGACTCTGGTCAATGGCGTGTGTGGACTGTC | 1968 |
| QY | 829 | TGGAAGCCGGTCTTGTGATCAGGATGATCTGGAAGAGAGATCAGGGGCTCGGCCAG | 888 | Db | 1921 | GTCTCCACCGCAACAACATCTTTCTCTGGCGACTCTGGTCAATGGCGTGTGTGGACTGTC | 1980 |
| Db | 841 | TGGAAGCCGGTCTTGTGATCAGGATGATCTGGAAGAGAGATCAGGGGCTCGGCCAG | 900 | QY | 1969 | TTATCATGTGCGGCTCAAGACCTTTCGCGCCCAAGAGGCCCAATCAACCAAAATGTAC | 2028 |
| QY | 889 | CGGAATGTTGCGCAGGCTCAAGGCGCGATCGCGACCGCGAGAGATCTCGTGTACCC | 948 | Db | 1981 | TATCATGTGTCGGCTCAAAAGACCTTTCGCGCCCAAGAGGCCCAATCAACCAAAATGTAC | 2040 |
| Db | 901 | CGGAATGTTGCGCAGGCTCAAGGCGCGATCGCGACCGCGAGAGATCTCGTGTACCC | 960 | QY | 2029 | ACCAATGTGACACAGGACCTCTGTCGGCTGGCAAGCGCCCCCGGGCGGCTTCTTGGACA | 2088 |
| QY | 949 | ATGGCGATCCCTGCTTGCAGATATCATGCTGGAAATGSCCGCTTTTCTGGATTCATCG | 1008 | Db | 2041 | ACCAATGTGACACAGGACCTCTGTCGGCTGGCAAGCGCCCCCGGGCGGCTTCTTGGACA | 2100 |
| Db | 961 | ATGGCGATCCCTGCTTGCAGATATCATGCTGGAAATGSCCGCTTTTCTGGATTCATCG | 1020 | QY | 2089 | CCATGACCTGCGGAGCTTCGGACCTTTACTTGGTCAAGAGGATCGGATGTCATTCCG | 2148 |
| QY | 1009 | ACTGTGCGCGGCTGGGTGGGAGCGGCTATCAGGACATAGGCTTGGCTACCGGTGATA | 1068 | Db | 2101 | CCATGACCTGCGGAGCTTCGGACCTTTACTTGGTCAAGAGGATCGGATGTCATTCCG | 2160 |
| Db | 1021 | ACTGTGCGCGGCTGGGTGGGAGCGGCTATCAGGACATAGGCTTGGCTACCGGTGATA | 1080 | QY | 2149 | GTGCGCGCGGCGGACAGCGGAGGCTTACTCTCCCGCAGGCGCGCTCTCTACTTG | 2208 |
| QY | 1069 | TTGCTGAAGAGCTTGGCGGAGATGGCTGACCGCTTCTCGTCTTACGGTATGCGCG | 1128 | Db | 2161 | GTGCGCGCGGCGGACAGCGGAGGCTTACTCTCCCGCAGGCGCGCTCTCTACTTG | 2220 |
| Db | 1081 | TTGCTGAAGAGCTTGGCGGAGATGGCTGACCGCTTCTCGTCTTACGGTATGCGCG | 1140 | QY | 2209 | AAGGGCTCTTTCGGCGGCTCCACTGCTCTGCCCCCTCGGGGACGCTGTGGGACATCTTTCG | 2268 |
| QY | 1129 | CTCCGATTCGAGCGCATCGCTTCTATCGCCTTCTTGACGAGTCTTCTGAGTTTAAA | 1188 | Db | 2221 | AAGGGCTCTTTCGGCGGCTCCACTGCTCTGCCCCCTCGGGGACGCTGTGGGACATCTTTCG | 2280 |
| Db | 1141 | CTCCGATTCGAGCGCATCGCTTCTATCGCCTTCTTGACGAGTCTTCTGAGTTTAAA | 1200 | QY | 2269 | GCTGCGGCTGTGACCCGAGGGTGTGGAAGCGGTGACTTTGTACCCGCTGAGTCTATG | 2328 |
| QY | 1189 | CAGACCAACAGGTTTCCCTTAGCGGATCAATTCGCGCCTCTCCCTCCCGCCCGCT | 1248 | Db | 2281 | GCTGCGGCTGTGACCCGAGGGTGTGGAAGCGGTGACTTTGTACCCGCTGAGTCTATG | 2340 |
| Db | 1201 | CAGACCAACAGGTTTCCCTTAGCGGATCAATTCGCGCCTCTCCCTCCCGCCCGCT | 1260 | QY | 2329 | GAAACCACTATGCGGTCCCGGCTTTCACGGAACAATCTGCTCCCTCGCGCGCTACCGCAG | 2388 |
| QY | 1249 | AAGCTTACTGCGAAGCGCTTGGAAATAGGCGGTGCTGCTTGTCTATATGTTATTT | 1308 | Db | 2341 | GAAACCACTATGCGGTCCCGGCTTTCACGGAACAATCTGCTCCCTCGCGCGCTACCGCAG | 2400 |
| Db | 1261 | AAGCTTACTGCGAAGCGCTTGGAAATAGGCGGTGCTGCTTGTCTATATGTTATTT | 1320 | QY | 2389 | ACATTCAGGTGGCGCATCTACAGCGCCCTTACTGTTAGCGCAAGAGCACTAAGGTGCG | 2448 |
| QY | 1309 | TCCACCATATGCGCGTCTTTTGGCAATGTGAGGCGCCGGAACCTGCGCCCTGCTTCTTG | 1368 | Db | 2401 | ACATTCAGGTGGCGCATCTACAGCGCCCTTACTGTTAGCGCAAGAGCACTAAGGTGCG | 2460 |
| Db | 1321 | TCCACCATATGCGCGTCTTTTGGCAATGTGAGGCGCCGGAACCTGCGCCCTGCTTCTTG | 1380 | QY | 2449 | GCTGCGTATGACGCCCAAGGGTATAGGTGCTTGTCTGACCCGCTCGCGCGCCACC | 2508 |
| QY | 1369 | ACGAGCATCTTAGGGTCTTTCCCTCTCCGCAAGAGATGCAAGGTCTGTTCAATGTC | 1428 | Db | 2461 | GCTGCGTATGACGCCCAAGGGTATAGGTGCTTGTCTGACCCGCTCGCGCGCCACC | 2520 |
| Db | 1381 | ACGAGCATCTTAGGGTCTTTCCCTCTCCGCAAGAGATGCAAGGTCTGTTCAATGTC | 1440 | QY | 2509 | CTAGGTTTTCGGGGGTATATGCTTAAGGCACTGTTATCGACCTTAACATCAGAATCGG | 2568 |
| QY | 1429 | GTGAAGGACAGTTCCTCTGGAAGCTTCTTGAAGCAAAACAGCTCTGTAGCGACCCCTT | 1488 | Db | 2521 | CTAGGTTTTCGGGGGTATATGCTTAAGGCACTGTTATCGACCTTAACATCAGAATCGG | 2580 |
| Db | 1441 | GTGAAGGACAGTTCCTCTGGAAGCTTCTTGAAGCAAAACAGCTCTGTAGCGACCCCTT | 1500 | QY | 2569 | GTAAGGACCATCACCAAGGGTGGCGGCTTACGTTACTTCCACTATGGCAAGTTCTTGGC | 2628 |
| QY | 1489 | TGCAAGGACAGGAAACCCCGGACAGGTGCTCTGCGGCAAAAGCGAGTGTGTA | 1548 | Db | 2581 | GTAAGGACCATCACCAAGGGTGGCGGCTTACGTTACTTCCACTATGGCAAGTTCTTGGC | 2640 |
| Db | 1501 | TGCAAGGACAGGAAACCCCGGACAGGTGCTCTGCGGCAAAAGCGAGTGTGTA | 1560 | QY | 2629 | GACGGTGTGCTCTGCGGGGCGCTTATGACATCATATATCTGATGAGTGGCACTCAACT | 2688 |
| QY | 1549 | TAAAGTACCTGCAAGGCGGACAAACCCAGTCCACGTTGTGAGTTGATAGTCTG | 1608 | Db | 2641 | GACGGTGTGCTCTGCGGGGCGCTTATGACATCATATATCTGATGAGTGGCACTCAACT | 2700 |
| Db | 1561 | TAAAGTACCTGCAAGGCGGACAAACCCAGTCCACGTTGTGAGTTGATAGTCTG | 1620 | QY | 2689 | GACTCGACCATCTCTCGGCGATCGGCACAGTCTTGGACCAAGCGGAGACGCGTGGAGCG | 2748 |
| QY | 1609 | GAAAGATCAATGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATGCCAGAG | 1668 | Db | 2701 | GACTCGACCATCTCTCGGCGATCGGCACAGTCTTGGACCAAGCGGAGACGCGTGGAGCG | 2760 |
| Db | 1621 | GAAAGATCAATGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATGCCAGAG | 1680 | QY | 2749 | CGACTCGTCTGCTCGCACCGCTACGCTTCGGGATCGGTCAACCGTGCACATCCAAAC | 2808 |
| QY | 1669 | GTACCCCATTTGATGGGATCTGATCTGGGCGCTCGGTGCAATGCTTTTACATGTTTAC | 1728 | Db | 2761 | CGACTCGTCTGCTCGCACCGCTACGCTTCGGGATCGGTCAACCGTGCACATCCAAAC | 2820 |
| Db | 1681 | GTACCCCATTTGATGGGATCTGATCTGGGCGCTCGGTGCAATGCTTTTACATGTTTAC | 1740 | QY | 2809 | ATCGAGGAGGTGGCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGGCACTCCCG | 2868 |
| QY | 1729 | TCGAGGTTAAAAAGCTTAGGCGCCCGGAAACCAAGGAGCGTGTGTTTCTTTTGAATAA | 1788 | Db | 2821 | ATCGAGGAGGTGGCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGGCACTCCCG | 2880 |
| Db | 1741 | TCGAGGTTAAAAAGCTTAGGCGCCCGGAAACCAAGGAGCGTGTGTTTCTTTTGAATAA | 1800 | QY | 2869 | ATCGAGACCATCAAGGGGAGGACCTCTATTTCTGCAATTCAGAGAAATGTGTAT | 2928 |
| QY | 1789 | CACGATAATACCATGCGCCTATTACGGCCTACTTCCCAACAGACGCGGCGCTACTTGGC | 1848 | | | | |

5089 TTCCAGAGTGGAGTGGGTCGGTTGACAGAGTACGCTCCAGCGTGCAAAACCCCTCCTTA 5148
5101 TTCCAGAGTGGAGTGGGTCGGTTGACAGAGTACGCTCCAGCGTGCAAAACCCCTCCTTA 5160
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VERSION AX937622.1 GI:40713673
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Duggal, R.A., Patick, A.K., Zhang, J.A. and Zhao, W.A.
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PRIMER INC. (US)
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ORIGIN

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Query Match 95.2%; Score 7611.8; DB 6; Length 12305;
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| QY | 2358 | GGACAACTCTGTCCTCCCGCGCTTACCGCAGACATTCACAGTGGCCCATCTACACGCC | 2417 | Db | 4600 | TTTCTTGTCCAGACTAAGCAGGAGAGCACTTCCCTTACCTGTGTAGCATACACAGG | 4659 |
| Db | 3520 | GGACAACTCTGTCCTCCCGCGCTTACCGCAGACATTCACAGTGGCCCATCTACACGCC | 3579 | QY | 3498 | TACGGTGTGGCGCAGGGCTCAGGCTCCACCTCCATCGTGGGACCAAAATGTGGAAGTCT | 3557 |
| QY | 2418 | TACTGTAGCGGCAAGACACTAAGTGTCCGGCTGCGGTATGACGCCCAAGGGTATAGGT | 2477 | Db | 4660 | TACGGTGTGGCGCAGGGCTCAGGCTCCACCTCCATCGTGGGACCAAAATGTGGAAGTCT | 4719 |
| Db | 3580 | TACTGTAGCGGCAAGACACTAAGTGTCCGGCTGCGGTATGACGCCCAAGGGTATAGGT | 3639 | QY | 3558 | CATACGGCTAAAGCTACGCTGCAACGGGCAACGCCCTCTGTGTATAGGCTGGAGCGT | 3617 |
| QY | 2478 | GCTTGTCTGAACCCGTCGTCGCGCACCTTAGTGTTCGGGGCTATATGTCTAAGG | 2537 | Db | 4720 | CATACGGCTAAAGCTACGCTGCAACGGGCAACGCCCTCTGTGTATAGGCTGGAGCGT | 4779 |
| Db | 3640 | GCTTGTCTGAACCCGTCGTCGCGCACCTTAGTGTTCGGGGCTATATGTCTAAGG | 3699 | QY | 3618 | TCAAAACGAGGTACTACACACACACCCCATTAACCAATATCATCATGATGATGTCGG | 3677 |
| QY | 2538 | ACATGGTATCGACCTAACATCAGAACGGGTAAAGACCATCACACGGGTGCCCCCAT | 2597 | Db | 4780 | TCAAAACGAGGTACTACACACACACCCCATTAACCAATATCATCATGATGATGTCGG | 4839 |
| Db | 3700 | ACATGGTATCGACCTAACATCAGAACGGGTAAAGACCATCACACGGGTGCCCCCAT | 3759 | QY | 3678 | TGACCTCGAGTCTGTACAGAGCACCTGGGTCTGTGTAGGGGAGTCTCTAGCAGCTGGC | 3737 |
| QY | 2598 | CACGTACTCCACCTATGCGCAAGTTCTTTCGCGACGGTGTGTCTGTGGGGCGCTATGA | 2657 | Db | 4840 | TGACCTCGAGTCTGTACAGAGCACCTGGGTCTGTGTAGGGGAGTCTCTAGCAGCTGGC | 4899 |
| Db | 3760 | CACGTACTCCACCTATGCGCAAGTTCTTTCGCGACGGTGTGTCTGTGGGGCGCTATGA | 3819 | QY | 3738 | CGGCTATTGGCTGACAAACAGGAGCGTGTCTATTTGGGAGGATCATCTTTGTCGGGAAA | 3797 |
| QY | 2658 | CATCAATATGATGATGAGTGCCACTCAACTGACTCGACCACTATCTGGGCATCGGCAC | 2717 | Db | 4900 | CGGCTATTGGCTGACAAACAGGAGCGTGTCTATTTGGGAGGATCATCTTTGTCGGGAAA | 4959 |
| Db | 3820 | CATCAATATGATGATGAGTGCCACTCAACTGACTCGACCACTATCTGGGCATCGGCAC | 3879 | QY | 3798 | GCGGGCCATCATTTCCGACAGGAGNAGTCTTTTACCGGGAGTTCATGATGATGGAAGTG | 3857 |
| QY | 2718 | AGTCTTGACCAAGCGAGAGCGGTGGAGCGGACTCGTGTGTCTGCGCACCGCTAGGCC | 2777 | Db | 4960 | GCGGGCCATCATTTCCGACAGGAGNAGTCTTTTACCGGGAGTTCATGATGATGGAAGTG | 5019 |
| Db | 3880 | AGTCTTGACCAAGCGAGAGCGGTGGAGCGGACTCGTGTGTCTGCGCACCGCTAGGCC | 3939 | QY | 3858 | CGCTCACACCTCCCTTACATCGAACAGGGAATCGAGCTCGCCGAAACAAATTCACACAGAA | 3917 |
| QY | 2778 | TCGGGATCGGTACCGGTGCGACATCCAAACATCGAGAGGTGTGTCTGACGACTGG | 2837 | Db | 5020 | CGCTCACACCTCCCTTACATCGAACAGGGAATCGAGCTCGCCGAAACAAATTCACACAGAA | 5079 |
| Db | 3940 | TCGGGATCGGTACCGGTGCGACATCCAAACATCGAGAGGTGTGTCTGACGACTGG | 3999 | QY | 3918 | GGCAATCGGGTGTGTGCAAAACAGCCACCAAGCAAGCGAGGCTGTCTCCCGTGGTGA | 3977 |
| QY | 2838 | AGAAATCCCTTTTATGGCAAGGATCCCATCGAGACCATCAAGGGGGGAGGCACCT | 2897 | Db | 5080 | GGCAATCGGGTGTGTGCAAAACAGCCACCAAGCAAGCGAGGCTGTCTCCCGTGGTGA | 5139 |
| Db | 4000 | AGAAATCCCTTTTATGGCAAGGATCCCATCGAGACCATCAAGGGGGGAGGCACCT | 4059 | QY | 3978 | ATCCAGTGGGGACCTTCGAGAGCTTCTGGCGAAGCATATGGAATTTTCATCAGCGG | 4037 |
| QY | 2898 | CATTTTCTGCCATTCGAAGAGAAATGTGATGAGCTCGCCGAGAGTGTCTCGGCGCTCGG | 2957 | Db | 5140 | ATCCAGTGGGGACCTTCGAGAGCTTCTGGCGAAGCATATGGAATTTTCATCAGCGG | 5199 |
| Db | 4060 | CATTTTCTGCCATTCGAAGAGAAATGTGATGAGCTCGCCGAGAGTGTCTCGGCGCTCGG | 4119 | QY | 4038 | GATACAAATTTTACGAGCTTGTCCACTCTCGCTGGCAACCCCGGATAGCATCACTGAT | 4097 |
| QY | 2958 | ACTCAATGCTAGCATATACCGGGGCTTGTATGATTCGCTATACCAATAGCGGAGA | 3017 | Db | 5200 | GATACAAATTTTACGAGCTTGTCCACTCTCGCTGGCAACCCCGGATAGCATCACTGAT | 5259 |
| Db | 4120 | ACTCAATGCTAGCATATACCGGGGCTTGTATGATTCGCTATACCAATAGCGGAGA | 4179 | QY | 4098 | GGCAATTCACAGCTTATACCAAGCGGCTCCACCCCAACATACCTCTCTGTTTAAACAT | 4157 |
| QY | 3018 | CGTCAATGCTAGCAAGGAGCTCTTAAGCGGGCTTACCGGCAATTCGACTCAGT | 3077 | Db | 5260 | GGCAATTCACAGCTTATACCAAGCGGCTCCACCCCAACATACCTCTCTGTTTAAACAT | 5319 |
| Db | 4180 | CGTCAATGCTAGCAAGGAGCTCTTAAGCGGGCTTACCGGCAATTCGACTCAGT | 4239 | QY | 4158 | CTGGGGGATGGGTGGCGCCCACTTGTCTCCAGAGCTGTCTCTGCTTTCTGTTAGG | 4217 |
| QY | 3078 | GATCGACTGCAATATGTGTACCCGACAGAGTTCGACTTCAGCTTCGAGCCCGACCTTCAC | 3137 | Db | 5320 | CTGGGGGATGGGTGGCGCCCACTTGTCTCCAGAGCTGTCTCTGCTTTCTGTTAGG | 5379 |
| Db | 4240 | GATCGACTGCAATATGTGTACCCGACAGAGTTCGACTTCAGCTTCGAGCCCGACCTTCAC | 4299 | QY | 4218 | CGCGGCACTCGCTGGAGCGGCTGTGGAGCATAGGCTTGGGAAAGGTGCTTGTGATAT | 4277 |
| QY | 3138 | CATTGAGAGCAGACCGTGCACCAAGAGCGGTGTACGCTCGAGCGGCGAGGACAGAC | 3197 | Db | 5380 | CGCGGCACTCGCTGGAGCGGCTGTGGAGCATAGGCTTGGGAAAGGTGCTTGTGATAT | 5439 |
| Db | 4300 | CATTGAGAGCAGACCGTGCACCAAGAGCGGTGTACGCTCGAGCGGCGAGGAC | 4359 | | | | |

Db 7600 GGCGCGCAAGCCAGCTCGCCTTATCTGATTTCCAGATTTGGGGGTTCTGTTGTGCGAGAA 7659
Qy 6498 AATGGCCCTTTACGATGTGTCTCCACCCTCCCTCAGCCGCTGATGGGCTCTTCATACGG 6557
Db 7660 AATGGCCCTTTACGATGTGTCTCCACCCTCCCTCAGCCGCTGATGGGCTCTTCATACGG 7719
Qy 6558 ATTCCATATCTCTCTGACAGCGGGTCTGAGTTCCTGTGTAATGCCCTGGAAAGCGAAGAA 6617
Db 7720 ATTCCATATCTCTCTGACAGCGGGTCTGAGTTCCTGTGTAATGCCCTGGAAAGCGAAGAA 7779
Qy 6618 ATGCCCTATGGGCTTCGATATGACACCCGCTGTTTGTACTCAACGGTCTACTGAAATGA 6677
Db 7780 ATGCCCTATGGGCTTCGATATGACACCCGCTGTTTGTACTCAACGGTCTACTGAAATGA 7839
Qy 6678 CATCCGTGTGAGAGTCAATCTACCAATGTTGTGACTTGGCCCCCGAAGCCACAGAGGC 6737
Db 7840 CATCCGTGTGAGAGTCAATCTACCAATGTTGTGACTTGGCCCCCGAAGCCACAGAGGC 7899
Qy 6738 CATAGGTTCGCTCACAGAGCGCTTTATCATCGGGGGCCCCCTGACTAATTTCTAAAGGSCA 6797
Db 7900 CATAGGTTCGCTCACAGAGCGCTTTATCATCGGGGGCCCCCTGACTAATTTCTAAAGGSCA 7959
Qy 6798 GAACCTGGGCTATCCCGGTCGCCGAGCGGTGTAATGACACCCAGCTCGGGTATATAC 6857
Db 7960 GAACCTGGGCTATCCCGGTCGCCGAGCGGTGTAATGACACCCAGCTCGGGTATATAC 8019
Qy 6858 CCTCACATGTTACTGAAGGCGCTGCGGCTGTGAGCTCGGAGCTCCAGGACTGCAC 6917
Db 8020 CCTCACATGTTACTGAAGGCGCTGCGGCTGTGAGCTCGGAGCTCCAGGACTGCAC 8079
Qy 6918 GATGCTCGTATGCGGAGACGACCTTGTCTTATCTGTGAAAGCGCGGGAACCAAGAGGA 6977
Db 8080 GATGCTCGTATGCGGAGACGACCTTGTCTTATCTGTGAAAGCGCGGGAACCAAGAGGA 8139
Qy 6978 CGAGCGAGCTACGGGCTTTACGAGGCTATGACTAGATCTCTGCCCCCCCTGGGGA 7037
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Qy 7038 CCGGCCCAACAGAAATAGCTTGGAGTTGATACATCTGCTCCATGCTCAGT 7097
Db 8200 CCGGCCCAACAGAAATAGCTTGGAGTTGATACATCTGCTCCATGCTCAGT 8259
Qy 7098 CGCGCAGCATGCTGCAAAAGGCTGTACTATCTCACCGGTGACCCACACCCCTCT 7157
Db 8260 CGCGCAGCATGCTGCAAAAGGCTGTACTATCTCACCGGTGACCCACACCCCTCT 8319
Qy 7158 TGCGCGGCTCGTGGGAGACAGCTAGACACACTCCAGTCAATTCCTGGCTAGGCAACAT 7217
Db 8320 TGCGCGGCTCGTGGGAGACAGCTAGACACACTCCAGTCAATTCCTGGCTAGGCAACAT 8379
Qy 7218 CATCATGTATGGCCACCTTGTGGCAAGGATGATCCTGATGACTCATTTCTTCCAT 7277
Db 8380 CATCATGTATGGCCACCTTGTGGCAAGGATGATCCTGATGACTCATTTCTTCCAT 8439
Qy 7278 CTTCTAGCTCAGGAACACTTGAAGAAAGCCCTAGATTCTCAGATCTACGGGCTGTGA 7337
Db 8440 CTTCTAGCTCAGGAACACTTGAAGAAAGCCCTAGATTCTCAGATCTACGGGCTGTGA 8499
Qy 7338 TPCCATTAGCCACTTACCTACCTCAGATCTTCAACGACTCCATTCCTAGGCTAGGCAAT 7397
Db 8500 TPCCATTAGCCACTTACCTACCTCAGATCTTCAACGACTCCATTCCTAGGCTAGGCAAT 8559
Qy 7398 TTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCTTCATGCTCAGGAACCT 7457
Db 8560 TTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCTTCATGCTCAGGAACCT 8619
Qy 7458 TGGGGTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAAAGTGTCCGGCTAGGCTACT 7517
Db 8620 TGGGGTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAAAGTGTCCGGCTAGGCTACT 8679
Qy 7518 GTCCCAAGGGGGAGGGCTGCGACATTTGTGGCAAGTACCTTCTCAACTGGGCGAGTAGGAC 7577
Db 8680 GTCCCAAGGGGGAGGGCTGCGACATTTGTGGCAAGTACCTTCTCAACTGGGCGAGTAGGAC 8739

Qy 7578 CAAGCTCAAACTCACTCCAAATCCCGGCTGCGTCCCAAGTTGGAATTTATCCAGCTGCTTCGT 7637
Db 8740 CAAGCTCAAACTCACTCCAAATCCCGGCTGCGTCCCAAGTTGGAATTTATCCAGCTGCTTCGT 8799
Qy 7638 TGCTGGTTACAGCGGGGAGACATATATACAGCTCTCTCGTCCCGACCCCGCTGCTT 7697
Db 8800 TGCTGGTTACAGCGGGGAGACATATATACAGCTCTCTCGTCCCGACCCCGCTGCTT 8859
Qy 7698 CATGTGCTGCTACTCTCTACTTTCTGTAGGGTAGGCATCTATCTACTCCCCAACCGATG 7757
Db 8860 CATGTGCTGCTACTCTCTACTTTCTGTAGGGTAGGCATCTATCTACTCCCCAACCGATG 8919
Qy 7758 AACGGGAGCTAAACACTCCAGGCCAATAGGCCAATCTGTTTTTTTCCCTTTTTTTTTT 7817
Db 8920 AACGGGAGCTAAACACTCCAGGCCAATAGGCCAATCTGTTTTTTTCCCTTTTTTTTTT 8979
Qy 7818 CTTC 7877
Db 8980 CTTC 9039
Qy 7878 CTTTTTTTCTTTTGGTGGCTCCATCTTAGCCCTTAGTACAGGCTAGCTGTGAAAGTCCG 7937
Db 9040 CTTTTTTTCTTTTGGTGGCTCCATCTTAGCCCTTAGTACAGGCTAGCTGTGAAAGTCCG 9099
Qy 7938 TGAGCCGCTTGAATGACAGAGAGTCTGATCTGGCCTCTCTGCGAGATCAAGTACT 7992
Db 9100 TGAGCCGCTTGAATGACAGAGAGTCTGATCTGGCCTCTCTGCGAGATCAAGTACT 9154

Search completed: November 9, 2004, 06:45:56
Job time : 21434 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 19:28:28 ; Search time 2220 Seconds
(without alignments)
18897.916 Million cell updates/sec

Title: US-10-005-469-1
Perfect score: 7992
Sequence: 1 gccagcccccagattgggggc.....ctctctgcagatcaagact 7992

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 23Sep04:.*
1: geneseqn1980s:.*
2: geneseqn1990s:.*
3: geneseqn2000s:.*
4: geneseqn2001as:.*
5: geneseqn2001bs:.*
6: geneseqn2002as:.*
7: geneseqn2002bs:.*
8: geneseqn2003as:.*
9: geneseqn2003bs:.*
10: geneseqn2003cs:.*
11: geneseqn2003ds:.*
12: geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|--------------------|
| 1 | 7992 | 100.0 | 7992 | 6 | AAL47276 Hepatitis |
| 2 | 7992 | 100.0 | 10690 | 6 | ABK91412 Hepatitis |
| 3 | 7992 | 100.0 | 10690 | 9 | ACA61697 Hepatitis |
| 4 | 7992 | 100.0 | 10690 | 10 | ADC83762 Hepatitis |
| 5 | 7990.4 | 100.0 | 7992 | 6 | AAL47281 Hepatitis |
| 6 | 7990.4 | 100.0 | 10690 | 6 | ABK91448 Hepatitis |
| 7 | 7990.4 | 100.0 | 10690 | 6 | ABK91435 Hepatitis |
| 8 | 7990.4 | 100.0 | 10690 | 6 | ABK91243 Hepatitis |
| 9 | 7990.4 | 100.0 | 10690 | 6 | ABK91434 Hepatitis |
| 10 | 7990.4 | 100.0 | 11313 | 12 | ADP86264 Hepatitis |
| 11 | 7989 | 100.0 | 7989 | 3 | AAA98968 Hepatitis |
| 12 | 7989 | 100.0 | 7989 | 12 | ADJ57845 HCV repli |
| 13 | 7988.8 | 100.0 | 10690 | 6 | ABK91440 Hepatitis |
| 14 | 7988.8 | 100.0 | 11313 | 12 | ADP86271 Hepatitis |
| 15 | 7987.4 | 99.9 | 7989 | 6 | AAD25322 Hepatitis |
| 16 | 7987.2 | 99.9 | 7992 | 6 | AAL47280 Hepatitis |
| 17 | 7987.2 | 99.9 | 7992 | 6 | AAL47277 Hepatitis |
| 18 | 7987.2 | 99.9 | 11313 | 12 | ADP86265 Hepatitis |
| 19 | 7985.8 | 99.9 | 7989 | 6 | AAD25326 Hepatitis |
| 20 | 7985.6 | 99.9 | 11313 | 12 | ADP86272 Hepatitis |
| 21 | 7984 | 99.9 | 10690 | 6 | ABK91242 Hepatitis |

| | | | | | |
|----|--------|------|-------|----|--------------------|
| 22 | 7982.6 | 99.9 | 7989 | 6 | AAD25325 Hepatitis |
| 23 | 7982.6 | 99.9 | 7989 | 10 | ADD93734 Hepatitis |
| 24 | 7982.4 | 99.9 | 11313 | 12 | ADP86275 Hepatitis |
| 25 | 7981 | 99.9 | 10691 | 6 | ABK91423 Hepatitis |
| 26 | 7980.8 | 99.9 | 11313 | 12 | ADP86273 Hepatitis |
| 27 | 7979.2 | 99.8 | 11313 | 12 | ADP86266 Hepatitis |
| 28 | 7979 | 99.8 | 10693 | 6 | ABK91438 Hepatitis |
| 29 | 7977.6 | 99.8 | 11313 | 12 | ADP86268 Hepatitis |
| 30 | 7977.4 | 99.8 | 10693 | 6 | ABK91443 Hepatitis |
| 31 | 7976.2 | 99.8 | 10691 | 6 | ABK91439 Hepatitis |
| 32 | 7975 | 99.8 | 7987 | 6 | AAD25321 Hepatitis |
| 33 | 7974.4 | 99.8 | 11313 | 12 | ADP86267 Hepatitis |
| 34 | 7973.6 | 99.8 | 7991 | 6 | AAL47279 Hepatitis |
| 35 | 7973.4 | 99.8 | 7987 | 6 | AAD25329 Hepatitis |
| 36 | 7971.8 | 99.7 | 7987 | 6 | AAD25324 Hepatitis |
| 37 | 7967 | 99.7 | 8001 | 3 | AAA98967 Hepatitis |
| 38 | 7966.2 | 99.7 | 7995 | 6 | AAL47278 Hepatitis |
| 39 | 7958.4 | 99.6 | 11313 | 12 | ADP86270 Hepatitis |
| 40 | 7955.2 | 99.5 | 11313 | 12 | ADP86269 Hepatitis |
| 41 | 7777.8 | 97.3 | 7989 | 10 | ADD93733 Hepatitis |
| 42 | 7714.4 | 96.5 | 11184 | 12 | ADP86274 Hepatitis |
| 43 | 7706.4 | 96.4 | 11184 | 12 | ADP86276 Hepatitis |
| 44 | 7701.6 | 96.4 | 11184 | 12 | ADP86277 Hepatitis |
| 45 | 7695.4 | 96.3 | 7848 | 6 | AAD25323 Hepatitis |

ALIGNMENTS

RESULT 1
AAL47276
ID AAL47276 standard; DNA; 7992 BP.
XX
AC AAL47276;
XX
DT 30-AUG-2002 (first entry)
XX
DE Hepatitis C virus sub-genomic replicon clone I377-NS3-3'UTR.
XX
KW Hepatitis; HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis;
KW virucide; hepatotropic; gene therapy; anti-viral; gene; ds.
XX
OS Hepatitis C virus.
FH Key Location/Qualifiers
FT CDS 342..1181
FT FT /*tag= a
FT FT /product= "core-neo fusion protein"
FT FT 1801..7758
FT FT /*tag= b
FT FT /product= "NS3 proteinase/helicase"
XX
XX WO200238793-A2.
XX
XX 16-MAY-2002.
XX
XX 02-NOV-2001; 2001WO-US046350.
XX
XX 07-NOV-2000; 2000US-0245866P.
XX
XX (ANAD-) ANADYS PHARM INC.
XX
XX Bichke V;
XX
XX WFI; 2002-490082/52.
XX
XX P-PSDB; AA018000, AA018001.
XX
XX Novel nucleic acid encoding replication competent recombinant hepatitis C
XX virus genome useful for screening anti-hepatitis C virus therapeutics and
XX for vaccine development.
XX
XX Claim 6; Page 43-47; 85pp; English.

CC The present invention provides protein and coding sequences from
CC Hepatitis C virus (HCV), comprising all or part of the HCV genome and
CC able to replicate efficiently when transfected into a susceptible cell
CC line without reducing the growth rate of the cell line by more than 10
CC fold. The sequences are useful for screening for anti-HCV therapeutics,
CC for detecting antibodies to HCV in a biological sample such as blood,
CC serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
CC for deriving authentic HCV components such as replication-complement non-
CC infectious, replication-defective infection-component, and replication-
CC defective non-infectious HCV, in gene therapy or gene vaccination
CC targeted to hepatic tissue for treating an animal infected or susceptible
CC to HCV infection and for studying HCV infection and propagation. The
CC present sequence is a clone of a fragment of the HCV genome which encodes
CC the core-neo and NS3 proteinase/helicase proteins
XX

SQ Sequence 7992 BP; 1648 A; 2369 C; 2243 G; 1732 T; 0 U; 0 Other;

| Query Match | 100.0% | Score 7992; | DB 6; | Length 7992; |
|-----------------------|--|---------------|-----------|--------------|
| Best Local Similarity | 100.0%; | Pred. No. 0; | | |
| Matches 7992; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| QY 1 | GGCAGCCCCCGATTGGGGGCGACATCCACATAGATCTATCCCTGTGAGGAACTACTG | 60 | | |
| Db 1 | GGCAGCCCCCGATTGGGGGCGACATCCACATAGATCTATCCCTGTGAGGAACTACTG | 60 | | |
| QY 61 | TCTTACGAGAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGNGCAGCCCTCCAGGAC | 120 | | |
| Db 61 | TCTTACGAGAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGNGCAGCCCTCCAGGAC | 120 | | |
| QY 121 | CCCCCTCCCGGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATTGCCAG | 180 | | |
| Db 121 | CCCCCTCCCGGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATTGCCAG | 180 | | |
| QY 181 | GACGACCGGTCCTTTCTTGGATCAACCCGCTCAATGCTCGGAGATTGGGGCGTGCCTCC | 240 | | |
| Db 181 | GACGACCGGTCCTTTCTTGGATCAACCCGCTCAATGCTCGGAGATTGGGGCGTGCCTCC | 240 | | |
| QY 241 | GCAGACTGTAGCGAGTAGTGTGGTCCGAAAGGCGCTGTGTACTGCTGATAGG | 300 | | |
| Db 241 | GCAGACTGTAGCGAGTAGTGTGGTCCGAAAGGCGCTGTGTACTGCTGATAGG | 300 | | |
| QY 301 | GTGCTTCGAGTGTCCCGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAAC | 360 | | |
| Db 301 | GTGCTTCGAGTGTCCCGGAGGTCTCGTAGACCGTGCACCATGAGCAGCAATCTTAAC | 360 | | |
| QY 361 | CTCAAGAAAAACCAAGGGCGCCCATGATTGAACAAGATGGATTGCACGAGGTTCTC | 420 | | |
| Db 361 | CTCAAGAAAAACCAAGGGCGCCCATGATTGAACAAGATGGATTGCACGAGGTTCTC | 420 | | |
| QY 421 | CGGCGCTTGGGTGAGAGGCTATTGCGCTATGACTGGCAGCAACACATCGGCTGCT | 480 | | |
| Db 421 | CGGCGCTTGGGTGAGAGGCTATTGCGCTATGACTGGCAGCAACACATCGGCTGCT | 480 | | |
| QY 481 | CTGATGCGCGCTGTTCGGCTGTGAGCGAGGGCGCCGGTTCTTTTGTCAAGACCG | 540 | | |
| Db 481 | CTGATGCGCGCTGTTCGGCTGTGAGCGAGGGCGCCGGTTCTTTTGTCAAGACCG | 540 | | |
| QY 541 | ACCTGTCCGFGCCCTGAATGAACTGCAAGGAGGAGGAGCGCGCTATCGTGGTGGCCA | 600 | | |
| Db 541 | ACCTGTCCGFGCCCTGAATGAACTGCAAGGAGGAGGAGCGCGCTATCGTGGTGGCCA | 600 | | |
| QY 601 | CGAGCGGTTCTTGGCGAGCTATTGCGCTATGACTGGCAGCAACAGCGGAGGAGCTGGC | 660 | | |
| Db 601 | CGAGCGGTTCTTGGCGAGCTATTGCGCTATGACTGGCAGCAACAGCGGAGGAGCTGGC | 660 | | |
| QY 661 | TGCTATTGGGCGAAGTGTCCGGGAGGATCTCTGTATCTCACTTGTCTCTCGCGAGA | 720 | | |
| Db 661 | TGCTATTGGGCGAAGTGTCCGGGAGGATCTCTGTATCTCACTTGTCTCTCGCGAGA | 720 | | |
| QY 721 | AAGTATCCATCATGCTGATGCAATGCGGCGCTGCATACGCTGATCGGCTACTGCC | 780 | | |
| Db 721 | AAGTATCCATCATGCTGATGCAATGCGGCGCTGCATACGCTGATCGGCTACTGCC | 780 | | |

| | | |
|---------|--|------|
| QY 781 | CATTGACCAACAAGCGAAACATCCATCGAGCGAGCAGTACTCGGATGGAAGCGGTC | 840 |
| Db 781 | CATTGACCAACAAGCGAAACATCCATCGAGCGAGCAGTACTCGGATGGAAGCGGTC | 840 |
| QY 841 | TTGTGATCAGATGATCTGAGCAGAGCAGTACAGGGCTCGCGCCAGCCGAACTGTCG | 900 |
| Db 841 | TTGTGATCAGATGATCTGAGCAGAGCAGTACAGGGCTCGCGCCAGCCGAACTGTCG | 900 |
| QY 901 | CCAGGCTCAAGGCGCGCATGCCCAGCGGAGGATCTCGTGTGACCCATGCGATGCT | 960 |
| Db 901 | CCAGGCTCAAGGCGCGCATGCCCAGCGGAGGATCTCGTGTGACCCATGCGATGCT | 960 |
| QY 961 | GCTTCCGGAATCATGTGTGAAATGCGCGCTTTTCTGGATTCATCGACTGCGCGG | 1020 |
| Db 961 | GCTTCCGGAATCATGTGTGAAATGCGCGCTTTTCTGGATTCATCGACTGCGCGG | 1020 |
| QY 1021 | TGGGTGTGCGGACCGCTATCAGGACATAGCTGCGTACCCTGATATGCTGAAGAGC | 1080 |
| Db 1021 | TGGGTGTGCGGACCGCTATCAGGACATAGCTGCGTACCCTGATATGCTGAAGAGC | 1080 |
| QY 1081 | TTGGGGCGGAATGGGCTGACCGCTTCTCGTGTGCTTACCGGTATCGCGCTCCGATCGC | 1140 |
| Db 1081 | TTGGGGCGGAATGGGCTGACCGCTTCTCGTGTGCTTACCGGTATCGCGCTCCGATCGC | 1140 |
| QY 1141 | AGCGATCGCTTCTATCGCTTCTTGACAGTCTTCTGAGTTTAAACAGACCAACAG | 1200 |
| Db 1141 | AGCGATCGCTTCTATCGCTTCTTGACAGTCTTCTGAGTTTAAACAGACCAACAG | 1200 |
| QY 1201 | GTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCTTAACTGCTGCTG | 1260 |
| Db 1201 | GTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCTTAACTGCTGCTG | 1260 |
| QY 1261 | CGAAGCGGTGGAATAAGCGCGGTGTGCTTGTCTATGTTATTTTCCACATATG | 1320 |
| Db 1261 | CGAAGCGGTGGAATAAGCGCGGTGTGCTTGTCTATGTTATTTTCCACATATG | 1320 |
| QY 1321 | CGGCTTTTGGCAATGTGAGGCGCGGAAACCTGCGGCTGCTTCTTGAAGAGATTCCT | 1380 |
| Db 1321 | CGGCTTTTGGCAATGTGAGGCGCGGAAACCTGCGGCTGCTTCTTGAAGAGATTCCT | 1380 |
| QY 1381 | AGGGGTCTTTCCTCTCGCAGGAAATGCAAGGTCTGTTGAATGTCGTGAAGAGAGCA | 1440 |
| Db 1381 | AGGGGTCTTTCCTCTCGCAGGAAATGCAAGGTCTGTTGAATGTCGTGAAGAGAGCA | 1440 |
| QY 1441 | GTTCCTCTGGAAGCTTTTGAAGACAAACAAAGTGTGTAGGACCTTTGAGGACGCG | 1500 |
| Db 1441 | GTTCCTCTGGAAGCTTTTGAAGACAAACAAAGTGTGTAGGACCTTTGAGGACGCG | 1500 |
| QY 1501 | AACCCCGCTGCGGACAGTGTGCTGCGGCGCAAGGACGCTGATAGATACACCT | 1560 |
| Db 1501 | AACCCCGCTGCGGACAGTGTGCTGCGGCGCAAGGACGCTGATAGATACACCT | 1560 |
| QY 1561 | GCAAGCGGCAACAAACCCAGTGCAGTGTGAGTTGGATGTTGTTGAAGAGTCAAA | 1620 |
| Db 1561 | GCAAGCGGCAACAAACCCAGTGCAGTGTGAGTTGGATGTTGTTGAAGAGTCAAA | 1620 |
| QY 1621 | TGGCTCTCTCAAGCGTATTCAACAGGCGTGAAGATGCCAGAGGTACCCCATGT | 1680 |
| Db 1621 | TGGCTCTCTCAAGCGTATTCAACAGGCGTGAAGATGCCAGAGGTACCCCATGT | 1680 |
| QY 1681 | ATGGATCTGATCTGGGCGCTCGGTGCACATGCTTACATGTTTGTAGTCGAGTTAAA | 1740 |
| Db 1681 | ATGGATCTGATCTGGGCGCTCGGTGCACATGCTTACATGTTTGTAGTCGAGTTAAA | 1740 |
| QY 1741 | AACCTCTAGGCGCGCGCAACCCAGGAGCGTGGTTTCTTTGAAACACAGATATACC | 1800 |
| Db 1741 | AACCTCTAGGCGCGCGCAACCCAGGAGCGTGGTTTCTTTGAAACACAGATATACC | 1800 |
| QY 1801 | ATGGCGCTATTAAGCGCTACTCCCAACAGAGCGGCGCTTCTGCTGATCATCACT | 1860 |
| Db 1801 | ATGGCGCTATTAAGCGCTACTCCCAACAGAGCGGCGCTTCTGCTGATCATCACT | 1860 |
| QY 1861 | AGCTCACAGGCGCGGACAGGAAACCAAGTTCGAGGGGAGGTCCAAAGTGTCTCCACCGCA | 1920 |

1861 AGCTTACAGGCGGACAGGAACCAAGTCCAGGGAGGTCCAAGTGTCTCCACCGCA 1920
1921 ACAAAATCTTCTGGCGAAGCTCGCTCAATGGCGTGTGTTGGACTGTCTATCATGTGCG 1980
1921 ACAAAATCTTCTGGCGAAGCTCGCTCAATGGCGTGTGTTGGACTGTCTATCATGTGCG 1980
1981 GGTCAAGACCTTGTGGCGGCAAGAGGCGCAATCAACCAATGTACACCAATGTGGAC 2040
1981 GGTCAAGACCTTGTGGCGGCAAGAGGCGCAATCAACCAATGTACACCAATGTGGAC 2040
2041 CAGGACTCTGTGGCGTGGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2100
2041 CAGGACTCTGTGGCGTGGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2100
2101 GGCAGCTCGGACCTTTACTTGTGTACAGGCGATGCCGATGTCAATCCGGTGGCGGCGG 2160
2101 GGCAGCTCGGACCTTTACTTGTGTACAGGCGATGCCGATGTCAATCCGGTGGCGGCGG 2160
2161 GCGGACAGAGGGGAGGACCTACTCTCCCGCAGCGCGCTCTCTACTTTGAAGGGCTCTCG 2220
2161 GCGGACAGAGGGGAGGACCTACTCTCCCGCAGCGCGCTCTCTACTTTGAAGGGCTCTCG 2220
2221 GCGGTCTCACTCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 2280
2221 GCGGTCTCACTCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 2280
2281 ACCGAGGGGTTCGAAAGCGGTGTGACTTTGTACCGCTCGAGTCTATGGAACCACTATG 2340
2281 ACCGAGGGGTTCGAAAGCGGTGTGACTTTGTACCGCTCGAGTCTATGGAACCACTATG 2340
2341 CGGTCCCGGCTTTTACCGGACACTCTGTCGCCCTCCGCGCGTACCGGAGGCTTCAGGTG 2400
2341 CGGTCCCGGCTTTTACCGGACACTCTGTCGCCCTCCGCGCGTACCGGAGGCTTCAGGTG 2400
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2401 GCCCATCTACAGCGCCCTACTGTTAGCGGCAAGGACTAAGTTCGCGGCTCGGTATGCA 2460
2461 GCCCAAGGTTAAGGTCCTTGTCTGAAACCGCTCGGTCGCGCGCACCCCTAGGTTTCGG 2520
2461 GCCCAAGGTTAAGGTCCTTGTCTGAAACCGCTCGGTCGCGCGCACCCCTAGGTTTCGG 2520
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2521 GCGTATATGCTAAGGACACTGTATCGACCTTAACATCAAGACCGGGTAAGGACCATC 2580
2581 ACCACGGTGCCTCCATCAGTACTTCCACTATGCGCAAGTTTCTTGGCGAGGTGTGC 2640
2581 ACCACGGTGCCTCCATCAGTACTTCCACTATGCGCAAGTTTCTTGGCGAGGTGTGC 2640
2641 TCTGGGCGCCTATGACATCAATATGTGATGAGTGCCACTCAACTGACTCGACCACT 2700
2641 TCTGGGCGCCTATGACATCAATATGTGATGAGTGCCACTCAACTGACTCGACCACT 2700
2701 ATCTGGGATCGGACAGTCTTGCAAGCGGAGACGGCTGAGCGGCGACTCGTGTG 2760
2701 ATCTGGGATCGGACAGTCTTGCAAGCGGAGACGGCTGAGCGGCGACTCGTGTG 2760
2761 CTGCGCACCGCTACGCTCGCGGATCGGTCAACCGTGCACATCGAACAATCGAGGAGGTG 2820
2761 CTGCGCACCGCTACGCTCGCGGATCGGTCAACCGTGCACATCGAACAATCGAGGAGGTG 2820
2821 GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCCATCGAGACCATC 2880
2821 GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCCATCGAGACCATC 2880
2881 AAGGGGGAGGACCTCATTTCTGCAATTCGAAGAAGAAATGTGATGAGTTCGCGCG 2940
2881 AAGGGGGAGGACCTCATTTCTGCAATTCGAAGAAGAAATGTGATGAGTTCGCGCG 2940
2941 AAGCTGTCCGGCTCGGACTCAATGTGTAGCATATTTACGGGGCTTGTATGATCCGTC 3000

2941 AAGCTGTCCGGCTCGGACTCAATGTGTAGCATATTTACCGGGCCCTTGTATGATCCGTC 3000
3001 ATACCAACTAGCGGAGACGCTCATTTGTGTAGCAACGGAAGCTCTAATAGCGGCTTTACC 3060
3001 ATACCAACTAGCGGAGACGCTCATTTGTGTAGCAACGGAAGCTCTAATAGCGGCTTTACC 3060
3061 GCGGATTTTCGACTCAGTGTAGTCAATATCATGTGTACCCAGACAGTGCAGTTCAGC 3120
3061 GCGGATTTTCGACTCAGTGTAGTCAATATCATGTGTACCCAGACAGTGCAGTTCAGC 3120
3121 CTGGACCCGACCTTACCAATTTGAGACGACCGTGCACACAGACCGGCTGTACGCTCG 3180
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3181 CAGCGGCGAGGACGACTGGTAGGGGACGATGGGCATTTACAGGTTTGTGACTCCAGGA 3240
3181 CAGCGGCGAGGACGACTGGTAGGGGACGATGGGCATTTACAGGTTTGTGACTCCAGGA 3240
3241 GAACGGCCCTCGGCGCATGTTCCGATTTCTCGGTTCTGTGCGAGTGTATGACGCGGCTGT 3300
3241 GAACGGCCCTCGGCGCATGTTCCGATTTCTCGGTTCTGTGCGAGTGTATGACGCGGCTGT 3300
3301 GCTTGTAACGACTCACGCCCGCGGAGACCTCAGTTAGGTTGCGGCTTACCTAAACACA 3360
3301 GCTTGTAACGACTCACGCCCGCGGAGACCTCAGTTAGGTTGCGGCTTACCTAAACACA 3360
3361 CAGGTTGCCGCTCTGCGAGACCATCTGGAGTTCTGGGAGAGGCTTTTACAGGCTTC 3420
3361 CAGGTTGCCGCTCTGCGAGACCATCTGGAGTTCTGGGAGAGGCTTTTACAGGCTTC 3420
3421 ACCACATAGACGCGCATTTCTTGTCCAGACTAAGCAGGAGGAGACAACTTCCCTTAC 3480
3421 ACCACATAGACGCGCATTTCTTGTCCAGACTAAGCAGGAGGAGACAACTTCCCTTAC 3480
3481 CTGTTAGCATACCAAGGCTACCGTGTGCGCAGGCTCAGGCTCCACCTCCTCTGTTGGAC 3540
3481 CTGTTAGCATACCAAGGCTACCGTGTGCGCAGGCTCAGGCTCCACCTCCTCTGTTGGAC 3540
3541 CAATGTGGAAGTGTCTCATAGCGCTAAGCGCTAAGCGCTGACGCGGCGCAACCGCCCTG 3600
3541 CAATGTGGAAGTGTCTCATAGCGCTAAGCGCTAAGCGCTGACGCGGCGCAACCGCCCTG 3600
3601 TATAGGCTGGAGCGGCTTCAAAAGGAGTTACTACCAACACCCCTTACCAATAATC 3660
3601 TATAGGCTGGAGCGGCTTCAAAAGGAGTTACTACCAACACCCCTTACCAATAATC 3660
3661 ATGGCATGCTGTGCGGTGACCTCGAGGCTGTGACGAGACCTGGGTGCTGTTAGGCGGA 3720
3661 ATGGCATGCTGTGCGGTGACCTCGAGGCTGTGACGAGACCTGGGTGCTGTTAGGCGGA 3720
3721 GTCTAGCAGCTGTGCGCGGTATTGCTGACAAACAGGCGGCTGCTCATTTGTTGGCAGG 3780
3721 GTCTAGCAGCTGTGCGCGGTATTGCTGACAAACAGGCGGCTGCTCATTTGTTGGCAGG 3780
3781 ATCATCTTGTCCGGAAGCGGCGCATCATTTCCGACAGGGAAGTCTTTTACCGGAGTTC 3840
3781 ATCATCTTGTCCGGAAGCGGCGCATCATTTCCGACAGGGAAGTCTTTTACCGGAGTTC 3840
3841 GATGAGATGGAAGTGTGCGCTCACACCTCCCTTACATCGAAGGGAATGACAGTCCGC 3900
3841 GATGAGATGGAAGTGTGCGCTCACACCTCCCTTACATCGAAGGGAATGACAGTCCGC 3900
3901 GAACAAATTCAGAAAGGCAATTCGGGTTGCTGCAAAACAGCCACCAAGCAAGCGGAGGCT 3960
3901 GAACAAATTCAGAAAGGCAATTCGGGTTGCTGCAAAACAGCCACCAAGCAAGCGGAGGCT 3960
3961 GCTGCTCCGCTGGTGAATTCAGAGGCGGACCTCGAAGCCTTCTGCGGCGAAGCATATG 4020
3961 GCTGCTCCGCTGGTGAATTCAGAGGCGGACCTCGAAGCCTTCTGCGGCGAAGCATATG 4020
4021 TGGAAATTCATCAGCGGGATCAATATTTAGCAGGCTTGTCCACTCTGCTGCTGCAACCC 4080
4021 TGGAAATTCATCAGCGGGATCAATATTTAGCAGGCTTGTCCACTCTGCTGCTGCAACCC 4080

| | | | | |
|----|------|-----|--|------|
| QY | 4081 | GC | GATAGCATCACTGATGGCAATTCACAGCGCTCTATCACAGCGCGCTACACACCAACAT | 4140 |
| Db | 4081 | GC | GATAGCATCACTGATGGCAATTCACAGCGCTCTATCACAGCGCGCTACACACCAACAT | 4140 |
| QY | 4141 | ACC | CTCTGTTTAAATCCTCTGGGGGAGATGGGTGGCGCGCCCACTTCTCTCCACGCGCT | 4200 |
| Db | 4141 | ACC | CTCTGTTTAAATCCTCTGGGGGAGATGGGTGGCGCGCCCACTTCTCTCCACGCGCT | 4200 |
| QY | 4201 | GCT | TCTGCTTTCGTAGGCGCGGCATCGCTGGAGCGGCTGTTGGCAGCATAGAGCCCTTGGG | 4260 |
| Db | 4201 | GCT | TCTGCTTTCGTAGGCGCGGCATCGCTGGAGCGGCTGTTGGCAGCATAGAGCCCTTGGG | 4260 |
| QY | 4261 | AAG | TGCTGTGGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGCGCTGTGGGC | 4320 |
| Db | 4261 | AAG | TGCTGTGGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGCGCTGTGGGC | 4320 |
| QY | 4321 | TTT | AAGGTCATAGAGCGGGAGATGCCCTCACCGAGGACCTGGTTAACTTACCTCCCTGCT | 4380 |
| Db | 4321 | TTT | AAGGTCATAGAGCGGGAGATGCCCTCACCGAGGACCTGGTTAACTTACCTCCCTGCT | 4380 |
| QY | 4381 | ATC | CTCTCCCTGGCGCCCTAGTCTCGGGTCTGTGGCAGCGATACTGCGTCGGCAC | 4440 |
| Db | 4381 | ATC | CTCTCTCCCTGGCGCCCTAGTCTCGGGTCTGTGGCAGCGATACTGCGTCGGCAC | 4440 |
| QY | 4441 | GTG | GGCCACAGGGAGGGGGCTGTGCAGTGTGATGAACCGGCTGTAGCGTTGCTTCCGG | 4500 |
| Db | 4441 | GTG | GGCCACAGGGAGGGGGCTGTGCAGTGTGATGAACCGGCTGTAGCGTTGCTTCCGG | 4500 |
| QY | 4501 | GGT | AAACCAAGCTCTCCCAACGCACTATGTGCTCAGAGCGACGCTGACAGCGTGCAC | 4560 |
| Db | 4501 | GGT | AAACCAACGCTCTCCCAACGCACTATGTGCTCAGAGCGACGCTGACAGCGTGCAC | 4560 |
| QY | 4561 | CAG | ATCCTCTCTAGTCTTACCATCACTCAGCTGCTGAAAGAGGCTTCCACAGTGTCAAC | 4620 |
| Db | 4561 | CAG | ATCCTCTCTCTAGTCTTACCATCACTCAGCTGCTGAAAGAGGCTTCCACAGTGTCAAC | 4620 |
| QY | 4621 | GAG | GACTGCTCCACGCCATGCTCCGGCTCGTGGCTTAAGAGATGTTTGGATTTGATATGC | 4680 |
| Db | 4621 | GAG | GACTGCTCTCCACGCCATGCTCCGGCTCGTGGCTTAAGAGATGTTTGGATTTGATATGC | 4680 |
| QY | 4681 | ACG | GTGTTGACTGATTTCAAGACCTTCCAGTCCAGTCCAGTCCCGCGATTCGCGGA | 4740 |
| Db | 4681 | ACG | GTGTTGACTGATTTCAAGACCTTCCAGTCCAGTCCAGTCCCGCGATTCGCGGA | 4740 |
| QY | 4741 | GTG | CCCTCTCTCATGTCAAGTGGGTCAAGGAGTCTTGGCGGGGCGAGGCATCATG | 4800 |
| Db | 4741 | GTG | CCCTCTCTCTCATGTCAAGTGGGTCAAGGAGTCTTGGCGGGGCGAGGCATCATG | 4800 |
| QY | 4801 | CAA | ACACCTGCCCATTGTGGAGCACAGATCAACCGACATGTGAATAAAGCGTTTCCATGAG | 4860 |
| Db | 4801 | CAA | ACACACCTGCCCATTGTGGAGCACAGATCAACCGACATGTGAATAAAGCGTTTCCATGAG | 4860 |
| QY | 4861 | ATG | TGGGGCTTAGGACCTGTAGTAACAGTGGCATGGAACATTCGCCATTAACCGCTAC | 4920 |
| Db | 4861 | ATG | TGGGGCTCTAGGACCTGTAGTAACAGTGGCATGGAACATTCGCCATTAACCGCTAC | 4920 |
| QY | 4921 | ACC | ACGGCCCTGACGCGCTCCCGCGCGCCAAATTAATCTAGGCGCGCTGTGGCGGGTG | 4980 |
| Db | 4921 | ACC | ACGGGCCCTCTGACGCGCTCCCGCGCGCCAAATTAATCTAGGCGCGCTGTGGCGGGTG | 4980 |
| QY | 4981 | GCT | GCTGAGGAGTACGTGGAGTTACCGGGTGGGGAATTCACATGAGTGAAGGAGGTC | 5040 |
| Db | 4981 | GCT | GCTGAGGAGTACGTGGAGTTACCGGGTGGGGAATTCACATGAGTGAAGGAGGTC | 5040 |
| QY | 5041 | ACC | ACTGACAGCTAAAGTCCCGTGTACAGTTCCGGCCCGGAAATTTCTTACAGAGTG | 5100 |
| Db | 5041 | ACC | ACTGACAGCTAAAGTCCCGTGTACAGTTCCGGCCCGGAAATTTCTTACAGAGTG | 5100 |
| QY | 5101 | GAT | GGGTGCGGTTGCAAGTACGCTCCAGCGTGCACCGCTCTCTTACGGGAGGAGGTC | 5160 |
| Db | 5101 | GAT | GGGTGCGGTTGCAAGTACGCTCCAGCGTGCACCGCTCTCTTACGGGAGGAGGTC | 5160 |
| QY | 5161 | AC | ATTCTGCTCGGGCTCAATCAATACCTGTTGGGTCAAGTCTCCATGCGAGCCCGAA | 5220 |
| Db | 5161 | AC | ATTCTCTGCTCGGGCTCAATCAATACCTGTTGGGTCAAGTCTCCATGCGAGCCCGAA | 5220 |
| QY | 5221 | CCG | ACGTAGAGTGTCTCATCTTCAATGCTCACCGACCCCTCCACATTAAGCGGAGACG | 5280 |
| Db | 5221 | CCG | ACGACGTAGAGTGTCTCATCTTCAATGCTCACCGACCCCTCCACATTAAGCGGAGACG | 5280 |
| QY | 5281 | GCT | TAAGCGTAGGCTGGCCAGGGGATCTCCCGCTCTCTTGGCCAGCTCATCAGCTAGCCAG | 5340 |
| Db | 5281 | GCT | TAAGCGTAGGCTGGCCAGGGGATCTCCCGCTCTCTTGGCCAGCTCATCAGCTAGCCAG | 5340 |
| QY | 5341 | CTG | CTGCGCTTCTCTTTGAAGGCAACATGCACTACCGGTATGATCTCCCGGAGCGTGC | 5400 |
| Db | 5341 | CTG | CTGCTGCGCTTCTCTTTGAAGGCAACATGCACTACCGGTATGATCTCCCGGAGCGTGC | 5400 |
| QY | 5401 | CTC | ATCGAGGCAACCTCTCTGCGGAGAGATGGCGGAGATCCACCGGCTGGAG | 5460 |
| Db | 5401 | CTC | ATCGAGGCAACCTCTCTGCGGAGAGATGGCGGAGATCCACCGGCTGGAG | 5460 |
| QY | 5461 | TCG | AAATAATAGGTAGTAATTTTGACACTTTTCAGAGCGCTTCCAAGCGGAGAGGATGAG | 5520 |
| Db | 5461 | TCG | AAATAATAGGTAGTAATTTTGACACTTTTCAGAGCGCTTCCAAGCGGAGAGGATGAG | 5520 |
| QY | 5521 | AGG | GAAGTATCCGTTCCGGCGAGATCTCGGAGGTCCAGAAATTTCCCTCGAGCGATG | 5580 |
| Db | 5521 | AGG | GAAGTATCCGTTCCGGCGAGATCTCGGAGGTCCAGAAATTTCCCTCGAGCGATG | 5580 |
| QY | 5581 | CCC | ATATGGGCAACCGCGGATTAACACCTTCCACTTTTAGTCTCTGGAAGACCCCGAC | 5640 |
| Db | 5581 | CCC | ATATGGGCAACCGCGGATTAACACCTTCCACTTTTAGTCTCTGGAAGACCCCGAC | 5640 |
| QY | 5641 | TAC | GTCCCTCCTCAGTGTCAACGGGTGTCATGCGCGCTTGCAGAGCGCCCTCCGATACCA | 5700 |
| Db | 5641 | TAC | GTCCCTCCTCAGTGTCAACGGGTGTCATGCGCGCTTGCAGAGCGCCCTCCGATACCA | 5700 |
| QY | 5701 | CCT | CCACGAGGAAGGACGCTGTCTGTCTCAGAAATCTACCGTGTCTTCTGCTTGGCG | 5760 |
| Db | 5701 | CCT | CCACGAGGAAGGACGCTGTCTGTCTCAGAAATCTACCGTGTCTTCTGCTTGGCG | 5760 |
| QY | 5761 | GAG | CTGCCACAAGACCTTCCGCGAGCTCCGAAATCTGCGGCGCTCGACAGCGGACCGCA | 5820 |
| Db | 5761 | GAG | CTGCCACAAGACCTTCCGCGAGCTCCGAAATCTGCGGCGCTCGACAGCGGACCGCA | 5820 |
| QY | 5821 | ACG | CGCTCTCTGACCAACCTTCCGAGCGCGGATCCG | |

Db 6241 GAAGCCTGTAAGCTGACGCCCCACATTCGGCCAGATCTAAATTTGGCTATCGGGCAAG 6300
 QY 6301 GACGTCGGGAACCTATTCAGCAAGCGCTTAAACCATCCGCTCCGCTGGGAAGACTTG 6360
 Db 6301 GACGTCGGGAACCTATTCAGCAAGCGCTTAAACCATCCGCTCCGCTGGGAAGACTTG 6360
 QY 6361 CTGGAAGCACTGAGACACCAATTGACACCAACCATCATGGCAAAAATGAGGTTTCTGC 6420
 Db 6361 CTGGAAGCACTGAGACACCAATTGACACCAACCATCATGGCAAAAATGAGGTTTCTGC 6420
 QY 6421 GTCCAAACAGAGAGAGGGGGCGGCAAGCAGCTCGCTTATCGTATTCACAGATTGGGG 6480
 Db 6421 GTCCAAACAGAGAGAGGGGGCGGCAAGCAGCTCGCTTATCGTATTCACAGATTGGGG 6480
 QY 6481 GTTCGTGTGTCGAGAAAATGSCCTTTTACGATGCTCTCCACCTCCCTCAGACCGTG 6540
 Db 6481 GTTCGTGTGTCGAGAAAATGSCCTTTTACGATGCTCTCCACCTCCCTCAGACCGTG 6540
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 Db 6541 ATGGGCTCTTCATACGGATTCCAATPACTCTCTGACAGCGGTCGAGTTCCTGCTGAAT 6600
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 Db 6601 GCCTGGAAGCAAGAAATGCGCTATGGCTTGGCATATGACACCCGCTGTTTGACTCA 6660
 QY 6661 ACAGTCACTGAGATGATCATCGCTGTTGAGGAGTCAATCTACCAATGTTGACTGGCC 6720
 Db 6661 ACAGTCACTGAGATGATCATCGCTGTTGAGGAGTCAATCTACCAATGTTGACTGGCC 6720
 QY 6721 CCCGAAGCAGACAGGCGCATAAAGTCTGCTCAGAGCGGCTTTACATCGGGGGCCCCCTG 6780
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 QY 6781 ACTAATTTAAAGGCGAAGTGGGCTATCGCGGTGCGCGGAGCGGTGTAAGC 6840
 Db 6781 ACTAATTTAAAGGCGAAGTGGGCTATCGCGGTGCGCGGAGCGGTGTAAGC 6840
 QY 6841 ACCAGCTGCGGTAATACCTCACAATGTTTACGAGCGGCTTTGAGGAGTCAATCTGTAAGC 6900
 Db 6841 ACCAGCTGCGGTAATACCTCACAATGTTTACGAGCGGCTTTGAGGAGTCAATCTGTAAGC 6900
 QY 6901 AAGCTCCAGGACTGACGATGCTCGTATGCGAGACGACCTTGTGCTTATCTGTAAGC 6960
 Db 6901 AAGCTCCAGGACTGACGATGCTCGTATGCGAGACGACCTTGTGCTTATCTGTAAGC 6960
 QY 6961 GCGGGACCCAAAGAGGAGGAGCGGCTACGGGCTTACGGGCTTACGGAGGCTATGACTAGATC 7020
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 Db 7021 TCTGCCCTCCCTGGGACCGGCCCCAAACACAGATACGACTTGGAGTTGATAACATCATGC 7080
 QY 7081 TCTTCCATGTGTCAGTGGCGACGATGCTATGCGCAAAAGGTTACTATCTCACCCGT 7140
 Db 7081 TCTTCCATGTGTCAGTGGCGACGATGCTATGCGCAAAAGGTTACTATCTCACCCGT 7140
 QY 7141 GACCCACACACCCCTTGGCGGGCTGCGTGGGAGACAGCTGACACATCCAGTCAAT 7200
 Db 7141 GACCCACACACCCCTTGGCGGGCTGCGTGGGAGACAGCTGACACATCCAGTCAAT 7200
 QY 7201 TCTTGGCTAGGCAACATCATCATGTATGCGCCACCTTGTGGCAAGGATGATCCCTGATG 7260
 Db 7201 TCTTGGCTAGGCAACATCATCATGTATGCGCCACCTTGTGGCAAGGATGATCCCTGATG 7260
 QY 7261 ACTCAATTTCTCCATCTCTAGCTCAGGAACTTGAAGGAGGCTTGTGTCAG 7320
 Db 7261 ACTCAATTTCTCCATCTCTAGCTCAGGAACTTGAAGGAGGCTTGTGTCAG 7320
 QY 7321 ATCTAGGGGCTGTTACTTCATTTAGCCACTTGACCTCAGATCATTCACGACTC 7380

Db 7321 ATCTAGGGGCTGTTACTTCCATTGAGCCACTTGACCTACCTCAGATCATTTCAAGACTC 7380
 QY 7381 CATGCCCTTAGGCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT 7440
 Db 7381 CATGCCCTTAGGCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCT 7440
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 Db 7441 TCATSCCTCAGAAACTTGGGGTACCGCCCTTGGAGTCTGGAGACATCGGGCCAGAAGT 7500
 QY 7501 GTCCGCTAGGCTACTCTCCAGGGGGGGGCTGCCACTTGTGGCAAGTACCTCTTC 7560
 Db 7501 GTCCGCTAGGCTACTCTCCAGGGGGGGGCTGCCACTTGTGGCAAGTACCTCTTC 7560
 QY 7561 AACTGGGAGTAAGAACCAAGCTCAAACTCACTCCCAATCCCGGCTGCGTCCAGTTGGAT 7620
 Db 7561 AACTGGGAGTAAGAACCAAGCTCAAACTCACTCCCAATCCCGGCTGCGTCCAGTTGGAT 7620
 QY 7621 TTATCCAGCTGTTGCTGTTGCTTACAGCGGGGGAGACATATATCACAGCTGTCTCGT 7680
 Db 7621 TTATCCAGCTGTTGCTGTTGCTTACAGCGGGGGAGACATATATCACAGCTGTCTCGT 7680
 QY 7681 GCCGAGCCCCCTGCTCATCTGCTGCTACTCTCTACTTTCTGAGGGGTAGGCATCTAT 7740
 Db 7681 GCCGAGCCCCCTGCTCATCTGCTGCTACTCTCTACTTTCTGAGGGGTAGGCATCTAT 7740
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 Db 7741 CTACTCCCAACCCGATGAACCGGGAGCTAAACATCCAGGCCAATAGGCCATCTCTGTTT 7800
 QY 7801 TTTCCCTT 7860
 Db 7801 TTTCCCTT 7860
 QY 7861 TTTTTCCTT 7920
 Db 7861 TTTTTCCTT 7920
 QY 7921 TAGCTGGAAGGTCCTGAGCCCTTGACTGAGAGTGTCTGATCTAGTGGCTCTCTGC 7980
 Db 7921 TAGCTGGAAGGTCCTGAGCCCTTGACTGAGAGTGTCTGATCTAGTGGCTCTCTGC 7980
 QY 7981 AGATCAAGTACT 7992
 Db 7981 AGATCAAGTACT 7992

RESULT 2
 ABK91412
 ID ABK91412 standard; DNA; 10690 BP.
 XX AC ABK91412;
 XX DT 15-NOV-2002 (first entry)
 XX DE Hepatitis C virus vector construct pHVNeo.17.
 XX KW HCV; ss; pHVNeo.17; adaptive mutation; liver failure; cirrhosis;
 KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
 KW internal ribosome entry site; IRES; NS5A; HCV replication.
 XX OS Hepatitis C virus.
 OS Encephalomyocarditis virus.
 OS Escherichia coli.
 OS Enterobacteria phage T7.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT 5'UTR 1..341
 FT /*tag= a
 FT 342..1181
 FT /*tag= b
 FT CDS /product= "Core-neo fusion protein"

```
FT misc_signal 1190..1800
FT /tag= c
FT /label= IRES
FT /note= "Internal ribosome entry site from EMCV"
FT CDS
FT 1801..7758
FT /tag= d
FT /product= "Polyprotein"
FT /note= "Comprising NS3, NS4A, NS4B, NS5A and NS5B"
FT 7759..7989
FT /tag= e
FT 7990..10690
FT /tag= f
FT /note= "Plasmid derived sequences"
XX
XX WO200259321-A2.
XX
XX 01-AUG-2002.
XX
XX 16-JAN-2002; 2002WO-BP000526.
XX
XX 23-JAN-2001; 2001US-0263479P.
XX
XX (RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.
XX
XX De Francesco R, Migliaccio G, Paonessa G;
XX WPI; 2002-599793/64.
XX
XX New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
XX NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
XX ribosome entry site (IRES) region, useful in studying HCV replication and
XX expression.
XX
XX Claim 1; Fig 1; 69pp; English.
XX
XX The invention relates to nucleic acid molecules comprising altered HCV
XX NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
XX internal ribosome entry site (IRES) region coding for one or more NS3,
XX NS5A, or EMCV IRES mutations, respectively. The location of the mutations
XX are detailed in the specification. Also included are (1) an expression
XX vector comprising a nucleotide sequence coding for the altered nucleic
XX acids, which is transcriptionally coupled to an exogenous promoter; (2) a
XX recombinant cell human hepatoma cell comprising the altered nucleic acids
XX ; (3) a recombinant cell produced by introducing into a human hepatoma
XX cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
XX replicon enhanced cell or which containing a functional HCV replicon; (5)
XX an HCV replicon enhanced cells made in the method; and (6) measuring the
XX ability of a compound to affect HCV activity. The HCV replicons and HCV
XX replicon enhanced cells are useful in studying HCV replication and
XX expression, and HCV and host cell interactions, producing HCV RNA and
XX proteins, and providing a system for measuring the ability of a compound
XX to modulate one or more HCV activities e.g. to discover drugs which may
XX treat HCV mediated diseases such as liver failure, cirrhosis and
XX hepatocellular carcinoma. The present sequence is the HCV based vector
XX pHCVNeo.17, used as a basis for the adaptive mutations of the invention
XX
XX Sequence 10690 BP; 2334 A; 3045 C; 2908 G; 2403 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 7992; DB 6; Length 10690;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 7992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GCCAGCCCCGATGGGGGCGACACTCCACCATAGATCACTCCCTCTGAGGAACACTG 60
XX |
XX 1 GCCAGCCCCGATGGGGGCGACACTCCACCATAGATCACTCCCTCTGAGGAACACTG 60
XX |
XX 61 TCCTTACGCGAAGACGCTTAGCCATGCGCTTAGTATGAGTGTGTCAGCCTCCAGGAC 120
XX |
XX 61 TCCTTACGCGAAGACGCTTAGCCATGCGCTTAGTATGAGTGTGTCAGCCTCCAGGAC 120
XX |
XX 121 CCCCCTCCCGGAGAGCCATAGTGTGCTGCGGAACCGGTGAGTACACCGGAATTGCCAG 180
XX |
XX 121 CCCCCTCCCGGAGAGCCATAGTGTGCTGCGGAACCGGTGAGTACACCGGAATTGCCAG 180
XX |
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QY 181 GACGACCGGGTCTTTTCTTGGATCAACCGCTCAATGCTCGAGATTGGGGTGCCTCC 240
Db 181 GACGACCGGGTCTTTTCTTGGATCAACCGCTCAATGCTCGAGATTGGGGTGCCTCC 240
QY 241 GCGAGACTGCTAGCCGAGTAGTGTGGGTGCGAAAGCCTTGTGGTACTGCTGATAGG 300
Db 241 GCGAGACTGCTAGCCGAGTAGTGTGGGTGCGAAAGCCTTGTGGTACTGCTGATAGG 300
QY 301 GTGCTTGGAGTGCCTCGGAGGTCTCGTAGACCTGACCATGAGCAGCAATCTTAAC 360
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QY 361 CTCAAAGAAAACCAAAGGCGCGCATGATTGAACAAGATGATGACAGAGTTCTC 420
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QY 421 CGGCGCTTGGTGGAGAGGCTATTGCGCTATGACTGGGCAACACAGAAATGGCTGCT 480
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QY 481 CTGATGCCCGCTGTTCCGGCTGTGAGCGAGGGCGCGGCTCTTTTGTCAAGACCG 540
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QY 541 ACCTGTCCGGTGCCTCTGAACTGACGAGCAGCGCGGCTATCGTGGCTGGCCA 600
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Db 901 CCAGGCTCAAGCGCGCATGCGCGAGGATCTGCTGTCGACCCATGGCGATGCTCT 960
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Db 1141 AGCGCATGCGCTTCTATCGCTTCTTACGAGTTCTTCTGAGTTTAAACAGACCAACG 1200
QY 1201 GTTTCCTCTAGGGGATCAATTCGCGCTCTCTCCCTCCCCCCCCCTAACGTTACTGGC 1260
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Db 1381 AGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTGTGAATGTCTGTAAGGAAGCA 1440
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QY 3421 ACCCAATAGAGCCCATTTCTTGTCCAGACTTAAGCGGACGAGACACACTTCCCTTAC 3480

| | | | | | | | |
|----|------|--|------|----|------|---|------|
| Db | 3421 | ACCCACATAGACGCCATTTCTTCTGCCAGACTAAGCAGGCGAGAGCAACTTCCCTTAC | 3480 | Qy | 4561 | CAGATCCTCTCTAGTCTTACCATCACTCAGCTGTGTAAGAGGCTTACCAGTGGATCAAC | 4620 |
| Qy | 3481 | CTGTAGCATACAGGCTACGGTGTGCCCAGGAGCTCAGGCTCCACCTCCATCTGTGGAC | 3540 | Db | 4561 | CAGATCCTCTCTAGTCTTACCATCACTCAGCTGTGTAAGAGGCTTACCAGTGGATCAAC | 4620 |
| Db | 3481 | CTGTAGCATACAGGCTACGGTGTGCCCAGGAGCTCAGGCTCCACCTCCATCTGTGGAC | 3540 | Qy | 4621 | GAGGACTGTCTCAGGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGATTGGATATGC | 4680 |
| Qy | 3541 | CAAAATGTGGAAGTGTCTCATACGGCTAAAGCTACGCTGCAGCGGCCCAAGCCCTCTGTG | 3600 | Db | 4621 | GAGGACTGTCTCAGGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGATTGGATATGC | 4680 |
| Db | 3541 | CAAAATGTGGAAGTGTCTCATACGGCTAAAGCTACGCTGCAGCGGCCCAAGCCCTCTGTG | 3600 | Qy | 4681 | ACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCCTGCCCGGATTGCCGGA | 4740 |
| Qy | 3601 | TATAGGCTGGAGCGCGTTCAAAACAGAGTTACTACCAACAGGTTTACTACCAACCCCATAAACCAATACATC | 3660 | Db | 4681 | ACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCCTGCCCGGATTGCCGGA | 4740 |
| Db | 3601 | TATAGGCTGGAGCGCGTTCAAAACAGAGTTACTACCAACAGGTTTACTACCAACCCCATAAACCAATACATC | 3660 | Qy | 4741 | GTCCCTCTTCTTCTCATGTCAAGTGGGTACAAAGGAGTCTGGCGGGGCGACGGCATCATG | 4800 |
| Qy | 3661 | ATGGCATGATGTCCGGCTGACCTGAGGTGCTCAGGACCTGGTGTCTGTAGGCGGA | 3720 | Db | 4741 | GTCCCTCTTCTTCTCATGTCAAGTGGGTACAAAGGAGTCTGGCGGGGCGACGGCATCATG | 4800 |
| Db | 3661 | ATGGCATGATGTCCGGCTGACCTGAGGTGCTCAGGACCTGGTGTCTGTAGGCGGA | 3720 | Qy | 4801 | CAAAACACCTGCCCATGTGGAGCAGATCACCGGACATGTGAAAACGGTTCCATGAGG | 4860 |
| Qy | 3721 | GTCCCTAGCAGCTCTGGCGCGTATTGCTGACAAAGGCGAGCGTGGTCAATTTGTGGGCGAGG | 3780 | Db | 4801 | CAAAACACCTGCCCATGTGGAGCAGATCACCGGACATGTGAAAACGGTTCCATGAGG | 4860 |
| Db | 3721 | GTCCCTAGCAGCTCTGGCGCGTATTGCTGACAAAGGCGAGCGTGGTCAATTTGTGGGCGAGG | 3780 | Qy | 4861 | ATCGTGGGCGCTTAGGACCTGTAGTAAACACGTGGGCAATTCGCCCATTTAACCGGTAC | 4920 |
| Qy | 3781 | ATCATCTTTTCCGGAAGCGGCCATCAATCCCGACAGGAAAGTCTTTTACGGGAGTTTC | 3840 | Db | 4861 | ATCGTGGGCGCTTAGGACCTGTAGTAAACACGTGGGCAATTCGCCCATTTAACCGGTAC | 4920 |
| Db | 3781 | ATCATCTTTTCCGGAAGCGGCCATCAATCCCGACAGGAAAGTCTTTTACGGGAGTTTC | 3840 | Qy | 4921 | ACCAACGGGCGCTGTCCCGGCGCCAAATTTATTCTAGGGCGCTGTGGCGGGTG | 4980 |
| Qy | 3841 | GATGAGTGAAGTGGCGCTCACACCTCCCTTACATCGACAGGGAATGAGCTCGCC | 3900 | Db | 4921 | ACCAACGGGCGCTGTCCCGGCGCCAAATTTATTCTAGGGCGCTGTGGCGGGTG | 4980 |
| Db | 3841 | GATGAGTGAAGTGGCGCTCACACCTCCCTTACATCGACAGGGAATGAGCTCGCC | 3900 | Qy | 4981 | GCTGTGAGGAGTACGTGGAGTTACGGGGTGGGGGATTTCCACTACGTGACGGGCATG | 5040 |
| Qy | 3901 | GAACAATTCACACAGAGGCAATCGGTTGCTGCAAAAGCCACCAAGCAAGCGGAGGCT | 3960 | Db | 4981 | GCTGTGAGGAGTACGTGGAGTTACGGGGTGGGGGATTTCCACTACGTGACGGGCATG | 5040 |
| Db | 3901 | GAACAATTCACACAGAGGCAATCGGTTGCTGCAAAAGCCACCAAGCAAGCGGAGGCT | 3960 | Qy | 5041 | ACCACTGACAAAGTAAAGTGGCCGTGTCAGGTTCCGGGCGCCCGAAATTTCTTACAGAGTG | 5100 |
| Qy | 3961 | GCTGCTCCCGTGGTGAATCCAGTGGCGGACCTCGAAGCCCTTTGGCGGAAGCATATG | 4020 | Db | 5041 | ACCACTGACAAAGTAAAGTGGCCGTGTCAGGTTCCGGGCGCCCGAAATTTCTTACAGAGTG | 5100 |
| Db | 3961 | GCTGCTCCCGTGGTGAATCCAGTGGCGGACCTCGAAGCCCTTTGGCGGAAGCATATG | 4020 | Qy | 5101 | GATGGGTGCGGTTCACAGGTACGCTCCAGCGTGCAAAACCCCTCTCTACGGGAGGAGTC | 5160 |
| Qy | 4021 | TGGAATTTATCAGCGGGATACAAATTTAGCAGGCTTTCCACTCTGCTGCGCAACCCC | 4080 | Db | 5101 | GATGGGTGCGGTTCACAGGTACGCTCCAGCGTGCAAAACCCCTCTCTACGGGAGGAGTC | 5160 |
| Db | 4021 | TGGAATTTATCAGCGGGATACAAATTTAGCAGGCTTTCCACTCTGCTGCGCAACCCC | 4080 | Qy | 5161 | ACATTCCTGCTGGGCTCAATCAATACCTGTTGGTCAAGCTCCATCGGAGCCCGAA | 5220 |
| Qy | 4081 | GGATAGCATCACTGATGCAATTTAGCAGGCTTTCCACTCTGCTGCGCAACCCC | 4140 | Db | 5161 | ACATTCCTGCTGGGCTCAATCAATACCTGTTGGTCAAGCTCCATCGGAGCCCGAA | 5220 |
| Db | 4081 | GGATAGCATCACTGATGCAATTTAGCAGGCTTTCCACTCTGCTGCGCAACCCC | 4140 | Qy | 5221 | CCGAGCTAGCAGTCTCACTTCCATGCTCACCGACCCCTCCACATTAACGGCGGAGAGC | 5280 |
| Qy | 4141 | ACCTCCTGTTAAATCCTGGGGGATGGGTGGCGGCCCAACTTGTCTCTCCAGCGCT | 4200 | Db | 5221 | CCGAGCTAGCAGTCTCACTTCCATGCTCACCGACCCCTCCACATTAACGGCGGAGAGC | 5280 |
| Db | 4141 | ACCTCCTGTTAAATCCTGGGGGATGGGTGGCGGCCCAACTTGTCTCTCCAGCGCT | 4200 | Qy | 5281 | GCTAAGCGTAGGCTGGCCAGGGGATCTCCCGCTCTCTGGCCAGCTCATCAGTAGCCAG | 5340 |
| Qy | 4201 | GCTTCTGCTTCTAGCGCGCATCGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG | 4260 | Db | 5281 | GCTAAGCGTAGGCTGGCCAGGGGATCTCCCGCTCTCTGGCCAGCTCATCAGTAGCCAG | 5340 |
| Db | 4201 | GCTTCTGCTTCTAGCGCGCATCGCTGGAGCGGCTGTGGCAGCATAGGCTTGGG | 4260 | Qy | 5341 | CTGTCTGCGCTTCTTGAAGGCAATGCACTACCCGTCATGCTCCCGGAGGATGAG | 5400 |
| Qy | 4261 | AAGGTGCTGTGATATTTGGCAGGTTATGAGCAGGGGTGGCAGCGCGCTCGTGGCC | 4320 | Db | 5341 | CTGTCTGCGCTTCTTGAAGGCAATGCACTACCCGTCATGCTCCCGGAGGATGAG | 5400 |
| Db | 4261 | AAGGTGCTGTGATATTTGGCAGGTTATGAGCAGGGGTGGCAGCGCGCTCGTGGCC | 4320 | Qy | 5401 | CTCATCGAGGCCAACCTCTCTGTGGCGGAGGATGGGGGAAATCAACCCCGGTGGAG | 5460 |
| Qy | 4321 | TTTAAAGTCAAGCGCGGAGTGCCTCCACGAGGACCTGGTTAACTACTCCCTGCT | 4380 | Db | 5401 | CTCATCGAGGCCAACCTCTCTGTGGCGGAGGATGGGGGAAATCAACCCCGGTGGAG | 5460 |
| Db | 4321 | TTTAAAGTCAAGCGCGGAGTGCCTCCACGAGGACCTGGTTAACTACTCCCTGCT | 4380 | Qy | 5461 | TCAGAAAATAAGTAGTAAATTTTGGACTCTTTTCGAGCCGCTCCAAAGGGAGGATGAG | 5520 |
| Qy | 4381 | ATCCTCTCCCTCGCGCTAGTCTCGGGGTCTGTGGCAGCGATCTGCTGCGCAC | 4440 | Db | 5461 | TCAGAAAATAAGTAGTAAATTTTGGACTCTTTTCGAGCCGCTCCAAAGGGAGGATGAG | 5520 |
| Db | 4381 | ATCCTCTCCCTCGCGCTAGTCTCGGGGTCTGTGGCAGCGATCTGCTGCGCAC | 4440 | Qy | 5521 | AGGGAAGTATCCCTTCCCGGCGAGATCTCGGAGGTCCAGGAAATTTCCCTCGAGCGATG | 5580 |
| Qy | 4441 | GTGGGCCAGGGAGGGGCTGTGCAAGTGAATGAACCGGCTGATAGCGTTGCTTCCGG | 4500 | Db | 5521 | AGGGAAGTATCCCTTCCCGGCGAGATCTCGGAGGTCCAGGAAATTTCCCTCGAGCGATG | 5580 |
| Db | 4441 | GTGGGCCAGGGAGGGGCTGTGCAAGTGAATGAACCGGCTGATAGCGTTGCTTCCGG | 4500 | Qy | 5581 | CCCATATGGCAGCGCCCGGATTAAACCCCTCCACTGTTAGAGTCTCTGGAAGGACCCGAC | 5640 |
| Qy | 4501 | GGTAAACAGCGTCTCCCCCAGCACTATGTGCTGAGAGCGACGCTGAGCAGCGTCACT | 4560 | Db | 5581 | CCCATATGGCAGCGCCCGGATTAAACCCCTCCACTGTTAGAGTCTCTGGAAGGACCCGAC | 5640 |
| Db | 4501 | GGTAAACAGCGTCTCCCCCAGCACTATGTGCTGAGAGCGACGCTGAGCAGCGTCACT | 4560 | | | | |

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Db 2041 CAGGACCTCTGTCGCTGCGTGGCAAGCGCCCGCGGGCGCGTTCCTTGACACCATGCACTGC 2100
QY 2101 GGCAGCTCGGACCTTTACTTGGTCAAGAGCATGCGATGTCTTCCGCTGCGCGGG 2160
Db 2101 GGCAGCTCGGACCTTTACTTGGTCAAGAGCATGCGATGTCTTCCGCTGCGCGGG 2160
QY 2161 GGCAGCAGCAGGGGAGCCTACTCTCCCGCAGGCCGCTCTCTACTTGAAGGCTCTTCG 2220
Db 2161 GGCAGCAGCAGGGGAGCCTACTCTCCCGCAGGCCGCTCTCTACTTGAAGGCTCTTCG 2220
QY 2221 GCGGTCCACTGCTCTGCGGCGCAGCTGTGGGCATCTTTTCGGGCTGCCGTGTC 2280
Db 2221 GCGGTCCACTGCTCTGCGGCGCAGCTGTGGGCATCTTTTCGGGCTGCCGTGTC 2280
QY 2281 ACCGAGGGGTGGCAAGCGGTGAGCTTTGTACCCGCTGAGTCTATGAAACCACTATG 2340
Db 2281 ACCGAGGGGTGGCAAGCGGTGAGCTTTGTACCCGCTGAGTCTATGAAACCACTATG 2340
QY 2341 CGGTCCCGGCTTTCAGGCAAACTCGTCCCGTCCCGCGCTACCGAGACATTCAGGTG 2400
Db 2341 CGGTCCCGGCTTTCAGGCAAACTCGTCCCGTCCCGCGCTACCGAGACATTCAGGTG 2400
QY 2401 GCCCATCTACAGCGCCCTACTGTGTAGCGGCAAGAGACTAAGGTGCGGCTGCGTATGCA 2460
Db 2401 GCCCATCTACAGCGCCCTACTGTGTAGCGGCAAGAGACTAAGGTGCGGCTGCGTATGCA 2460
QY 2461 GCCCAAGGTTAAGGTGCTTCTCTGAAACCGCTGCGCGCCACCTAGGTTTCGGG 2520
Db 2461 GCCCAAGGTTAAGGTGCTTCTCTGAAACCGCTGCGCGCCACCTAGGTTTCGGG 2520
QY 2521 GCGTATATGCTAAGGCACATGTTATCGACCTTAACATCAGAACGGGTTAAGACCATC 2580
Db 2521 GCGTATATGCTAAGGCACATGTTATCGACCTTAACATCAGAACGGGTTAAGACCATC 2580
QY 2581 ACCACGGGTGCCCGCATCACTACTCACTATGGAAGTTTCTTCCGACGGTGTGTC 2640
Db 2581 ACCACGGGTGCCCGCATCACTACTCACTATGGAAGTTTCTTCCGACGGTGTGTC 2640
QY 2641 TCTGGGGCGCTTATGACATCAATAATGATGAGTGCCACTCACTGACTCGACCACT 2700
Db 2641 TCTGGGGCGCTTATGACATCAATAATGATGAGTGCCACTCACTGACTCGACCACT 2700
QY 2701 ATCTTGGGATCGGCACAGTCTTGGACCAAGCGGAGCGCTGAGCGCGCTGCTGTCG 2760
Db 2701 ATCTTGGGATCGGCACAGTCTTGGACCAAGCGGAGCGCTGAGCGCGCTGCTGTCG 2760
QY 2761 CTGCGCACGCTACGCTCGGATCGGTCACTGCACATCAACATCGAGGAGGTG 2820
Db 2761 CTGCGCACGCTACGCTCGGATCGGTCACTGCACATCAACATCGAGGAGGTG 2820
QY 2821 GCTCTGTCCAGCTCGAGAAATCCCTTTTATGGCAAGGCCATCCCATCGAGACCATC 2880
Db 2821 GCTCTGTCCAGCTCGAGAAATCCCTTTTATGGCAAGGCCATCCCATCGAGACCATC 2880

QY 2881 AAGGGGGGAGGACCTCATTTCTGCCATTCGAAGAAATGATGATGCTCCGCG 2940
DB |||||
QY 2881 AAGGGGGGAGGACCTCATTTCTGCCATTCGAAGAAATGATGATGCTCCGCG 2940
DB |||||
QY 2941 AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTAACGGGGGCTTGATATCCGTC 3000
DB |||||
QY 2941 AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTAACGGGGGCTTGATATCCGTC 3000
DB |||||
QY 3001 ATACCAACTAGCGGAGAGCTGATTTGTGTAGCAAGCGAGCTCTAATGACGGGCTTTACC 3060
DB |||||
QY 3001 ATACCAACTAGCGGAGAGCTGATTTGTGTAGCAAGCGAGCTCTAATGACGGGCTTTACC 3060
DB |||||
QY 3061 GAGGATTTGCACTGAGTGACAGTCAATGCTGTAGCAAGCGAGCTCTAATGACGGGCTTTACC 3120
DB |||||
QY 3061 GAGGATTTGCACTGAGTGACAGTCAATGCTGTAGCAAGCGAGCTCTAATGACGGGCTTTACC 3120
DB |||||
QY 3121 CTGGACCCGACCTTACCAATTTAGAGACGACCGTGTCCCAAGACGCGGTGTACGCTCG 3180
DB |||||
QY 3121 CTGGACCCGACCTTACCAATTTAGAGACGACCGTGTCCCAAGACGCGGTGTACGCTCG 3180
DB |||||
QY 3181 CAGCGGAGGAGGAGCTGTTAGGGGAGGATGAGTGTCCAGAGCTGTACAGGCTGTACGCTGT 3240
DB |||||
QY 3181 CAGCGGAGGAGGAGCTGTTAGGGGAGGATGAGTGTCCAGAGCTGTACAGGCTGTACGCTGT 3240
DB |||||
QY 3241 GAACGGCCCTCGGGCATGTTGATTCCTCGTTCTGTGCGAGTGTATGACGCGGCTGT 3300
DB |||||
QY 3241 GAACGGCCCTCGGGCATGTTGATTCCTCGTTCTGTGCGAGTGTATGACGCGGCTGT 3300
DB |||||
QY 3301 GCTTGTGTAGAGCTACGCGCGGAGACCTCAGTTAGTTTGGGGCTTACCTAAACACA 3360
DB |||||
QY 3301 GCTTGTGTAGAGCTACGCGCGGAGACCTCAGTTAGTTTGGGGCTTACCTAAACACA 3360
DB |||||
QY 3361 CAGGGTGGCCGTGTGCGAGGACCTGAGTCTGGAGAGCGCTTTTACAGGCTC 3420
DB |||||
QY 3361 CAGGGTGGCCGTGTGCGAGGACCTGAGTCTGGAGAGCGCTTTTACAGGCTC 3420
DB |||||
QY 3421 ACCACATAGACGCCATTTCTGTCCAGACTAAGCAGGAGGAGACAACTTCCCTAC 3480
DB |||||
QY 3421 ACCACATAGACGCCATTTCTGTCCAGACTAAGCAGGAGGAGACAACTTCCCTAC 3480
DB |||||
QY 3481 CTGATAGCATACAGGCTACGGTGTGCGCAGGCTCAGGCTCAGCTCCTCATGTGGGAC 3540
DB |||||
QY 3481 CTGATAGCATACAGGCTACGGTGTGCGCAGGCTCAGGCTCAGCTCCTCATGTGGGAC 3540
DB |||||
QY 3541 CAATGTGGAAGTGTCTATACGCTAAAGCTTACGCTGACGCGGCAACGCGCTCTG 3600
DB |||||
QY 3541 CAATGTGGAAGTGTCTATACGCTAAAGCTTACGCTGACGCGGCAACGCGCTCTG 3600
DB |||||
QY 3601 TATAGGCTGGAGCGGCTTCAAAAGAGTTACTACACACACACCCCAATACATC 3660
DB |||||
QY 3601 TATAGGCTGGAGCGGCTTCAAAAGAGTTACTACACACACACCCCAATACATC 3660
DB |||||
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DB |||||
QY 3661 ATGSCATGCACTGCTGGGCTGACCTGGAGTGTGCTACGAGACCTGGGCTGTGGTGGGGA 3720
DB |||||
QY 3721 GTCCTAGAGCTGTGGCGGCTATGCTGACACAGCAGCGGCTGCTATGTCGGCAGG 3780
DB |||||
QY 3721 GTCCTAGAGCTGTGGCGGCTATGCTGACACAGCAGCGGCTGCTATGTCGGCAGG 3780
DB |||||
QY 3781 ATCATCTTGTCCGAAAGCGGCTCATATCCGACAGGAGTCTTTTACCGGAGTTC 3840
DB |||||
QY 3781 ATCATCTTGTCCGAAAGCGGCTCATATCCGACAGGAGTCTTTTACCGGAGTTC 3840
DB |||||
QY 3841 GATGAGATGGAAGTGTGGCTTCACTCCCTTACATGCAACAGGAGTGTGCTGCC 3900
DB |||||
QY 3841 GATGAGATGGAAGTGTGGCTTCACTCCCTTACATGCAACAGGAGTGTGCTGCC 3900
DB |||||
QY 3901 GAACAATTAACAGAGGATCGGTTGTGCAACAGCAGCCACCAAGCAAGCGAGGCT 3960
DB |||||
QY 3901 GAACAATTAACAGAGGATCGGTTGTGCAACAGCAGCCACCAAGCAAGCGAGGCT 3960
DB |||||
QY 3961 GCTGTCCCGTGGTGGAAATCCAAAGTGGGAGCCCTCGAAGCCTTCTGGGCGAAGCATATG 4020
DB |||||

DB 3961 GCTGTCCCGTGGTGGAAATCCAAAGTGGGAGCCCTCGAAGCCTTCTGGGCGAAGCATATG 4020
QY |||||
QY 4021 TGGAAATTCATCAGGGGATCAATATTTAGCAGGCTTTGTCCACTCTCTGCTGGCAACCCC 4080
DB |||||
QY 4021 TGGAAATTCATCAGGGGATCAATATTTAGCAGGCTTTGTCCACTCTCTGCTGGCAACCCC 4080
DB |||||
QY 4081 GCGATAGCATCACTGATGGCATTCACAGCTCTATACAGCCCGCTACACCCCAACAT 4140
DB |||||
QY 4081 GCGATAGCATCACTGATGGCATTCACAGCTCTATACAGCCCGCTACACCCCAACAT 4140
DB |||||
QY 4141 ACCCTCTGTTTAAATCTCTGGGGGATGGGTCGCCCAACTTGTCTCTCCACGCGCT 4200
DB |||||
QY 4141 ACCCTCTGTTTAAATCTCTGGGGGATGGGTCGCCCAACTTGTCTCTCCACGCGCT 4200
DB |||||
QY 4201 GCTTCTGCTTCTGTTAGGCGCGGATCGCTGAGGCGGCTTTGGCAGCATAGGCTTTGG 4260
DB |||||
QY 4201 GCTTCTGCTTCTGTTAGGCGCGGATCGCTGAGGCGGCTTTGGCAGCATAGGCTTTGG 4260
DB |||||
QY 4261 AAGGTGCTTGTGGATATTTTGGCAGGTTATGAGCAGGGGTGGCAGCGGCTCGTGCGC 4320
DB |||||
QY 4261 AAGGTGCTTGTGGATATTTTGGCAGGTTATGAGCAGGGGTGGCAGCGGCTCGTGCGC 4320
DB |||||
QY 4321 TTTAAGGTCTATGAGCGCGGATGCCCTCCACGAGGACCTGTGTTAACTACTTCCCTGCT 4380
DB |||||
QY 4321 TTTAAGGTCTATGAGCGCGGATGCCCTCCACGAGGACCTGTGTTAACTACTTCCCTGCT 4380
DB |||||
QY 4381 ATCTCTCCCTCGGCGGCTAGTCTGTCGGGGTCTGTGCGCAGCGATATGCTGCTGGCAC 4440
DB |||||
QY 4381 ATCTCTCCCTCGGCGGCTAGTCTGTCGGGGTCTGTGCGCAGCGATATGCTGCTGGCAC 4440
DB |||||
QY 4441 GTGGGCCCGGAGGCGGCTGTGCACTGATGATGAAACGGCTGATAGGTTGCTTCCGCG 4500
DB |||||
QY 4441 GTGGGCCCGGAGGCGGCTGTGCACTGATGATGAAACGGCTGATAGGTTGCTTCCGCG 4500
DB |||||
QY 4501 GGTAAACACGCTCTCCCGCAGCCTATGTCCTGAGAGCAGCCTGTCAGCAGCTGTCACT 4560
DB |||||
QY 4501 GGTAAACACGCTCTCCCGCAGCCTATGTCCTGAGAGCAGCCTGTCAGCAGCTGTCACT 4560
DB |||||
QY 4561 CAGATCTCTCTAGTCTTACCATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 4620
DB |||||
QY 4561 CAGATCTCTCTAGTCTTACCATCACTCACTCACTCACTCACTCACTCACTCACTCACT 4620
DB |||||
QY 4621 GAGGACTGTCTCCAGCATCTCGGCTCGTGGCTGATGATGATGATGATGATGATGATGATG 4680
DB |||||
QY 4621 GAGGACTGTCTCCAGCATCTCGGCTCGTGGCTGATGATGATGATGATGATGATGATGATG 4680
DB |||||
QY 4681 ACCTGTGTTGACTGATTTCAAGACTGCTGCTCCAGTCCAGCTCTCTGCGCGGATTCGCGGA 4740
DB |||||
QY 4681 ACCTGTGTTGACTGATTTCAAGACTGCTGCTCCAGTCCAGCTCTCTGCGCGGATTCGCGGA 4740
DB |||||
QY 4741 GTCCCTTCTTCTCATGTCATCAACGTTGAGTCAAGGAGTCTGGCGGGGCGAGCGCATATG 4800
DB |||||
QY 4741 GTCCCTTCTTCTCATGTCATCAACGTTGAGTCAAGGAGTCTGGCGGGGCGAGCGCATATG 4800
DB |||||
QY 4801 CAAACACCTGCTGCTGAGGACATCAACGAGATGATGAAACGTTTCCATGAGG 4860
DB |||||
QY 4801 CAAACACCTGCTGCTGAGGACATCAACGAGATGATGAAACGTTTCCATGAGG 4860
DB |||||
QY 4861 ATCTGTGGGCTTAGGACTGTTAGTAAACAGTGGCATGGAACATTTCCCATTAACGCTTAC 4920
DB |||||
QY 4861 ATCTGTGGGCTTAGGACTGTTAGTAAACAGTGGCATGGAACATTTCCCATTAACGCTTAC 4920
DB |||||
QY 4921 ACCACGGGCTTCTGACGCTTCCCGGCGCAAAATTTATTCTAGGGGCTGTGGCGGCTG 4980
DB |||||
QY 4921 ACCACGGGCTTCTGACGCTTCCCGGCGCAAAATTTATTCTAGGGGCTGTGGCGGCTG 4980
DB |||||
QY 4981 GCTGTGAGGAGTGTAGTGGAGTGTACGCGGCTGGGATTTCCATCTAGTACGCGGCTG 5040
DB |||||
QY 4981 GCTGTGAGGAGTGTAGTGGAGTGTACGCGGCTGGGATTTCCATCTAGTACGCGGCTG 5040
DB |||||
QY 5041 ACCACTGACAAAGTAAAGTCCCGGCTGTCAGGTTCCGCGCCCGCAATTTCTTACAGAGTG 5100
DB |||||

| | | | |
|----|------|--|------|
| Db | 5041 | ACCACTGACAAAGTAAAGTGCCCGGTGTCAAGTTCCGGCCCCCGAAATTTCTTACAGAAAGTG | 5100 |
| Qy | 5101 | GATGGGGTCCGGTTGCACAGGTACGCTCCAGCGTGCAAAACCCCTCCTACGGGAGGAGTTC | 5160 |
| Db | 5101 | GATGGGGTCCGGTTGCACAGGTACGCTCCAGCGTGCAAAACCCCTCCTACGGGAGGAGTTC | 5160 |
| Qy | 5161 | ACATTCCTGGTCCGGCTCAATCAATACCTGTGGTGGGTCAAGTCCCATGCGAGCCCGAA | 5220 |
| Db | 5161 | ACATTCCTGGTCCGGCTCAATCAATACCTGTGGTGGGTCAAGTCCCATGCGAGCCCGAA | 5220 |
| Qy | 5221 | CCGACGTAGCAGTGCCTCACATTCCTCAATGCTCCAGCGGAGTCCCGAGTCCCGAGCCCGAA | 5280 |
| Db | 5221 | CCGACGTAGCAGTGCCTCACATTCCTCAATGCTCCAGCGGAGTCCCGAGTCCCGAGCCCGAA | 5280 |
| Qy | 5281 | GCTAAGCGTAGGCTGGCCAGGCGATCTCCCGCTCTTGGCCAGTCAATCAGCTAGCCAG | 5340 |
| Db | 5281 | GCTAAGCGTAGGCTGGCCAGGCGATCTCCCGCTCTTGGCCAGTCAATCAGCTAGCCAG | 5340 |
| Qy | 5341 | CTGTCTGGGCTTCTTGAAGGCAACATGCACTACCCGTATGACTCCCGGAGCGCTGAC | 5400 |
| Db | 5341 | CTGTCTGGGCTTCTTGAAGGCAACATGCACTACCCGTATGACTCCCGGAGCGCTGAC | 5400 |
| Qy | 5401 | CTCATCGAGGCAACCTCTCTGGCGGAGGATGGCGGGAACATCACCCGGTGGAG | 5460 |
| Db | 5401 | CTCATCGAGGCAACCTCTCTGGCGGAGGATGGCGGGAACATCACCCGGTGGAG | 5460 |
| Qy | 5461 | TCGAAATAAGGTAGTAATTTTGGACTCTTTTCGAGCGCTTCCAAAGCGGAGGAGATGAG | 5520 |
| Db | 5461 | TCGAAATAAGGTAGTAATTTTGGACTCTTTTCGAGCGCTTCCAAAGCGGAGGAGATGAG | 5520 |
| Qy | 5521 | AGGAAAGTATCCGTTCGGCGGAGATCTCTGGGAGGTCCAGGAAATTCCTTCGAGCGATG | 5580 |
| Db | 5521 | AGGAAAGTATCCGTTCGGCGGAGATCTCTGGGAGGTCCAGGAAATTCCTTCGAGCGATG | 5580 |
| Qy | 5581 | CCCATATGGCAGCCCGGATTAACAACCTCCACTGTAGAGTCTCTGGAGGACCCGGAC | 5640 |
| Db | 5581 | CCCATATGGCAGCCCGGATTAACAACCTCCACTGTAGAGTCTCTGGAGGACCCGGAC | 5640 |
| Qy | 5641 | TACGTCCCTCCAGTGATACAGGTGTCCATTTGGCGCTGCGAAGGCCCTCCGATACCA | 5700 |
| Db | 5641 | TACGTCCCTCCAGTGATACAGGTGTCCATTTGGCGCTGCGAAGGCCCTCCGATACCA | 5700 |
| Qy | 5701 | CTTCCAGGAGGAGGAGCGTTGTCTGTGAGAACTTACCGTGTCTTCTGCTTGGCG | 5760 |
| Db | 5701 | CTTCCAGGAGGAGGAGCGTTGTCTGTGAGAACTTACCGTGTCTTCTGCTTGGCG | 5760 |
| Qy | 5761 | GAGCTGCCACAAAGACTTTCCGAGCTCCGAACTCGTGGCGCTCGACAGGCGACGCA | 5820 |
| Db | 5761 | GAGCTGCCACAAAGACTTTCCGAGCTCCGAACTCGTGGCGCTCGACAGGCGACGCA | 5820 |
| Qy | 5821 | ACGGCTCTCTCTGACAGCCCTCCGACAGCGGAGTCCGAGCTTGGAGTTCGTAC | 5880 |
| Db | 5821 | ACGGCTCTCTCTGACAGCCCTCCGACAGCGGAGTCCGAGCTTGGAGTTCGTAC | 5880 |
| Qy | 5881 | TCTTCCATGCCCCCTTGAAGGAGGAGCGGGGATCCCGATCTCAGCAGCGGTCTTGG | 5940 |
| Db | 5881 | TCTTCCATGCCCCCTTGAAGGAGGAGCGGGGATCCCGATCTCAGCAGCGGTCTTGG | 5940 |
| Qy | 5941 | TCTTACCGTAAGCAGGAGGCTAGTGAGGAGCTGTCTGCTGCTCGATGCTTACATAGG | 6000 |
| Db | 5941 | TCTTACCGTAAGCAGGAGGCTAGTGAGGAGCTGTCTGCTGCTCGATGCTTACATAGG | 6000 |
| Qy | 6001 | ACAGGCGCTCTGATCAGCCATCGCTGCGGAGGAAACCAAGCTGCCATCAATGCACTG | 6060 |
| Db | 6001 | ACAGGCGCTCTGATCAGCCATCGCTGCGGAGGAAACCAAGCTGCCATCAATGCACTG | 6060 |
| Qy | 6061 | AGCAACTTTTGTCTCGTCAACCAACTTGGTCTATGCTTACCAATCTCGCAGCGCAAGC | 6120 |
| Db | 6061 | AGCAACTTTTGTCTCGTCAACCAACTTGGTCTATGCTTACCAATCTCGCAGCGCAAGC | 6120 |
| Qy | 6121 | CTCGCGCAGAGAGGCTTTCAGACTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT | 6180 |
| Db | 6121 | CTCGCGCAGAGAGGCTTTCAGACTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT | 6180 |
| Qy | 6181 | GTGCTCRAAGGAGTAAAGCGGCGAAGCGCTCCACAGTTAAAGCTTAACTTCTATCCGTGGAG | 6240 |
| Db | 6181 | GTGCTCRAAGGAGTAAAGCGGCGAAGCGCTCCACAGTTAAAGCTTAACTTCTATCCGTGGAG | 6240 |
| Qy | 6241 | GAAGCTCTAAGCTGACGCCGCCCAATTCGCGCAGATCTAAATTTGGCTATGGGCGCAAG | 6300 |
| Db | 6241 | GAAGCTCTAAGCTGACGCCGCCCAATTCGCGCAGATCTAAATTTGGCTATGGGCGCAAG | 6300 |
| Qy | 6301 | GACGTCCGGAACCTTATCCAGCAAGCGCGTTAAACCAATCCGCTCCGTGGAAGACTTG | 6360 |
| Db | 6301 | GACGTCCGGAACCTTATCCAGCAAGCGCGTTAAACCAATCCGCTCCGTGGAAGACTTG | 6360 |
| Qy | 6361 | CTGGAAGACACTGAGACACCAATTTGACACCAATTCATGCGCAAAATGAGTTTCTGC | 6420 |
| Db | 6361 | CTGGAAGACACTGAGACACCAATTTGACACCAATTCATGCGCAAAATGAGTTTCTGC | 6420 |
| Qy | 6421 | GTCCAAACAGAGAGGGGGCGCAAGCGCTCGCCCTTATCGATGTGTCTCCACCTCCCTCAGGCCGTG | 6480 |
| Db | 6421 | GTCCAAACAGAGAGGGGGCGCAAGCGCTCGCCCTTATCGATGTGTCTCCACCTCCCTCAGGCCGTG | 6480 |
| Qy | 6481 | GTTCTGTGTGCGAGAAATGGCCCTTTAGATGTGTCTCCACCTCCCTCAGGCCGTG | 6540 |
| Db | 6481 | GTTCTGTGTGCGAGAAATGGCCCTTTAGATGTGTCTCCACCTCCCTCAGGCCGTG | 6540 |
| Qy | 6541 | ATGGGCTCTTTCATACGATTCCTTCCATCTCTCTGGAAGCGGCTCGAGTCTCTGCTGAT | 6600 |
| Db | 6541 | ATGGGCTCTTTCATACGATTCCTTCCATCTCTCTGGAAGCGGCTCGAGTCTCTGCTGAT | 6600 |
| Qy | 6601 | GCCTGGAAGCGAAGAAATGCCCTTATGGGCTTCCCATATGACACCCGCTGTTTGACTCA | 6660 |
| Db | 6601 | GCCTGGAAGCGAAGAAATGCCCTTATGGGCTTCCCATATGACACCCGCTGTTTGACTCA | 6660 |
| Qy | 6661 | ACGCTCATCTGAGAAATGATCCCGTGTGAGAGTCAATCTACCAATGTGTGACTGCGCC | 6720 |
| Db | 6661 | ACGCTCATCTGAGAAATGATCCCGTGTGAGAGTCAATCTACCAATGTGTGACTGCGCC | 6720 |
| Qy | 6721 | CCGGAAGCCAGACAGGCCATTAAGGTCCTCACAGAGCGGCTTACATCGGGGGCCCCGTG | 6780 |
| Db | 6721 | CCGGAAGCCAGACAGGCCATTAAGGTCCTCACAGAGCGGCTTACATCGGGGGCCCCGTG | 6780 |
| Qy | 6781 | ACTAATTTTAAAGGCGAAGAACTGCGGCTATTCGCGGTGCGCGGAGCGGTGACTGACG | 6840 |
| Db | 6781 | ACTAATTTTAAAGGCGAAGAACTGCGGCTATTCGCGGTGCGCGGAGCGGTGACTGACG | 6840 |
| Qy | 6841 | ACCAGCTGCGGTAAATACCCCTCACATGTACTTGAAGCGCGCTCGCGCTGTGAGCTGCG | 6900 |
| Db | 6841 | ACCAGCTGCGGTAAATACCCCTCACATGTACTTGAAGCGCGCTCGCGCTGTGAGCTGCG | 6900 |
| Qy | 6901 | AAGCTCCAGGACTGCGAGTCTGATGCGGAGACGACCTTGTGTTATCTGTGAAAGC | 6960 |
| Db | 6901 | AAGCTCCAGGACTGCGAGTCTGATGCGGAGACGACCTTGTGTTATCTGTGAAAGC | 6960 |
| Qy | 6961 | GCGGGGACCCAGAGGACGAGGCGAGCTACGGGCTTCAACGAGGCTATGACTAGATAC | 7020 |
| Db | 6961 | GCGGGGACCCAGAGGACGAGGCGAGCTACGGGCTTCAACGAGGCTATGACTAGATAC | 7020 |
| Qy | 7021 | TCTGCCCCCTTGGGACCCGCCAAACAGATACTGAGTTGAGTTGATAATCATATGC | 7080 |
| Db | 7021 | TCTGCCCCCTTGGGACCCGCCAAACAGATACTGAGTTGAGTTGATAATCATATGC | 7080 |
| Qy | 7081 | TCTTCCAAATGTGTGACTGCGGACGATGATCTGGGCAAAAGGTTGATCTATCTCACCCGT | 7140 |
| Db | 7081 | TCTTCCAAATGTGTGACTGCGGACGATGATCTGGGCAAAAGGTTGATCTATCTCACCCGT | 7140 |
| Qy | 7141 | GACCCCAACACCCCTTGGGCGGCTGCGTGGGAGACAGCTAGACACTCCAGTCAAT | 7200 |
| Db | 7141 | GACCCCAACACCCCTTGGGCGGCTGCGTGGGAGACAGCTAGACACTCCAGTCAAT | 7200 |
| Qy | 7201 | TCTGCTAGGCAACATCATATGATGCGGCCACCTTGTGGGCAAGGATGATCTCTGATG | 7260 |
| Db | 7201 | TCTGCTAGGCAACATCATATGATGCGGCCACCTTGTGGGCAAGGATGATCTCTGATG | 7260 |

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QY 7261 ACTATTCTCTCCATCTCTAGCTCAGGAACAATTGAAAGAGCCCTAGATTGTGAG 7320
DB |||||
QY 7261 ACTATTCTCTCCATCTCTAGCTCAGGAACAATTGAAAGAGCCCTAGATTGTGAG 7320
DB |||||
QY 7321 ATCTACGGGGGCTGTACTCCATTGAGCCACTTGACCTCAGATCATTCACGACTC 7380
DB |||||
QY 7321 ATCTACGGGGGCTGTACTCCATTGAGCCACTTGACCTCAGATCATTCACGACTC 7380
DB |||||
QY 7381 CATGCCCTTAGCGCAATTTTCACTCATAGTACTCTCCAGGTGAGATCAATAGGTGGCT 7440
DB |||||
QY 7381 CATGCCCTTAGCGCAATTTTCACTCATAGTACTCTCCAGGTGAGATCAATAGGTGGCT 7440
DB |||||
QY 7441 TCATCCCTCAGGAACCTTGGGTACCGCTTGCAGTCTGAGACATCGGCCAGAAAGT 7500
DB |||||
QY 7441 TCATCCCTCAGGAACCTTGGGTACCGCTTGCAGTCTGAGACATCGGCCAGAAAGT 7500
DB |||||
QY 7501 GTCCGGCTTAGCTACTGTGCCAGGGGGAGGGTGGCCACTTGTGGCAAGTACTCTTC 7560
DB |||||
QY 7501 GTCCGGCTTAGCTACTGTGCCAGGGGGAGGGTGGCCACTTGTGGCAAGTACTCTTC 7560
DB |||||
QY 7561 AACTGGGAGTAAGGACCAAGCTCAAACTCACTCCAACTCCCGCTGCGTCCAGTTGGAT 7620
DB |||||
QY 7561 AACTGGGAGTAAGGACCAAGCTCAAACTCACTCCAACTCCCGCTGCGTCCAGTTGGAT 7620
DB |||||
QY 7621 TTATCCAGCTGTTCCTGCTGCTTACAGCGGGGAGACATATACAGCCCTGTCTCGT 7680
DB |||||
QY 7621 TTATCCAGCTGTTCCTGCTGCTTACAGCGGGGAGACATATATACAGCCCTGTCTCGT 7680
DB |||||
QY 7681 GCCCGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7740
DB |||||
QY 7681 GCCCGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7740
DB |||||
QY 7741 CTACTCCCAACCGATGAAGGGGAGCTAAACTCCAGCCCAATAGGCCATCTCTTT 7800
DB |||||
QY 7741 CTACTCCCAACCGATGAAGGGGAGCTAAACTCCAGCCCAATAGGCCATCTCTTT 7800
DB |||||
QY 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 7860
DB |||||
QY 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 7860
DB |||||
QY 7861 TTTTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 7920
DB |||||
QY 7861 TTTTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 7920
DB |||||
QY 7921 TAGCTGTGAAGTCCGTGAGCCGCTTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 7980
DB |||||
QY 7921 TAGCTGTGAAGTCCGTGAGCCGCTTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 7980
DB |||||
QY 7981 AGATCAAGTACT 7992
DB |||||
QY 7981 AGATCAAGTACT 7992
DB |||||

RESULT 4
AD:283762
ID ADC83762 standard; DNA; 10690 BP.
XX
AC ADC83762;
DB
XX
XX 01-JAN-2004 (first entry)
XX pHCVNeo17.wt plasmid containing an HCV bicistronic replicon.
XX
XX Hepatitis C virus; thiosemicarbazone; RHEPLISA; Ia; hepatitis C;
XX 4-(cinamylloxy)benzaldehyde thiosemicarbazone; RHEPLISA; Ia; hepatitis C;
XX HCV replication system; bicistronic RNA replicon;
XX neomycin phosphotransferase; human hepatoma cell line; Huh-7;
XX neomycin sulphate; G418; pHCVNeo17.wt; replicon I377neo/NS3-3'/wt.;
XX hepatotropic; virucide; antiinflammatory; ds.
XX
XX Synthetic.
XX Unidentified.
XX Hepatitis C virus.
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XX US2003176503-A1.
PN 18-SEP-2003.
XX
XX 19-APR-2002; 2002US-00125920.
XX
XX 20-APR-2001; 2001US-0285195P.
XX
XX (ALTA/) ALTAMURA S.
XX (KOH/) KOCH U.
XX
XX Altamura S, Koch U;
XX WPI; 2003-778475/73.
XX
XX Use of thiosemicarbazone compounds for e.g. treating and preventing
XX hepatitis C or its related condition, and delaying the onset of hepatitis
XX C or its related condition.
XX
XX Example 3; SEQ ID NO 1; 30pp; English.
XX
XX The invention discloses a method for the treatment and prevention of
XX hepatitis C, or its related condition, which involves the administration
XX of thiosemicarbazone compounds, or its salts. The inhibitory activity of
XX 4-(cinamylloxy)benzaldehyde thiosemicarbazone was evaluated using
XX RHEPLISA assay in a 96-well microplate format. The route of
XX administration is oral, parenteral (e.g. subcutaneous, intravenous,
XX intramuscular, intrasternal injection, or infusion), by inhalation spray
XX or rectal. The use of the 35 compounds disclosed is specifically claimed,
XX e.g. 4-(cinamylloxy)benzaldehyde thiosemicarbazone (Ia). The compounds
XX are useful for treating and preventing hepatitis C or its related
XX condition, delaying the onset of hepatitis C virus. The compounds are potent
XX inhibiting replication of the hepatitis C virus. HCV replication
XX inhibitor of replication of the hepatitis C virus. HCV replication
XX systems can be obtained using various techniques. Selection of cells
XX capable of supporting HCV replication can be achieved using bicistronic
XX RNA replicons expressing a selectable marker, the neomycin
XX phosphotransferase. Transfection of these replicons in the human hepatoma
XX cell line, Huh-7, followed by cultivation in the presence of neomycin
XX sulphate (G418), permits the isolation of clones that support HCV
XX replication. The sequence presented is the pHCVNeo17.wt plasmid which
XX contains the cDNA coding for an HCV bicistronic replicon identical to
XX replicon I377neo/NS3-3'/wt.
XX
XX Sequence 10690 BP; 2334 A; 3045 C; 2908 G; 2403 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 7992; DB 10; Length 10690;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 7992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GCCAGCCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAACACTG 60
DB |||||
QY 1 GCCAGCCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAACACTG 60
DB |||||
QY 61 TCTTACGCAGAAAAGCGTCTAGCCATGGCGCTTATAGTATAGTGTGCGAGCTCCAGAC 120
DB |||||
QY 61 TCTTACGCAGAAAAGCGTCTAGCCATGGCGCTTATAGTATAGTGTGCGAGCTCCAGAC 120
DB |||||
QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACACCGGAATTGCCAG 180
DB |||||
QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGAAACCGGTGAGTACACCGGAATTGCCAG 180
DB |||||
QY 181 GAGACACGGGTCTCTTTTGGATCAACCCCGCTCAATGCTCGGAGATTGGGGGTGCCCCC 240
DB |||||
QY 181 GAGACACGGGTCTCTTTTGGATCAACCCCGCTCAATGCTCGGAGATTGGGGGTGCCCCC 240
DB |||||
QY 241 GCAGAGCTGTAGCCGAGTGTGTGGTGTGCGAAAGCGCTTGTGCTACTGCCCTGATAGG 300
DB |||||
QY 241 GCAGAGCTGTAGCCGAGTGTGTGGTGTGCGAAAGCGCTTGTGCTACTGCCCTGATAGG 300
DB |||||
QY 301 GTGCTTCGAGTGTCCCGGGAGGTCTCGTAGACCGTGTGAGCAGCAGCAATCTAAAC 360
DB |||||
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Db 301 GTGCTTGGAGTGGCCCCGGAGGTCTCTGTAGACCGGTGACCATGAGCACGAATCTCTAAAC 360
QY 361 CTCAAGAAAAACCAAGGGCGCGCATGATTGAACAAGATGCAATGGACGAGTTCTC 420
Db 361 CTCAAGAAAAACCAAGGGCGCGCATGATTGAACAAGATGCAATGGACGAGTTCTC 420
QY 421 CGGCGCTTGGGTGAGAGGCTATTGCGCTATGACTGGGCAACAAGACAATCGGCTGT 480
Db 421 CGGCGCTTGGGTGAGAGGCTATTGCGCTATGACTGGGCAACAAGACAATCGGCTGT 480
QY 481 CTGATGCCCGGTGTCGGCTGTGTCAGCGAGGGGGCGCGCTCTCTTTTTCAGACGG 540
Db 481 CTGATGCCCGGTGTCGGCTGTGTCAGCGAGGGGGCGCGCTCTCTTTTTCAGACGG 540
QY 541 ACTGTCCGGTCCCTGAATGAATGCAGAGCAGGCGAGCGGCTATCTGTCGGTGGCA 600
Db 541 ACTGTCCGGTCCCTGAATGAATGCAGAGCAGGCGAGCGGCTATCTGTCGGTGGCA 600
QY 601 CGACGGGGTTCCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGACTGCG 660
Db 601 CGACGGGGTTCCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGACTGCG 660
QY 661 TGCTATTGGGGAAGTGGCGGAGGATCTCCTGTCACTCACTTGTCTGTCGGCGAGA 720
Db 661 TGCTATTGGGGAAGTGGCGGAGGATCTCCTGTCACTCACTTGTCTGTCGGCGAGA 720
QY 721 AAGTATCCATCATGGCTGATGCAATGCGCGCGCTGCATACGTTGATCGGCTACCTGCC 780
Db 721 AAGTATCCATCATGGCTGATGCAATGCGCGCGCTGCATACGTTGATCGGCTACCTGCC 780
QY 781 CATTCGACCAACAAGCGAAAATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTC 840
Db 781 CATTCGACCAACAAGCGAAAATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTC 840
QY 841 TTGTCGATCAGATGATCTGACGAAGAGCATCAGGGCTCGGCGCAGCCGAACTGTTCG 900
Db 841 TTGTCGATCAGATGATCTGACGAAGAGCATCAGGGCTCGGCGCAGCCGAACTGTTCG 900
QY 901 CAGGCTCAAGCGCGCATGCCGACGCGGAGGATCTCGTGTGACCCATCGCGATGCT 960
Db 901 CAGGCTCAAGCGCGCATGCCGACGCGGAGGATCTCGTGTGACCCATCGCGATGCT 960
QY 961 GCTTGGCGAATATCATGGTGAATAATGGCGCTTTCTGGAATTCATCGACTGTGGCGGG 1020
Db 961 GCTTGGCGAATATCATGGTGAATAATGGCGCTTTCTGGAATTCATCGACTGTGGCGGG 1020
QY 1021 TGGGTGCGGACCGCTATCAGACATAGGTGGTACCCGTGATTCGTGAAGAGC 1080
Db 1021 TGGGTGCGGACCGCTATCAGACATAGGTGGTACCCGTGATTCGTGAAGAGC 1080
QY 1081 TTGCGCGCAATGGGCTGACCGCTTCTCGTGTCTTACGGTATCGCGCTCCCGATTCGC 1140
Db 1081 TTGCGCGCAATGGGCTGACCGCTTCTCGTGTCTTACGGTATCGCGCTCCCGATTCGC 1140
QY 1141 AGGCATCGGCTTCTATCGGCTTCTGACGAGTTCTTCTGAGTTTAAACAGACCAACG 1200
Db 1141 AGGCATCGGCTTCTATCGGCTTCTGACGAGTTCTTCTGAGTTTAAACAGACCAACG 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTAACGTTATGCGC 1260
Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTAACGTTATGCGC 1260
QY 1261 CGAAGCGCTTGAATAAGCGCGGTGTGCTTGTCTATATGTTATTTTCCACCATATG 1320
Db 1261 CGAAGCGCTTGAATAAGCGCGGTGTGCTTGTCTATATGTTATTTTCCACCATATG 1320
QY 1321 CCGTCTTTTGGCAATGTAGGGGCGGAAACCTGGCCCTGTCTTCTGAGGAGCATTCCT 1380
Db 1321 CCGTCTTTTGGCAATGTAGGGGCGGAAACCTGGCCCTGTCTTCTGAGGAGCATTCCT 1380
QY 1381 AGGGGTCTTTCCTCTCGCAAGGATCGAAGGTCTGTGTAATGTGTTGAAGGAGCA 1440
Db 1381 AGGGGTCTTTCCTCTCGCAAGGATCGAAGGTCTGTGTAATGTGTTGAAGGAGCA 1440

QY 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACAAGCTCTGTAGCAACCTTTTCAGGCGAGCG 1500
Db 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACAAGCTCTGTAGCAACCTTTTCAGGCGAGCG 1500
QY 1501 AACCCCCACCTGGCGACAGGTGCTCTGCGSCCAAAAGCCACGTTATAGATACACT 1560
Db 1501 AACCCCCACCTGGCGACAGGTGCTCTGCGSCCAAAAGCCACGTTATAGATACACT 1560
QY 1561 GCAAGGGCGGCAACACCCAGTGCACAGTTGTGATGTGATGTGTAAGAGAGTCAAA 1620
Db 1561 GCAAGGGCGGCAACACCCAGTGCACAGTTGTGATGTGATGTGTAAGAGAGTCAAA 1620
QY 1621 TGGCTCTCTCAAGCGTATTCAACAAGGGCTGAAGGATGCCAGAAGTACCCATTGT 1680
Db 1621 TGGCTCTCTCAAGCGTATTCAACAAGGGCTGAAGGATGCCAGAAGTACCCATTGT 1680
QY 1681 ATGGATCTGATCTGGGCTCTCGGTGCACATGCTTTACATGTTTACTCGAGGTTAAA 1740
Db 1681 ATGGATCTGATCTGGGCTCTCGGTGCACATGCTTTACATGTTTACTCGAGGTTAAA 1740
QY 1741 AACGTCTAGGCCCCCGAACCAACCGGAGCGTGGTTTCTTTGAAAAACACATATACC 1800
Db 1741 AACGTCTAGGCCCCCGAACCAACCGGAGCGTGGTTTCTTTGAAAAACACATATACC 1800
QY 1801 ATGGCGCTATTAGGCGCTACTCCCAACAGACGGAGGCTACTTGGCTGCATCACT 1860
Db 1801 ATGGCGCTATTAGGCGCTACTCCCAACAGACGGAGGCTACTTGGCTGCATCACT 1860
QY 1861 AGCTCAAGCGCGGACAGAACAGGTGAGGGGAGGTCCAAAGTGTCTTCCACCGCA 1920
Db 1861 AGCTCAAGCGCGGACAGAACAGGTGAGGGGAGGTCCAAAGTGTCTTCCACCGCA 1920
QY 1921 ACACAATCTTCTGGGACCTGCTCAATGGCGTGTGTTGGAGTGTCTATCATGTGGC 1980
Db 1921 ACACAATCTTCTGGGACCTGCTCAATGGCGTGTGTTGGAGTGTCTATCATGTGGC 1980
QY 1981 GGCTCAAGAGCCTTGGCGGCGCAAGGGGCGCAATCAACCAATGTACACCAATGTGAC 2040
Db 1981 GGCTCAAGAGCCTTGGCGGCGCAAGGGGCGCAATCAACCAATGTACACCAATGTGAC 2040
QY 2041 CAGGACCTGTCGCTGCAAGCGCCCGCGGCGGCTTCTGACACCAATGACCTTGC 2100
Db 2041 CAGGACCTGTCGCTGCAAGCGCCCGCGGCGGCTTCTGACACCAATGACCTTGC 2100
QY 2101 GGCAGCTCGACCTTACTTGGTCAAGGATGCGGATGTCTATCCGCTGCGCGCGG 2160
Db 2101 GGCAGCTCGACCTTACTTGGTCAAGGATGCGGATGTCTATCCGCTGCGCGCGG 2160
QY 2161 GCGCAGCAGCGGGGAGCTACTCTCCCGCAGGCGCTCTCTACTTTGAAGGGCTCTTCG 2220
Db 2161 GCGCAGCAGCGGGGAGCTACTCTCCCGCAGGCGCTCTCTACTTTGAAGGGCTCTTCG 2220
QY 2221 GCGGCTCCACTGTCTGCGGCGAGCTGTGGGATCTTTCGGGCTGCGGTGTC 2280
Db 2221 GCGGCTCCACTGTCTGCGGCGAGCTGTGGGATCTTTCGGGCTGCGGTGTC 2280
QY 2281 ACCGAGGGGTTCGGAAGGCGGTGAGCTTTGTACCGCTCGAGTCTATGGAACCACTATG 2340
Db 2281 ACCGAGGGGTTCGGAAGGCGGTGAGCTTTGTACCGCTCGAGTCTATGGAACCACTATG 2340
QY 2341 CGGTCCCGGTCTTACGAGCAACTCTGTCCTCCCGCGGTACCGCAGATTCAGGTG 2400
Db 2341 CGGTCCCGGTCTTACGAGCAACTCTGTCCTCCCGCGGTACCGCAGATTCAGGTG 2400
QY 2401 GCCCATCTACGCCCTTACTGTAAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 2460
Db 2401 GCCCATCTACGCCCTTACTGTAAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 2460
QY 2461 GCCCAAGGTTAAGGTGCTTGTCTGAAACCGCTGCGCGCCACCTTAGGTTCGGG 2520
Db 2461 GCCCAAGGTTAAGGTGCTTGTCTGAAACCGCTGCGCGCCACCTTAGGTTCGGG 2520

| | | | |
|----|------|--|------|
| Db | 4681 | ACGGTGTGACGATTTCAAGACCTGGCTCCAGTCCAAAGCTCCTCGCGGATTTGCGGGA | 4740 |
| Qy | 4741 | GTCCCTTTCTTCTCATGTCAAGTGGGTACAAAGGAGTCTGGCGGGGACGGCATCATG | 4800 |
| Db | 4741 | GTCCCTTTCTTCTCATGTCAAGTGGGTACAAAGGAGTCTGGCGGGGACGGCATCATG | 4800 |
| Qy | 4801 | CNAACCACTGCGCATGTGGAGCAGATCAACGGACATGTGAAAAAGGTTCCATGAGG | 4860 |
| Db | 4801 | CNAACCACTGCGCATGTGGAGCAGATCAACGGACATGTGAAAAAGGTTCCATGAGG | 4860 |
| Qy | 4861 | ATCGTGGGCGCTAGGACCTGTAGTAAACAGTGGCATGGAACATTTCCCATTAACCGGTAC | 4920 |
| Db | 4861 | ATCGTGGGCGCTAGGACCTGTAGTAAACAGTGGCATGGAACATTTCCCATTAACCGGTAC | 4920 |
| Qy | 4921 | ACCAAGGCGCCCTGCACGCCCTCCCGGCGCCAAATTTATTTAGGGCGCTGTGGCGGGTG | 4980 |
| Db | 4921 | ACCAAGGCGCCCTGCACGCCCTCCCGGCGCCAAATTTATTTAGGGCGCTGTGGCGGGTG | 4980 |
| Qy | 4981 | GCTGCTGAGGAGTACGTGGAGGTACGGGTTACGGGGTGGGGGATTTCCACTAGTGAACGGCATG | 5040 |
| Db | 4981 | GCTGCTGAGGAGTACGTGGAGGTACGGGTTACGGGGTGGGGGATTTCCACTAGTGAACGGCATG | 5040 |
| Qy | 5041 | ACCACTGACAAAGTAAAGTCCCGGTGTCAAGTTCCGGGCCCGGAATTTCTTACAGAAAGTG | 5100 |
| Db | 5041 | ACCACTGACAAAGTAAAGTCCCGGTGTCAAGTTCCGGGCCCGGAATTTCTTACAGAAAGTG | 5100 |
| Qy | 5101 | GATGGGGTGGGTGCACAGTACGCTCCAGCGTGCAGAAACCCCTCCTACGGGAGGAGTGC | 5160 |
| Db | 5101 | GATGGGGTGGGTGCACAGTACGCTCCAGCGTGCAGAAACCCCTCCTACGGGAGGAGTGC | 5160 |
| Qy | 5161 | ACATTCCTGGTGGGCTCAATCAATACCTGTGTGGTCAAGTCCCATGCGAGCCGAA | 5220 |
| Db | 5161 | ACATTCCTGGTGGGCTCAATCAATACCTGTGTGGTCAAGTCCCATGCGAGCCGAA | 5220 |
| Qy | 5221 | CCGACCTAGCAGTGTCTACCTTCATGCTCACCGACCCCTCCCACTTACCGGGGAGACG | 5280 |
| Db | 5221 | CCGACCTAGCAGTGTCTACCTTCATGCTCACCGACCCCTCCCACTTACCGGGGAGACG | 5280 |
| Qy | 5281 | GCTAAGCGTAGGCTGGCGAGGGATCTCCCGCTCTTGGCGAGCTCATAGCTAGCCAG | 5340 |
| Db | 5281 | GCTAAGCGTAGGCTGGCGAGGGATCTCCCGCTCTTGGCGAGCTCATAGCTAGCCAG | 5340 |
| Qy | 5341 | CTGCTCGGCTTCTTGAAGGAAACATGACCTACCGGTATGACTCCCGGACGCTGAC | 5400 |
| Db | 5341 | CTGCTCGGCTTCTTGAAGGAAACATGACCTACCGGTATGACTCCCGGACGCTGAC | 5400 |
| Qy | 5401 | CTCATCGAGGCAACCTCTGTGGCGCAGGAGATGGCGGACATCACCCCGGTGGAG | 5460 |
| Db | 5401 | CTCATCGAGGCAACCTCTGTGGCGCAGGAGATGGCGGACATCACCCCGGTGGAG | 5460 |
| Qy | 5461 | TCAGAAATAGGTAGTAAATTTTGGACTTTTCGAGCCGCTCCAGCGGAGGAGATGAG | 5520 |
| Db | 5461 | TCAGAAATAGGTAGTAAATTTTGGACTTTTCGAGCCGCTCCAGCGGAGGAGATGAG | 5520 |
| Qy | 5521 | AGGGAAGTATCCGTTCCGGCGGAGATCTCGGAGGTCCAGGAAATTCCTTCGAGCGATG | 5580 |
| Db | 5521 | AGGGAAGTATCCGTTCCGGCGGAGATCTCGGAGGTCCAGGAAATTCCTTCGAGCGATG | 5580 |
| Qy | 5581 | CCCATATGGGACCGCCCGATTAACACCTTCCACTGTGTAGAGTCCCTGGAGAGCCCGGAC | 5640 |
| Db | 5581 | CCCATATGGGACCGCCCGATTAACACCTTCCACTGTGTAGAGTCCCTGGAGAGCCCGGAC | 5640 |
| Qy | 5641 | TAGTCTCTCCAGTGTGACAGGGTGTCAATTTGCGCTGCCAGGCGCCCTCCGATACCA | 5700 |
| Db | 5641 | TAGTCTCTCCAGTGTGACAGGGTGTCAATTTGCGCTGCCAGGCGCCCTCCGATACCA | 5700 |
| Qy | 5701 | CCTCCAGGAGGAGGAGCGGTGTCTGTCAAGATCTACCGTGTCTTCTGCTTGGCG | 5760 |
| Db | 5701 | CCTCCAGGAGGAGGAGCGGTGTCTGTCAAGATCTACCGTGTCTTCTGCTTGGCG | 5760 |
| Qy | 5761 | GAGCTGCCACAAAGACCTTCGGAGCTCCGAATCTCGGCGCTTCGACAGCGCAGGCA | 5820 |
| Db | 5761 | GAGCTGCCACAAAGACCTTCGGAGCTCCGAATCTCGGCGCTTCGACAGCGCAGGCA | 5820 |

| | | | |
|----|------|---|------|
| Qy | 5821 | ACGGCTCTCTGACGAGCCCTCCGACGCGGAGCGGGATCCGACGTTGAGTGGTAC | 5880 |
| Db | 5821 | ACGGCTCTCTGACGAGCCCTCCGACGCGGAGCGGGATCCGACGTTGAGTGGTAC | 5880 |
| Qy | 5881 | TCCTCCATGCCCCCTTTGAGGGGAGCCGGGGATCCCGATCTCAGCGACGGGTCTTGG | 5940 |
| Db | 5881 | TCCTCCATGCCCCCTTTGAGGGGAGCCGGGGATCCCGATCTCAGCGACGGGTCTTGG | 5940 |
| Qy | 5941 | TCTACCGTAAGCGAGGAGGTAGTGAGGACGTCTGCTGCTCGATGCTTACACATGG | 6000 |
| Db | 5941 | TCTACCGTAAGCGAGGAGGTAGTGAGGACGTCTGCTGCTCGATGCTTACACATGG | 6000 |
| Qy | 6001 | ACAGCGCCCTGATCACGCCATCGCTCGGAGGAAACCAAGCTCCCATCAATGCACTG | 6060 |
| Db | 6001 | ACAGCGCCCTGATCACGCCATCGCTCGGAGGAAACCAAGCTCCCATCAATGCACTG | 6060 |
| Qy | 6061 | AGCAACTCTTTGCTCCGTCACCAAACTTGTCTATGCTACAACTCTCGAGCGCAAGC | 6120 |
| Db | 6061 | AGCAACTCTTTGCTCCGTCACCAAACTTGTCTATGCTACAACTCTCGAGCGCAAGC | 6120 |
| Qy | 6121 | CTGGCGAAGAAAGGTCACTTTGACAGACTGACAGTCTCTGGACGACCACTACCGGAC | 6180 |
| Db | 6121 | CTGGCGAAGAAAGGTCACTTTGACAGACTGACAGTCTCTGGACGACCACTACCGGAC | 6180 |
| Qy | 6181 | GTGCTCAAGGAGATGAAGGCGGCTCCAGCTTAAGGCTAAACTTCTATCCGTGGAG | 6240 |
| Db | 6181 | GTGCTCAAGGAGATGAAGGCGGCTCCAGCTTAAGGCTAAACTTCTATCCGTGGAG | 6240 |
| Qy | 6241 | GAAGCTGTAGCTGAAGCCGCCACATTCGCGCCAGATCTAAATTTGGCTATGGGSCAAAG | 6300 |
| Db | 6241 | GAAGCTGTAGCTGAAGCCGCCACATTCGCGCCAGATCTAAATTTGGCTATGGGSCAAAG | 6300 |
| Qy | 6301 | GACGTCGGAACCTTATCCAGCAAGCGCGTTAAACACATCCGCTCGGTGGAAGGACTTG | 6360 |
| Db | 6301 | GACGTCGGAACCTTATCCAGCAAGCGCGTTAAACACATCCGCTCGGTGGAAGGACTTG | 6360 |
| Qy | 6361 | CTGGAAGCACTGAGACCACTTGAACACCACTCATGCGCAAAATAGAGTTTCTGCG | 6420 |
| Db | 6361 | CTGGAAGCACTGAGACCACTTGAACACCACTCATGCGCAAAATAGAGTTTCTGCG | 6420 |
| Qy | 6421 | GTCCAAACAGAGAGGGGGCGGCAAGCAGCTCGCTTATCGTATTCACGATTTGGG | 6480 |
| Db | 6421 | GTCCAAACAGAGAGGGGGCGGCAAGCAGCTCGCTTATCGTATTCACGATTTGGG | 6480 |
| Qy | 6481 | GTTCGTGTGTGCGAGAAATTTGGCCCTTTACGATGTGTCTCCACCTCTCCAGCCGCTG | 6540 |
| Db | 6481 | GTTCGTGTGTGCGAGAAATTTGGCCCTTTACGATGTGTCTCCACCTCTCCAGCCGCTG | 6540 |
| Qy | 6541 | ATGGGCTCTTTCATACGATTTCCAAATCTCTCGGACAGCGGTTCGAGTTCTCGTGAAT | 6600 |
| Db | 6541 | ATGGGCTCTTTCATACGATTTCCAAATCTCTCGGACAGCGGTTCGAGTTCTCGTGAAT | 6600 |
| Qy | 6601 | GCCTGGAACGCGAGAAATGCCCTATGGGCTTCGCAATATCACACCCGCTGTTTGACTCA | 6660 |
| Db | 6601 | GCCTGGAACGCGAGAAATGCCCTATGGGCTTCGCAATATCACACCCGCTGTTTGACTCA | 6660 |
| Qy | 6661 | ACGGTCACTGAGAAATGACATCCCGTGTGAGGAGTCAATCTTACCAATGTTGACTGGCC | 6720 |
| Db | 6661 | ACGGTCACTGAGAAATGACATCCCGTGTGAGGAGTCAATCTTACCAATGTTGACTGGCC | 6720 |
| Qy | 6721 | CCCGAAGCCAGACAGGCGCATAGGTCGCTCACAGAGGGCTTTACATCGGGGGCCCCCTG | 6780 |
| Db | 6721 | CCCGAAGCCAGACAGGCGCATAGGTCGCTCACAGAGGGCTTTACATCGGGGGCCCCCTG | 6780 |
| Qy | 6781 | ACTAATTTAAAGGGCAGAACTCGCGCTATCGCGGTGCGCGCGGAGCGGTGACTGACG | 6840 |
| Db | 6781 | ACTAATTTAAAGGGCAGAACTCGCGCTATCGCGGTGCGCGCGGAGCGGTGACTGACG | 6840 |
| Qy | 6841 | ACAGCTCGGTAAATACCTCTCATGTTACTTTGAAGGCGCTGCGGCTGTCTGAGCTGGG | 6900 |
| Db | 6841 | ACAGCTCGGTAAATACCTCTCATGTTACTTTGAAGGCGCTGCGGCTGTCTGAGCTGGG | 6900 |

6901 AAGCTCCAGGACTGCACGATGCTCGTATGCGGAGACGACCTGTGCTTATCTGTGAAAGC 6960
6901 AAGCTCCAGGACTGCACGATGCTCGTATGCGGAGACGACCTGTGCTTATCTGTGAAAGC 6960
6961 GCGGGGACCCAGAGAGAGAGCGAGCGCTTACGGGCTTTCACGGAGGCTATGACTAGATAC 7020
6961 GCGGGGACCCAGAGAGAGAGCGAGCGCTTACGGGCTTTCACGGAGGCTATGACTAGATAC 7020
7021 TCTGCCCCCTTGGGGACCCGCCCAAACAGAAATACGACTTGGAGTTGATAATCATATGC 7080
7021 TCTGCCCCCTTGGGGACCCGCCCAAACAGAAATACGACTTGGAGTTGATAATCATATGC 7080
7081 TCTCCATGCTCAGTCCGACGATGATCTGCGAAAGGCTGACTATCTCAACCCGT 7140
7081 TCTCCATGCTCAGTCCGACGATGATCTGCGAAAGGCTGACTATCTCAACCCGT 7140
7141 GACCCCAACACCCCTTGGGGGCTGGGTGGGAGACAGCTAGACACATCCAGTCAAT 7200
7141 GACCCCAACACCCCTTGGGGGCTGGGTGGGAGACAGCTAGACACATCCAGTCAAT 7200
7201 TCTGGCTAGGCAACATCATATGATGATGCGCCACCTTGGGCAAGGATGATCTGATG 7260
7201 TCTGGCTAGGCAACATCATATGATGATGCGCCACCTTGGGCAAGGATGATCTGATG 7260
7261 ACTCATTTCTTCTCCATCTTCTAGCTCAGGAAACAACTTGAAAAAGCCCTAGATTCTCAG 7320
7261 ACTCATTTCTTCTCCATCTTCTAGCTCAGGAAACAACTTGAAAAAGCCCTAGATTCTCAG 7320
7321 ATCTACGGGCTGTGTTACTTCAATGAGCCACTTGACCTACCTCAGATCATATCAACGACTC 7380
7321 ATCTACGGGCTGTGTTACTTCAATGAGCCACTTGACCTACCTCAGATCATATCAACGACTC 7380
7381 CATGGCTTAGCCATTTTCACTCCATGATTAATCTCCAGGTGAGATCAATAGGTGGCT 7440
7381 CATGGCTTAGCCATTTTCACTCCATGATTAATCTCCAGGTGAGATCAATAGGTGGCT 7440
7441 TCATGCTCAGGAAACTTGGGTTACCGCCCTTGGAGTCTGGAGATCGGGCCAGAAAT 7500
7441 TCATGCTCAGGAAACTTGGGTTACCGCCCTTGGAGTCTGGAGATCGGGCCAGAAAT 7500
7501 GTCGGCTTAGGCTAGTCTCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACTCTTC 7560
7501 GTCGGCTTAGGCTAGTCTCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACTCTTC 7560
7561 AACTGGCAGTAAGGACCAAGCTCAACTCACTCCATCCCGTGGTCCCAAGTTGGAT 7620
7561 AACTGGCAGTAAGGACCAAGCTCAACTCACTCCATCCCGTGGTCCCAAGTTGGAT 7620
7621 TTATCCAGCTGGTTCGTTGCTGTTACAGGGGGGAGACATATATACAGCCTGTCTCGT 7680
7621 TTATCCAGCTGGTTCGTTGCTGTTACAGGGGGGAGACATATATACAGCCTGTCTCGT 7680
7681 GCCCGACCCGCTGGTTCAATGTTGCTTACTCTTCTTCTAGGGGTAGGATCATAT 7740
7681 GCCCGACCCGCTGGTTCAATGTTGCTTACTCTTCTTCTAGGGGTAGGATCATAT 7740
7741 CTACTCCCAACCATGAGCGGAGCTAAACACTCCAGGCCAATAGCCCATCTGTTTT 7800
7741 CTACTCCCAACCATGAGCGGAGCTAAACACTCCAGGCCAATAGCCCATCTGTTTT 7800
7801 TTTCCCTTT 7860
7801 TTTCCCTTT 7860
7861 TTTTTCCTTT 7920
7861 TTTTTCCTTT 7920
7921 TAGCTGTGAAGGTCCTGAGCGCTTCACTGCAGAGAGTCTCATATCTGACCTCTCTGCG 7980
7921 TAGCTGTGAAGGTCCTGAGCGCTTCACTGCAGAGAGTCTCATATCTGACCTCTCTGCG 7980
7981 AGATCAAGTACT 7992

Db 7981 AGATCAAGTACT 7992
RESULT 5
ID AAL47281 standard; DNA; 7992 BP.
XX AAL47281;
AC AAL47281;
XX 30-AUG-2002 (first entry)
XX Hepatitis C virus sub-genomic replicon recombinant clone HCV224.
XX Hepatitis; HCV; core-neo; NS3 proteinase/helicase; vaccine; diagnosis;
XX virucide; hepatotropic; gene therapy; anti-viral; gene; ds.
XX Hepatitis C virus.
XX WO200238793-A2.
XX 16-MAY-2002.
XX 02-NOV-2001; 2001WO-US046350.
XX 07-NOV-2000; 2000US-0245866P.
XX (ANAD-) ANADYS PHARM INC.
XX Bichko V;
XX WPI; 2002-490082/52.
XX Novel nucleic acid encoding replication competent recombinant hepatitis C
XX virus genome useful for screening anti-hepatitis C virus therapeutics and
XX for vaccine development.
XX Claim 11; Page 70-75; 85pp; English.
XX The present invention provides protein and coding sequences from
XX Hepatitis C virus (HCV), comprising all or part of the HCV genome and
XX able to replicate efficiently when transfected into a susceptible cell
XX line without reducing the growth rate of the cell line by more than 10
XX fold. The sequences are useful for screening for anti-HCV therapeutics,
XX for detecting antibodies to HCV in a biological sample such as blood,
XX serum, plasma, blood cells, lymphocytes, or liver cells from a subject,
XX for deriving authentic HCV components such as replication-competent non-
XX infectious, replication-defective infection-component, and replication-
XX defective non-infectious HCV, in gene therapy or gene vaccination
XX targeted to hepatic tissue for treating an animal infected or susceptible
XX to HCV infection and for studying HCV infection and propagation. The
XX present sequence is a clone of a fragment of the HCV genome designated
XX HCV24
SQ Sequence 7992 BP; 1648 A; 2369 C; 2242 G; 1733 T; 0 U; 0 Other;
Query Match 100.0%; Score 7990.4; DB 6; Length 7992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCCAGCCCCGATTTGGGGGACACTCCACATAGATCACTCCCTCTGAGGAATCACTG 60
Db 1 GCCAGCCCCGATTTGGGGGACACTCCACATAGATCACTCCCTCTGAGGAATCACTG 60
QY 61 TCTTCACGACAGAAAGCGCTTAGCCATGGCTTAGTATGATGCTGTCAGCCTCCAGAC 120
Db 61 TCTTCACGACAGAAAGCGCTTAGCCATGGCTTAGTATGATGCTGTCAGCCTCCAGAC 120
QY 121 CCCCCCTCCCGGGAGAGCCATAGTGGTCTCGGGAACCGGTGAGTACACCGAATTGCCAG 180
Db 121 CCCCCCTCCCGGGAGAGCCATAGTGGTCTCGGGAACCGGTGAGTACACCGAATTGCCAG 180
QY 181 GACGACCGGGTCTTTTCTTGGATCAACCCGCTCAATGCTGGAGATTTGGGCGTGCCCC 240

QY 2401 GCCCATCTACAGCCCTACTGTTAGCGGACAGACCTAAGTGCCTGCGTATGCA 2460
DB |||||
QY 2401 GCCCATCTACAGCCCTACTGTTAGCGGACAGACCTAAGTGCCTGCGTATGCA 2460
DB |||||
QY 2461 GCCCAAGGTTAAGGTGCTTCTGTAACCCGTCCTGCGCGCCACCCCTAGTTCGGG 2520
DB |||||
QY 2461 GCCCAAGGTTAAGGTGCTTCTGTAACCCGTCCTGCGCGCCACCCCTAGTTCGGG 2520
DB |||||
QY 2521 GCGTATATGTTAAGGACATGGTATCGACCCCTAAACATCAGAACCCGGGTAAAGACCATC 2580
DB |||||
QY 2521 GCGTATATGTTAAGGACATGGTATCGACCCCTAAACATCAGAACCCGGGTAAAGACCATC 2580
DB |||||
QY 2581 ACCAGGGTCCCGCCATCAGTCTCCACCTATGGCAAGTTCCTGCGCGACGGTCTTCG 2640
DB |||||
QY 2581 ACCAGGGTCCCGCCATCAGTCTCCACCTATGGCAAGTTCCTGCGCGACGGTCTTCG 2640
DB |||||
QY 2641 TCTGGGGGCGCTATGACATCATATATGTAGTGAGTGCCACTCAACTGACTCGACCAT 2700
DB |||||
QY 2641 TCTGGGGGCGCTATGACATCATATATGTAGTGAGTGCCACTCAACTGACTCGACCAT 2700
DB |||||
QY 2701 ATCTGGGATCGGACAGTCTCTGACCAAGGGAGACGGCTGGAGCGGACTCTGTCGTG 2760
DB |||||
QY 2701 ATCTGGGATCGGACAGTCTCTGACCAAGGGAGACGGCTGGAGCGGACTCTGTCGTG 2760
DB |||||
QY 2761 CTGCGCACCGCTACGCTCGGGATCGGTACCGTGCACATCCAAACATCGAGGAGGTG 2820
DB |||||
QY 2761 CTGCGCACCGCTACGCTCGGGATCGGTACCGTGCACATCCAAACATCGAGGAGGTG 2820
DB |||||
QY 2821 GCTCTCTCAGCACTGGAGAAATCCCTTTTATGCGAAAGCCATCCCATCGAGACCATC 2880
DB |||||
QY 2821 GCTCTCTCAGCACTGGAGAAATCCCTTTTATGCGAAAGCCATCCCATCGAGACCATC 2880
DB |||||
QY 2881 AAGGGGGAGGACCTCATTTTCTGCAATTCCTCAAGAGAAATGTATGAGTCTCGCGG 2940
DB |||||
QY 2881 AAGGGGGAGGACCTCATTTTCTGCAATTCCTCAAGAGAAATGTATGAGTCTCGCGG 2940
DB |||||
QY 2941 AAGCTGCGGCTCGGACTCAATGTGTAGCATATTCAGGGGCTTGATGATCGCTC 3000
DB |||||
QY 2941 AAGCTGCGGCTCGGACTCAATGTGTAGCATATTCAGGGGCTTGATGATCGCTC 3000
DB |||||
QY 3001 ATACCAACTAGCGAGACGTCATTTGCTGTAGCAACCGACGCTCTAATGACGGGCTTACC 3060
DB |||||
QY 3001 ATACCAACTAGCGAGACGTCATTTGCTGTAGCAACCGACGCTCTAATGACGGGCTTACC 3060
DB |||||
QY 3061 GGGCATTTGACTCAGTGATCGATGCAATACATGTGTCAACCGACAGTCTCAGC 3120
DB |||||
QY 3061 GGGCATTTGACTCAGTGATCGATGCAATACATGTGTCAACCGACAGTCTCAGC 3120
DB |||||
QY 3121 CTGACCCGACCTTCACTTGTAGACGACGACGCTGCCACAAGACGGGTGTCAACGCTCG 3180
DB |||||
QY 3121 CTGACCCGACCTTCACTTGTAGACGACGACGCTGCCACAAGACGGGTGTCAACGCTCG 3180
DB |||||
QY 3181 CAGCGCGAGCGAGGACTGTTAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGGA 3240
DB |||||
QY 3181 CAGCGCGAGCGAGGACTGTTAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGGA 3240
DB |||||
QY 3241 GAACGGCCCTCGGGCATGTCGATTCCTCGGTCTGTGCGAGTCTATGACGGGCTGT 3300
DB |||||
QY 3241 GAACGGCCCTCGGGCATGTCGATTCCTCGGTCTGTGCGAGTCTATGACGGGCTGT 3300
DB |||||
QY 3301 GCTTGTACGAGCTCACGCCCGCGAGACCTCAGTTAGTTTGGGGCTTACTAAACACA 3360
DB |||||
QY 3301 GCTTGTACGAGCTCACGCCCGCGAGACCTCAGTTAGTTTGGGGCTTACTAAACACA 3360
DB |||||
QY 3361 CCAGGGTGGCCGCTCTGCCAGGACCACTCTGAGTTCTGGGAGAGGCTTTTACAGGCTC 3420
DB |||||
QY 3361 CCAGGGTGGCCGCTCTGCCAGGACCACTCTGAGTTCTGGGAGAGGCTTTTACAGGCTC 3420
DB |||||
QY 3421 ACCACATAGACGCTCTTCTGCGAGACTAAGCAGGAGGAGACCACTTCCCTTAC 3480
DB |||||
QY 3421 ACCACATAGACGCTCTTCTGCGAGACTAAGCAGGAGGAGACCACTTCCCTTAC 3480
DB |||||

QY 3481 CTGTGTAGCATACAGGCTACGGTGTGCGCAGGGCTCAGGCTCCACCTCCATCGTGGAC 3540
DB |||||
QY 3481 CTGTGTAGCATACAGGCTACGGTGTGCGCAGGGCTCAGGCTCCACCTCCATCGTGGAC 3540
DB |||||
QY 3541 CAAATGTGGAAGTGTCTCATAGGCTAAGCCTAGCTGACGCGCCCAACGCCCTGCTG 3600
DB |||||
QY 3541 CAAATGTGGAAGTGTCTCATAGGCTAAGCCTAGCTGACGCGCCCAACGCCCTGCTG 3600
DB |||||
QY 3601 TATAGGCTGGGAGCCGTTCAAAACGAGGTTACTACCAACACCCCATAAACCAATACATC 3660
DB |||||
QY 3601 TATAGGCTGGGAGCCGTTCAAAACGAGGTTACTACCAACACCCCATAAACCAATACATC 3660
DB |||||
QY 3661 ATGGCATGATGCTCGGCTGACCTGAGGTCGTCAAGAGCCTGCTGCTAGCGGGA 3720
DB |||||
QY 3661 ATGGCATGATGCTCGGCTGACCTGAGGTCGTCAAGAGCCTGCTGCTAGCGGGA 3720
DB |||||
QY 3721 GTCTTAGCAGCTCTGCGCGGTATTCCTGTGACAAAGGAGGTCGTGCTATGTTGGGCAGG 3780
DB |||||
QY 3721 GTCTTAGCAGCTCTGCGCGGTATTCCTGTGACAAAGGAGGTCGTGCTATGTTGGGCAGG 3780
DB |||||
QY 3781 ATCATCTTCTCGGAAAGCCGCCATCATTTCCGACAGGAAAGTCTTTACCGGGAGTTTC 3840
DB |||||
QY 3781 ATCATCTTCTCGGAAAGCCGCCATCATTTCCGACAGGAAAGTCTTTACCGGGAGTTTC 3840
DB |||||
QY 3841 GATGATGGAAGAGTGCCTCTCACCTCCCTTACATCGAAGGAAATGCAAGTCCGC 3900
DB |||||
QY 3841 GATGATGGAAGAGTGCCTCTCACCTCCCTTACATCGAAGGAAATGCAAGTCCGC 3900
DB |||||
QY 3901 GACAAATTCAAACAGAGGAAATCGGGTTGCTGAAACAGCCACCAAGAAAGGAGGCT 3960
DB |||||
QY 3901 GACAAATTCAAACAGAGGAAATCGGGTTGCTGAAACAGCCACCAAGAAAGGAGGCT 3960
DB |||||
QY 3961 GCTGCTCCGCTGGTGAATTCGAAGTGGCGGACCTCCGAAGCCTTTCTGGGGAAGCATATG 4020
DB |||||
QY 3961 GCTGCTCCGCTGGTGAATTCGAAGTGGCGGACCTCCGAAGCCTTTCTGGGGAAGCATATG 4020
DB |||||
QY 4021 TGGAAATTCATAGCGGGATCAATATTTAGCAGGCTTGTCCACTGTGCTGCCAGACCCC 4080
DB |||||
QY 4021 TGGAAATTCATAGCGGGATCAATATTTAGCAGGCTTGTCCACTGTGCTGCCAGACCCC 4080
DB |||||
QY 4081 GCGATAGCATCACTGATGCAATTCACAGCTCTATCACAGCCCGCTCACACCCCAACAT 4140
DB |||||
QY 4081 GCGATAGCATCACTGATGCAATTCACAGCTCTATCACAGCCCGCTCACACCCCAACAT 4140
DB |||||
QY 4141 ACCCTCTGTTTAAACATCTCTGGGGGATGGGTGGCGCCCAACTTGTCTCTCCAGGCT 4200
DB |||||
QY 4141 ACCCTCTGTTTAAACATCTCTGGGGGATGGGTGGCGCCCAACTTGTCTCTCCAGGCT 4200
DB |||||
QY 4201 GCTTCTGCTTTCGTAGCGCGCATCGCTGGAGCGGCTGTTGGCAGCATAGGCTTTGGG 4260
DB |||||
QY 4201 GCTTCTGCTTTCGTAGCGCGCATCGCTGGAGCGGCTGTTGGCAGCATAGGCTTTGGG 4260
DB |||||
QY 4261 AAGGTGCTTCTGATATTTTGGCAGGTTATGAGCAGGGGTGGCAGCGCTGCTGGCC 4320
DB |||||
QY 4261 AAGGTGCTTCTGATATTTTGGCAGGTTATGAGCAGGGGTGGCAGCGCTGCTGGCC 4320
DB |||||
QY 4321 TTTAAGGTCTATGAGCGCGAGATGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCT 4380
DB |||||
QY 4321 TTTAAGGTCTATGAGCGCGAGATGCCCTCCACCGAGGACCTGGTTAACTACTCCCTGCT 4380
DB |||||
QY 4381 ATCTCTCCCTTGGCGCCCTAGTGTGCGGGTGTGTCGAGCATACTGCGTCGCAC 4440
DB |||||
QY 4381 ATCTCTCCCTTGGCGCCCTAGTGTGCGGGTGTGTCGAGTCAGCATACTGCGTCGCAC 4440
DB |||||
QY 4441 GTGGGCCAGGGAGGGGGCTGTGCACTGAGTAACCGGCTGATAGCGTTTCGTTTCGGG 4500
DB |||||
QY 4441 GTGGGCCAGGGAGGGGGCTGTGCACTGAGTAACCGGCTGATAGCGTTTCGTTTCGGG 4500
DB |||||
QY 4501 GGTAAACACGCTCTCCCCCAGCAGCATATGTCCTGAGAGCGCTGTCAGCAGCTGCTACT 4560
DB |||||
QY 4501 GGTAAACACGCTCTCCCCCAGCAGCATATGTCCTGAGAGCGCTGTCAGCAGCTGCTACT 4560
DB |||||
QY 4561 CAGATCTCTCTAGTCTTACCATCACTCAGTGTCTGTAAGAGGCTTTCACAGTGGATCAAC 4620
DB |||||

| | | | |
|----|------|---|------|
| Db | 4561 | CAGATCCCTCTAGTCTTTACCATCACTCAGCTGCTGAAGAGCCTTCCACATGGATCAAC | 4620 |
| Qy | 4621 | GAGGACTGCTCCACGCCATGCTCGGCTCGTGGCTTAAGAGATGTTTGGGATTGGATATGC | 4680 |
| Db | 4621 | GAGGACTGCTCCACGCCATGCTCGGCTCGTGGCTTAAGAGATGTTTGGGATTGGATATGC | 4680 |
| Qy | 4681 | ACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCTCGCCGATTCGCCGGA | 4740 |
| Db | 4681 | ACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAAAGCTCTCTGCCGATTCGCCGGA | 4740 |
| Qy | 4741 | GTCCCTCTCTTCTCATGTCAACGTGGGTACAGGAGGATCTGGCGGGGACGGCATCATG | 4800 |
| Db | 4741 | GTCCCTCTCTTCTCATGTCAACGTGGGTACAGGAGGATCTGGCGGGGACGGCATCATG | 4800 |
| Qy | 4801 | CAAACCACTGCCCCATGTGGAGCACAGATCACCGGACATGTGAAAAACGGTTCATCAGG | 4860 |
| Db | 4801 | CAAACCACTGCCCCATGTGGAGCACAGATCACCGGACATGTGAAAAACGGTTCATCAGG | 4860 |
| Qy | 4861 | ATCGTGGGCTTAGACCTGTAGTAAACAGTGGGATGAAACATTTCCCAATTAACGGGTAC | 4920 |
| Db | 4861 | ATCGTGGGCTTAGACCTGTAGTAAACAGTGGGATGAAACATTTCCCAATTAACGGGTAC | 4920 |
| Qy | 4921 | ACCACGGCCCCCTGCACGCCCTCCCCGGCGCCAAATTTATTTAGGGCGCTGTGCGCGGTG | 4980 |
| Db | 4921 | ACCACGGCCCCCTGCACGCCCTCCCCGGCGCCAAATTTATTTAGGGCGCTGTGCGCGGTG | 4980 |
| Qy | 4981 | GCTGCTGAGGAGTAGCTGGAGGTTACGCGGTGGGGATTTTCCACTACGTGACGGGCATG | 5040 |
| Db | 4981 | GCTGCTGAGGAGTAGCTGGAGGTTACGCGGTGGGGATTTTCCACTACGTGACGGGCATG | 5040 |
| Qy | 5041 | ACCACTGACACGTAAGTAGTCCCGTGTCAAGTTCGCGCCCCCGAAATTTCTTACAGAAATG | 5100 |
| Db | 5041 | ACCACTGACACGTAAGTAGTCCCGTGTCAAGTTCGCGCCCCCGAAATTTCTTACAGAAATG | 5100 |
| Qy | 5101 | GATGGGTGCGGTTGCAACAGTACGCTCCAGCGTGCNAACCCCTCCTACGGGAGGCTC | 5160 |
| Db | 5101 | GATGGGTGCGGTTGCAACAGTACGCTCCAGCGTGCNAACCCCTCCTACGGGAGGCTC | 5160 |
| Qy | 5161 | ACAATCTGCTGGGCTCAATCAATCACTGTTGGGTACAGCTCCCATGCGGACCGGAA | 5220 |
| Db | 5161 | ACAATCTGCTGGGCTCAATCAATCACTGTTGGGTACAGCTCCCATGCGGACCGGAA | 5220 |
| Qy | 5221 | CCGACGTAGAGTGCTCATTCATGCTCAACGACCCCTCCACATTAACGCGGAGACG | 5280 |
| Db | 5221 | CCGACGTAGAGTGCTCATTCATGCTCAACGACCCCTCCACATTAACGCGGAGACG | 5280 |
| Qy | 5281 | GCTAAGCGTAGGCTGGCCAGGGATCTCCCCCTCTTGGCAGCTCATCAGTACCGAG | 5340 |
| Db | 5281 | GCTAAGCGTAGGCTGGCCAGGGATCTCCCCCTCTTGGCAGCTCATCAGTATCCAG | 5340 |
| Qy | 5341 | CTGTCTGCGCTTCTTTGAAGGCAAATGACACTACCCCTCATGACTCCCCCGACGCTAC | 5400 |
| Db | 5341 | CTGTCTGCGCTTCTTTGAAGGCAAATGACACTACCCCTCATGACTCCCCCGACGCTAC | 5400 |
| Qy | 5401 | CTCATGAGGCCAACTCTGTGGCGGAGAGATGGGCGGAAACATCACCCGCTGGAG | 5460 |
| Db | 5401 | CTCATGAGGCCAACTCTGTGGCGGAGAGATGGGCGGAAACATCACCCGCTGGAG | 5460 |
| Qy | 5461 | TCAGAAAAAAGTACTGATTTTGGACTCTTTGAGCCGCTCCAGCGGAGGAGATCAG | 5520 |
| Db | 5461 | TCAGAAAAAAGTACTGATTTTGGACTCTTTGAGCCGCTCCAGCGGAGGAGATCAG | 5520 |
| Qy | 5521 | AGGGAAGTATCCCTTCCGGCGGAGATCTTCGAGGCTCCAGGAAATTCCTTCAGCGATG | 5580 |
| Db | 5521 | AGGGAAGTATCCCTTCCGGCGGAGATCTTCGAGGCTCCAGGAAATTCCTTCAGCGATG | 5580 |
| Qy | 5581 | CCCATATGGGCACGCCCGGATTACAAACCTCCACTGTTAGAGTCTCTGAAAGACCCGAC | 5640 |
| Db | 5581 | CCCATATGGGCACGCCCGGATTACAAACCTCCACTGTTAGAGTCTCTGAAAGACCCGAC | 5640 |
| Qy | 5641 | TACGTCCTCCATGCTACACGGGTGTCATTTGCGGCTGCGAAGGCCCTCTCCGATCCA | 5700 |

| | | | |
|----|------|--|------|
| Db | 5641 | TACGTCCTCCAGTGGTACACGGGTGCTCATTTGCCCGCTGCCAAGSCCCTCCGATACCA | 5701 |
| Qy | 5701 | CCTCCACGGAGAGAGAGCGGTTCCTCTGTGAGAACTACCGTGTCTTCTGCTCTGGCG | 5760 |
| Db | 5701 | | |
| Qy | 5761 | GAGCTCGCCACAAAGACTCTCGGCAGCTCCGAATCTGTCGGCCCTCGACACGCGCACGGCA | 5820 |
| Db | 5761 | GAGCTCGCCACAAAGACTCTCGGCAGCTCCGAATCTGTCGGCCCTCGACACGCGCACGGCA | 5820 |
| Qy | 5821 | ACGGCTCTCTGTACACGACCTTCGACGACGGGAGACGGGATCCGAGTCTACGACGCGGTCTTGG | 5940 |
| Db | 5821 | ACGGCTCTCTGTACACGACCTTCGACGACGGGAGACGGGATCCGAGTCTACGACGCGGTCTTGG | 5940 |
| Qy | 5881 | TCCTCCATGCCCCCTTGAGGGGGAGCGGGGGATCCCGATCTACGACGCGGTCTTGG | 5940 |
| Db | 5881 | TCCTCCATGCCCCCTTGAGGGGGAGCGGGGGATCCCGATCTACGACGCGGTCTTGG | 5940 |
| Qy | 5941 | TCTACCGTAAGCAGGAGGCTAGTGAGGACGTCGTCCTGCTGCTGATGTCCTACACATGG | 6000 |
| Db | 5941 | TCTACCGTAAGCAGGAGGCTAGTGAGGAGCTGTCGTCGTCGATGTCCTACACATGG | 6000 |
| Qy | 6001 | ACAGCGCCCTGATCACGCCATCGCTGCGGAGGAAACCAAGTGCCTCAATGCATG | 6060 |
| Db | 6001 | ACAGCGCCCTGATCACGCCATCGCTGCGGAGGAAACCAAGTGCCTCAATGCATG | 6060 |
| Qy | 6061 | AGCAACTCTTTGCTCCGTACCAACAATTTGGTCTATGCTTACAACTCTCGACGCGCAAGC | 6120 |
| Db | 6061 | AGCAACTCTTTGCTCCGTACCAACAATTTGGTCTATGCTTACAACTCTCGACGCGCAAGC | 6120 |
| Qy | 6121 | CTGCGGCAGAGAAGGTCACCTTTTGACAGACTGCAGTCTCTCGAGCACCACTACCGGAC | 6180 |
| Db | 6121 | CTGCGGCAGAGAAGGTCACCTTTTGACAGACTGCAGTCTCTCGAGCACCACTACCGGAC | 6180 |
| Qy | 6181 | GTGCTCAGAGATGAAGGGAAGGCGTCCAAGTTAAGGCTAACTTCTATCCGTGAG | 6240 |
| Db | 6181 | GTGCTCAGAGATGAAGGGAAGGCGTCCAAGTTAAGGCTAACTTCTATCCGTGAG | 6240 |
| Qy | 6241 | GAAGCCTGTAAGCTGACGCCCCACATTCGGCCAGATCTAAATTTGGCTATGGGCAAG | 6300 |
| Db | 6241 | GAAGCCTGTAAGCTGACGCCCCACATTCGGCCAGATCTAAATTTGGCTATGGGCAAG | 6300 |
| Qy | 6301 | GAGCTCGGAACCTATCCAGCAAGGCGTTAAACCACATCCGCTCCGCTGGAAGGACTTG | 6360 |
| Db | 6301 | GAGCTCGGAACCTATCCAGCAAGGCGTTAAACCACATCCGCTCCGCTGGAAGGACTTG | 6360 |
| Qy | 6361 | CTGGAGACACTGAGACACCAATTGACACCACTCATGCGAATAAATGAGTTTCTGC | 6420 |
| Db | 6361 | CTGGAGACACTGAGACACCAATTGACACCACTCATGCGAATAAATGAGTTTCTGC | 6420 |
| Qy | 6421 | GTCCAAACGAGAGAGGGGGCGCAAGCCAGCTCCGCTTATCGTATTCACAGATTTGGG | 6480 |
| Db | 6421 | GTCCAAACGAGAGAGGGGGCGCAAGCCAGCTCCGCTTATCGTATTCACAGATTTGGG | 6480 |
| Qy | 6481 | GTTCTGTGTGCGAGAAATGSCCTTTACGATGCTGCTCCACCTCCCTCAGGCGGTG | 6540 |
| Db | 6481 | GTTCTGTGTGCGAGAAATGSCCTTTACGATGCTGCTCCACCTCCCTCAGGCGGTG | 6540 |
| Qy | 6541 | ATGGGCTCTTACATCGGATTCCAATCTCTCTGAGACGCGGTGCGATTCCTGGTGAAT | 6600 |
| Db | 6541 | ATGGGCTCTTACATCGGATTCCAATCTCTCTGAGACGCGGTGCGATTCCTGGTGAAT | 6600 |
| Qy | 6601 | GCTGTAAACGAGAAATGCCCATTGGGCTTCGCATATGACACCGCTGTTTGACTCA | 6660 |
| Db | 6601 | GCTGTAAACGAGAAATGCCCATTGGGCTTCGCATATGACACCGCTGTTTGACTCA | 6660 |
| Qy | 6661 | ACGGTCACTGAGATGACATCCGTTGAGGAGTCAATCTAGCAATGTGTGACTTGGCC | 6720 |
| Db | 6661 | ACGGTCACTGAGATGACATCCGTTGAGGAGTCAATCTAGCAATGTGTGACTTGGCC | 6720 |
| Qy | 6721 | CCGGAAGCCAGACGCGCATAGTCCGTACACAGCGGCTTTACATCGGGGGCCCCCTG | 6780 |
| Db | 6721 | CCGGAAGCCAGACGCGCATAGTCCGTACACAGCGGCTTTACATCGGGGGCCCCCTG | 6780 |

| | | | | | |
|----|--|-----|------|--|------|
| XX | Claim 16; Page; 69pp; English. | Db | 601 | CGACGGGGTTCCTTGGCAGCTGTCTCGAGCTGTCTGACGAGCGGAGGAGTGGC | 660 |
| XX | The invention relates to nucleic acid molecules comprising altered HCV NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) region coding for one or more NS3, NS5A, or EMCV IRES mutations, respectively. The location of the mutations are detailed in the specification. Also included are (1) an expression vector comprising a nucleotide sequence coding for the altered nucleic acids, which is transcriptionally coupled to an exogenous promoter; (2) a recombinant cell human hepatoma cell comprising the altered nucleic acids; (3) a recombinant cell produced by introducing into a human hepatoma cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus) replicon enhanced cell or which containing a functional HCV replicon; (5) an HCV replicon enhanced cells made in the method; and (6) measuring the ability of a compound to affect HCV activity. The HCV replicons and HCV expression, and HCV and host cell interactions, producing HCV RNA and proteins, and providing a system for measuring the ability of a compound to modulate one or more HCV activities e.g. to discover drugs which may treat HCV mediated diseases such as liver failure, cirrhosis and hepatocellular carcinoma. The present sequence is an HCV based vector pHCVNeo.17 mutant of the invention. Note: The present sequence is not shown in the specification but was created by the indexer using the HCV vector sequence appearing as ABK91412 and the information in Claim 16 | QY | 661 | TGCTATTGGGCGAAGTGCAGGGGAGGATCTCTGTATCTCACCTTCTCTCGCCGAGA | 720 |
| | | Db | 661 | TGCTATTGGGCGAAGTGCAGGGGAGGATCTCTGTATCTCACCTTCTCTCGCCGAGA | 720 |
| | | QY | 721 | AAGTATCCATCATCGCTGATGCAATGCGGCGCTGCATACGCTTGATCCGGTACCTGCC | 780 |
| | | Db | 721 | AAGTATCCATCATCGCTGATGCAATGCGGCGCTGCATACGCTTGATCCGGTACCTGCC | 780 |
| | | QY | 781 | CATTTCGACCAACAAAGCGAATCATCGCATCGAGCGAGCAGCTACTCGGATGGAAGCCGGTC | 840 |
| | | Db | 781 | CATTTCGACCAACAAAGCGAATCATCGCATCGAGCGAGCAGCTACTCGGATGGAAGCCGGTC | 840 |
| | | QY | 841 | TTGTGATTCAGGATGATCTGGAACGAGCATCAGGGGCTCGGCCAGCCGAACTGTTTCG | 900 |
| | | Db | 841 | TTGTGATTCAGGATGATCTGGAACGAGCATCAGGGGCTCGGCCAGCCGAACTGTTTCG | 900 |
| | | QY | 901 | CCAGGCTCAAGGCGCGCATGCCCCGACGCGGAGGATCTCGTGTGACCCATGGCGATGCT | 960 |
| | | Db | 901 | CCAGGCTCAAGGCGCGCATGCCCCGACGCGGAGGATCTCGTGTGACCCATGGCGATGCT | 960 |
| | | QY | 961 | GCTTTCGGAATATCATGCTGGAATAATGCGCGCTTTCTTGGATTTCATCGACTGTGCGCGGC | 1020 |
| | | Db | 961 | GCTTTCGGAATATCATGCTGGAATAATGCGCGCTTTCTTGGATTTCATCGACTGTGCGCGGC | 1020 |
| | | QY | 1021 | TGGTGTGGCGGACCGCTATCAGGACATAGCTTGGCTACCGGTGATTTGCTGAAGAGC | 1080 |
| | | Db | 1021 | TGGTGTGGCGGACCGCTATCAGGACATAGCTTGGCTACCGGTGATTTGCTGAAGAGC | 1080 |
| | | QY | 1081 | TTGCGGCGAATGCGCTGACCGCTTCTCGTGTGTTTACGGTATCGCGCTCCCGATTGCG | 1140 |
| | | Db | 1081 | TTGCGGCGAATGCGCTGACCGCTTCTCGTGTGTTTACGGTATCGCGCTCCCGATTGCG | 1140 |
| | | QY | 1141 | AGCGCATTCGCTTCTATCGCTTCTTACGAGTTCCTTCTGAGTTTAAACAGACCACAAACG | 1200 |
| | | Db | 1141 | AGCGCATTCGCTTCTATCGCTTCTTACGAGTTCCTTCTGAGTTTAAACAGACCACAAACG | 1200 |
| | | QY | 1201 | GTTTCCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCCCCCCCTAACGTTACTGGC | 1260 |
| | | Db | 1201 | GTTTCCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCCCCCCCTAACGTTACTGGC | 1260 |
| | | QY | 1261 | CGAAGCGCTTGAATAAGCCGCTGCTTGTCTATATGTTATTTCCACCATATTG | 1320 |
| | | Db | 1261 | CGAAGCGCTTGAATAAGCCGCTGCTTGTCTATATGTTATTTCCACCATATTG | 1320 |
| | | QY | 1321 | CCGTCTTTTGGCAATGTAGGGGCGCGAAACCTGGGCTCTCTTCTTGTAGAGCATTCCT | 1380 |
| | | Db | 1321 | CCGTCTTTTGGCAATGTAGGGGCGCGAAACCTGGGCTCTCTTCTTGTAGAGCATTCCT | 1380 |
| | | QY | 1381 | AGGGGTCTTTCCCTCTCGCCTAAAGGAATGCAAGTCTGTTGAATGTGCTGAAGGAGCA | 1440 |
| | | Db | 1381 | AGGGGTCTTTCCCTCTCGCCTAAAGGAATGCAAGTCTGTTGAATGTGCTGAAGGAGCA | 1440 |
| | | QY | 1441 | GTTTCTCTGGAAGTCTTTGAAGCAAAACAAAGTCTGTAGCGACCCCTTTGACGCGCGG | 1500 |
| | | Db | 1441 | GTTTCTCTGGAAGTCTTTGAAGCAAAACAAAGTCTGTAGCGACCCCTTTGACGCGCGG | 1500 |
| | | QY | 1501 | AACCCCTCCACCTTGGCGACAGGTGCTCTCGGCGAAAGCCAGCTGTATAAGGATACACCT | 1560 |
| | | Db | 1501 | AACCCCTCCACCTTGGCGACAGGTGCTCTCGGCGAAAGCCAGCTGTATAAGGATACACCT | 1560 |
| | | QY | 1561 | GCAAGGCGGCAAAACCCAGTGCACCGTTGTAGTTGATAGTTGTGGAAGAGTCAAA | 1620 |
| | | Db | 1561 | GCAAGGCGGCAAAACCCAGTGCACCGTTGTAGTTGATAGTTGTGGAAGAGTCAAA | 1620 |
| | | QY | 1621 | TGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATGCCAGAGGATACCCATTGT | 1680 |
| | | Db | 1621 | TGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATGCCAGAGGATACCCATTGT | 1680 |
| | | QY | 1681 | ATGGGATCTGATCTGGGCGCTCGGTGCAATCTTTACATGTTTGTAGTCGAGGTTAAA | 1740 |
| | | Db | 1681 | ATGGGATCTGATCTGGGCGCTCGGTGCAATCTTTACATGTTTGTAGTCGAGGTTAAA | 1740 |
| XX | Query Match 100.0%; Score 7990.4; DB 6; Length 10690; | | | | |
| XX | Best Local Similarity 100.0%; Pred. No. 0; | | | | |
| XX | Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | | | | |
| QY | 1 GCCAGCCCCCGATTGGGGCGACACTCCACATAGATCACTCCCTCTGAGGAACTACTG | 60 | | | |
| Db | 1 GCCAGCCCCCGATTGGGGCGACACTCCACATAGATCACTCCCTCTGAGGAACTACTG | 60 | | | |
| QY | 61 TCTTTCAGCAGAAAGCGTCTAGCCATCGGCTGTAGTGTGCTGCAGCCCTCCAGGAC | 120 | | | |
| Db | 61 TCTTTCAGCAGAAAGCGTCTAGCCATCGGCTGTAGTGTGCTGCAGCCCTCCAGGAC | 120 | | | |
| QY | 121 CCCCCCTCCCGGAGAGCCATAGTGCTCGGNAACGGTGTAGTACACCGGAATTGCCAG | 180 | | | |
| Db | 121 CCCCCCTCCCGGAGAGCCATAGTGCTCGGNAACGGTGTAGTACACCGGAATTGCCAG | 180 | | | |
| QY | 181 GACGACCGGCTCTTCTTGATCAACCCCGTCAATGCTTGGAGTTGGCGCTGCCCCC | 240 | | | |
| Db | 181 GACGACCGGCTCTTCTTGATCAACCCCGTCAATGCTTGGAGTTGGCGCTGCCCCC | 240 | | | |
| QY | 241 GCGAGACTGTAGCCGAGTGTGTGGTTCGGAAGCCCTTGTGTACTGCTGTATAGG | 300 | | | |
| Db | 241 GCGAGACTGTAGCCGAGTGTGTGGTTCGGAAGCCCTTGTGTACTGCTGTATAGG | 300 | | | |
| QY | 301 GTCTTTCGAGTCCCGGGAGTCTCGTAGCCGTCAATGCTTGGAGTTGGCGCTGCC | 360 | | | |
| Db | 301 GTCTTTCGAGTCCCGGGAGTCTCGTAGCCGTCAATGCTTGGAGTTGGCGCTGCC | 360 | | | |
| QY | 361 CTCAAGAGAAAAACCAAGGCGCGCCATGTTGAACAAGATGATGTCAGCGAGTTCTC | 420 | | | |
| Db | 361 CTCAAGAGAAAAACCAAGGCGCGCCATGTTGAACAAGATGATGTCAGCGAGTTCTC | 420 | | | |
| QY | 421 CGGCGCTTGGTGGAGAGCTTATTCGGTATGATGCTGGGCACACAGCAATCGGCTGCT | 480 | | | |
| Db | 421 CGGCGCTTGGTGGAGAGCTTATTCGGTATGATGCTGGGCACACAGCAATCGGCTGCT | 480 | | | |
| QY | 481 CTGATCCGCGCTGTTCCGCTGTAGCGAGCGCGCGCTTCTTTTGTCAAGACCG | 540 | | | |
| Db | 481 CTGATCCGCGCTGTTCCGCTGTAGCGAGCGCGCGCTTCTTTTGTCAAGACCG | 540 | | | |
| QY | 541 ACTGTGCGGTGCTTCCCTGAATGAATCGAGGACGAGGCGCGCTTATCGTGGCTG3CCA | 600 | | | |
| Db | 541 ACTGTGCGGTGCTTCCCTGAATGAATCGAGGACGAGGCGCGCTTATCGTGGCTG3CCA | 600 | | | |
| QY | 601 CGACGGCGCTTCTTGGCAGCTGTCTCGAGCTGTCTGACGAGCGGAGGAGTGGC | 660 | | | |

Db 1681 ATGGGATCTGATCTGGGGCTCGGTGACATGCTTTTACATGTTTACTCGAGGTAAAA 1740
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Db 1741 AACGTCTAGGCCCCCGGAACACACGGGACGTGTTTCTCTTGAABACAGATAATACC 1800
Qy 1801 ATGGCGCTATTACGGCTTACTCCCAACAGACGCGAGGCTTACTTGGCTGCATCATCACT 1860
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Qy 1861 AGCTTCACAGCGCGGACAGGAACACAGGTTCGAGGGGAGGTCCAAAGTGTCTCCACCGCA 1920
Db 1861 AGCTTCACAGCGCGGACAGGAACACAGGTTCGAGGGGAGGTCCAAAGTGTCTCCACCGCA 1920
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Db 2101 GGAGCTCGGACCTTACTTGTGTACGAGGCATGCCATGTCAATCTCCGTTGCCGCGG 2160
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Db 2161 GGCGACAGCAGGGGAGGCTACTCTCCCGCAGGCGGCTCTCTTCTTGAAGGCTCTTCG 2220
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Db 2281 ACCGAGGGTTCGGAAGCGGTGGACTTGTACCGCTCGAGTCTATGGAACCACTATG 2340
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Db 2341 CGGTCCCGGCTTTCACGAGCACTCGTCCCTCGGCGGTACCGCAGACATTCACAGTG 2400
Qy 2401 GGCATCTACAGCCCTTACTGCTAGCGGCAAGAGCACTAAGGTGCGGCTGCGTATGCA 2460
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Db 3721 GTCTTAGAGCTGTGCGCGGTTATGCTGACAAAGGAGGCTGCTATGTTGGGAGG 3780
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Db 3781 ATCATCTGTTCGGAAAGCGGCGCATCTTCCCGACAGGGAAGTCTTTTACCAGGAGTTC 3840
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RESULT 7

ABK91435
ID ABK91435 standard; DNA; 10690 BP.

XX ABK91435;

XX AC

XX XX

XX 15-NOV-2002 (first entry)

XX Hepatitis C virus vector construct pHVNeo.17m2.

XX HCV; ss; pHVNeo.17m2; adaptive mutation; liver failure; cirrhosis;

XX hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;

XX internal ribosome entry site; IRES; NS5A; HCV replication; mutant.

XX Hepatitis C virus.

OS Encephalomyocarditis virus.
OS Escherichia coli.
OS Enterobacteria phage T7.
OS Synthetic.

XX Key Location/Qualifiers
XX FH 1..341
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XX CDS 342..1181
XX /*tag= b
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XX misc_signal 1190..1800
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XX misc_feature 7992..10690
XX /*tag= g
XX /note= "Plasmid derived sequences"

XX WO200259321-A2.

XX 01-AUG-2002.

XX 16-JAN-2002; 2002WO-EP000526.

XX 23-JAN-2001; 2001US-0263479P.

XX (RICE-) 1ST RICERCHIE BIOL MOLECOLARE ANGELETTI.

XX De Francesco R, Migliaccio G, Paonessa G;

XX WPI; 2002-599793/64.

XX New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
XX NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
XX ribosome entry site (IRES) region, useful in studying HCV replication and
XX expression.

XX Claim 16; Page; 69pp; English.

XX The invention relates to nucleic acid molecules comprising altered HCV
XX NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
XX internal ribosome entry site (IRES) region coding for one or more NS3,
XX NS5A, or EMCV IRES mutations, respectively. The location of the mutations
XX are detailed in the specification. Also included are (1) an expression
XX vector comprising a nucleotide sequence coding for the altered nucleic
XX acids, which is transcriptionally coupled to an exogenous promoter; (2) a
XX recombinant cell human hepatoma cell comprising the altered nucleic acids
XX ; (3) a recombinant cell produced by introducing into a human hepatoma
XX cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
XX replicon enhanced cell or which containing a functional HCV replicon; (5)
XX an HCV replicon enhanced cells made in the method; and (6) measuring the
XX ability of a compound to affect HCV activity. The HCV replicons and HCV
XX replicon enhanced cells are useful in studying HCV replication and
XX expression, and HCV and host cell interactions, producing HCV RNA and
XX proteins, and providing a system for measuring the ability of a compound
XX to modulate one or more HCV activities e.g. to discover drugs which may
XX treat HCV mediated diseases such as liver failure, cirrhosis and
XX hepatocellular carcinoma. The present sequence is an HCV based vector
XX pHCNeo.17 mutant of the invention. Note: The present sequence is not
XX shown in the specification but was created by the indexer using the HCV
XX vector sequence appearing as ABK91412 and the information in Claim 16

XX Sequence 10690 BP; 2334 A; 3044 C; 2908 G; 2404 T; 0 U; 0 Other;

| | Query Match | 100.0%; | Score 7990.4; | DB 6; | Length 10690; |
|---------|--|-----------------|---------------|-----------|---------------|
| | Best Local Similarity | 100.0%; | Pred. No. 0; | | |
| | Matches 7991; | Conservative 0; | Mismatches 1; | Indels 0; | Gaps 0; |
| QY 1 | GCACGCCCGGATTTGGGGCGGACACTCCACCATAGATCACTCCCTCTGTGAGAACTACTG | 60 | | | |
| DB 1 | GCACGCCCGGATTTGGGGCGGACACTCCACCATAGATCACTCCCTCTGTGAGAACTACTG | 60 | | | |
| QY 61 | TCTTCACGAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGTGAGCCTCCAGGAC | 120 | | | |
| DB 61 | TCTTCACGAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGTGAGCCTCCAGGAC | 120 | | | |
| QY 121 | CCCCCTCCCGGAGAGCCATAGTGGTCTGGGAACCGGTAGATACACGGAAATGCCAG | 180 | | | |
| DB 121 | CCCCCTCCCGGAGAGCCATAGTGGTCTGGGAACCGGTAGATACACGGAAATGCCAG | 180 | | | |
| QY 181 | GACGACCGGGTCTTCTTGGATCAACCCCGCTCAATGCTCGAGATTTGGGGTCCGCC | 240 | | | |
| DB 181 | GACGACCGGGTCTTCTTGGATCAACCCCGCTCAATGCTCGAGATTTGGGGTCCGCC | 240 | | | |
| QY 241 | CGGAGACTGTAGCCGAGTAGTGTGGTTCGGAAGGCCCTTGTGTAATCGCTGATAGG | 300 | | | |
| DB 241 | CGGAGACTGTAGCCGAGTAGTGTGGTTCGGAAGGCCCTTGTGTAATCGCTGATAGG | 300 | | | |
| QY 301 | GTGCTTGGAGTGCCTCCGGAGGTCTCTAGACCGTGCACCATGAGCAAGTCTTAAC | 360 | | | |
| DB 301 | GTGCTTGGAGTGCCTCCGGAGGTCTCTAGACCGTGCACCATGAGCAAGTCTTAAC | 360 | | | |
| QY 361 | CTCAAGAAACCAACCAAGGGCGGCCCATGATTGAACAAGATGGATTGCACGAGTCTTC | 420 | | | |
| DB 361 | CTCAAGAAACCAACCAAGGGCGGCCCATGATTGAACAAGATGGATTGCACGAGTCTTC | 420 | | | |
| QY 421 | CGGCCGCTTGGGTGAGAGGCTATTCGGCTATGACTGGGCAACACAGCAATCGGCTCT | 480 | | | |
| DB 421 | CGGCCGCTTGGGTGAGAGGCTATTCGGCTATGACTGGGCAACACAGCAATCGGCTCT | 480 | | | |
| QY 481 | CTGATGCCGCGTGTCCGGCTGCAGGCGAGGGCGCCGGTCTTTTGTGAAGACCG | 540 | | | |
| DB 481 | CTGATGCCGCGTGTCCGGCTGCAGGCGAGGGCGCCGGTCTTTTGTGAAGACCG | 540 | | | |
| QY 541 | ACCTGTCCGGTGCCTGAATGAATCTGACGACGAGGCGCGGCTATCGTGGCTGGCCA | 600 | | | |
| DB 541 | ACCTGTCCGGTGCCTGAATGAATCTGACGACGAGGCGCGGCTATCGTGGCTGGCCA | 600 | | | |
| QY 601 | CGACGGCGTTCCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGACTGGC | 660 | | | |
| DB 601 | CGACGGCGTTCCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGACTGGC | 660 | | | |
| QY 661 | TGCTATTGGCGAAGTCCCGGGCAGGATCTCTGTCTATCTCACCTTGTCTCTCCGAGA | 720 | | | |
| DB 661 | TGCTATTGGCGAAGTCCCGGGCAGGATCTCTGTCTATCTCACCTTGTCTCTCCGAGA | 720 | | | |
| QY 721 | AAGTATCCATCATGGCTGATGCAATCGCGGCTGTGATCGCTTGTATCCGGTACCTGCC | 780 | | | |
| DB 721 | AAGTATCCATCATGGCTGATGCAATCGCGGCTGTGATCGCTTGTATCCGGTACCTGCC | 780 | | | |
| QY 781 | CATTTCACCAACCAAGCGAAACATCGCATCGAGCGACACGACTCGGATGGAAGCGGTC | 840 | | | |
| DB 781 | CATTTCACCAACCAAGCGAAACATCGCATCGAGCGACACGACTCGGATGGAAGCGGTC | 840 | | | |
| QY 841 | TTGTCGATCAGGATGATCTGGACGAGAGCATCAGGGGCTCGGCCAGCCGAACTGTTCG | 900 | | | |
| DB 841 | TTGTCGATCAGGATGATCTGGACGAGAGCATCAGGGGCTCGGCCAGCCGAACTGTTCG | 900 | | | |
| QY 901 | CCAGGCTCAAGGCGCATGCCCGAGGATCTCGTGTGACCCATGGCGGATGCCCT | 960 | | | |
| DB 901 | CCAGGCTCAAGGCGCATGCCCGAGGATCTCGTGTGACCCATGGCGGATGCCCT | 960 | | | |
| QY 961 | GCTTGCAGAAATCATGTGTGGAATAATGGCGCTTTTCTGGAATTCATCGACTGTGGCGGC | 1020 | | | |
| DB 961 | GCTTGCAGAAATCATGTGTGGAATAATGGCGCTTTTCTGGAATTCATCGACTGTGGCGGC | 1020 | | | |
| QY 1021 | TGGGTGTGGCGGACCCCTATCAGGACATAGCTTGGCTACCCGTGATTTGCTGAAGAGC | 1080 | | | |

| | | | |
|----|------|---|------|
| QY | 3241 | GAACGGCCCTCGGCATGTTTCGATTCTTCGTTCTGTCGAGTGTATGACGCGGGCTGT | 3300 |
| Db | 3241 | GAACGGCCCTCGGCATGTTTCGATTCTTCGTTCTGTCGAGTGTATGACGCGGGCTGT | 3300 |
| QY | 3301 | GCTTGGTAGAGCTACAGCCCGCGGAGACCTCAGTTAGTTGCGGGCTTACTAAACACA | 3360 |
| Db | 3301 | GCTTGGTAGAGCTACAGCCCGCGGAGACCTCAGTTAGTTGCGGGCTTACTAAACACA | 3360 |
| QY | 3361 | CCAGGTTGCGCGTCTGCAGACCATCTGAGTTCTGGGAGAGCGTTTTCACAGGCTC | 3420 |
| Db | 3361 | CCAGGTTGCGCGTCTGCAGACCATCTGAGTTCTGGGAGAGCGTTTTCACAGGCTC | 3420 |
| QY | 3421 | ACCACATAGAGCCCACTTTCTGTCCAGACTAAGCAGGAGGAGACAACTTCCCTTAC | 3480 |
| Db | 3421 | ACCACATAGAGCCCACTTTCTGTCCAGACTAAGCAGGAGGAGACAACTTCCCTTAC | 3480 |
| QY | 3481 | CTGGTAGATACAGGCTACCGGTGTCGCGCAGGGCTCAGGCTCCACCTCCATCGTGGAC | 3540 |
| Db | 3481 | CTGGTAGATACAGGCTACCGGTGTCGCGCAGGGCTCAGGCTCCACCTCCATCGTGGAC | 3540 |
| QY | 3541 | CAAAATGGAGTGTCTCATACGGCTAAAGCCTACGCTGCAACCGGCTCAAGCTCCATCGTGGCT | 3600 |
| Db | 3541 | CAAAATGGAGTGTCTCATACGGCTAAAGCCTACGCTGCAACCGGCTCAAGCTCCATCGTGGCT | 3600 |
| QY | 3601 | TATAGGCTGGAGCGGTTCAAAACGAGTTACTACACACACACCCCAATAACCAATAATC | 3660 |
| Db | 3601 | TATAGGCTGGAGCGGTTCAAAACGAGTTACTACACACACACCCCAATAACCAATAATC | 3660 |
| QY | 3661 | ATGCGATCATGTCGGCTGACCTGGAGTGTGTACAGACCTGGGTGTGTAGGCGGA | 3720 |
| Db | 3661 | ATGCGATCATGTCGGCTGACCTGGAGTGTGTACAGACCTGGGTGTGTAGGCGGA | 3720 |
| QY | 3721 | GTCCTAGAGCTCTGGCGCGTATGCTGACACAGCAGCGGTGTCATTTACCGGAGTTC | 3780 |
| Db | 3721 | GTCCTAGAGCTCTGGCGCGTATGCTGACACAGCAGCGGTGTCATTTACCGGAGTTC | 3780 |
| QY | 3781 | ATCATCTTGTCCGAAAGCCGGCCATCATTTCCCGACAGGGAAGTCTTTTACCGGAGTTC | 3840 |
| Db | 3781 | ATCATCTTGTCCGAAAGCCGGCCATCATTTCCCGACAGGGAAGTCTTTTACCGGAGTTC | 3840 |
| QY | 3841 | GATGAGATGAAGTGGCTTACACCTCTCTTACATGGAACAGGGAATGCACTCGCC | 3900 |
| Db | 3841 | GATGAGATGAAGTGGCTTACACCTCTCTTACATGGAACAGGGAATGCACTCGCC | 3900 |
| QY | 3901 | GAACAAATCAACAGAGGCAATCGGTTGCTGCAACAGCCACCAAGCAAGCGGAGGCT | 3960 |
| Db | 3901 | GAACAAATCAACAGAGGCAATCGGTTGCTGCAACAGCCACCAAGCAAGCGGAGGCT | 3960 |
| QY | 3961 | GCTGCTCCCGTGGGAATCCAAAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG | 4020 |
| Db | 3961 | GCTGCTCCCGTGGGAATCCAAAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG | 4020 |
| QY | 4021 | TGGAATTTATCAGCGGATACATATTTAGCAGGCTTGTCCACTGTGCTGGCAACCCC | 4080 |
| Db | 4021 | TGGAATTTATCAGCGGATACATATTTAGCAGGCTTGTCCACTGTGCTGGCAACCCC | 4080 |
| QY | 4081 | GCATAGATCACTGATGGCATTCACAGCCTCTATCACAGCGCGCTCACACCCACAT | 4140 |
| Db | 4081 | GCATAGATCACTGATGGCATTCACAGCCTCTATCACAGCGCGCTCACACCCACAT | 4140 |
| QY | 4141 | ACCTCTCTGTTTAACTCTCTGGGGGATGGTGGCGCCCAACTTGTCTCTCCAGCGCT | 4200 |
| Db | 4141 | ACCTCTCTGTTTAACTCTCTGGGGGATGGTGGCGCCCAACTTGTCTCTCCAGCGCT | 4200 |
| QY | 4201 | GCTTCTGCTTTTCTAGCGCGGATCGCTGGAGCGGCTTGGCAGCATAGCCCTTGGG | 4260 |
| Db | 4201 | GCTTCTGCTTTTCTAGCGCGGATCGCTGGAGCGGCTTGGCAGCATAGCCCTTGGG | 4260 |
| QY | 4261 | AAGGTCTTGTGATATTTTGGCAGGTTATGAGCAGGGGTGCGAGCGGCTGTGGCC | 4320 |
| Db | 4261 | AAGGTCTTGTGATATTTTGGCAGGTTATGAGCAGGGGTGCGAGCGGCTGTGGCC | 4320 |
| QY | 4321 | TTTAAAGTTCATAGCGCGAGATGCCTCCACCGAGGACCTGGTTAACTACTCCCTGCT | 4380 |
| Db | 4321 | TTTAAAGTTCATAGCGCGAGATGCCTCCACCGAGGACCTGGTTAACTACTCCCTGCT | 4380 |
| QY | 4381 | ATCCTCTCTCCCTGGCGCCCTAGTGTGCGGGTCTGTGTCGCGAGGATATCTCGTGGCAC | 4440 |
| Db | 4381 | ATCCTCTCTCCCTGGCGCCCTAGTGTGCGGGTCTGTGTCGCGAGGATATCTCGTGGCAC | 4440 |
| QY | 4441 | GTGGGCGCAGGGAGGGGCTGTGTCAGTGTGATGTAACCGGCTGTAGTCGTTTCGCTCGCG | 4500 |
| Db | 4441 | GTGGGCGCAGGGAGGGGCTGTGTCAGTGTGATGTAACCGGCTGTAGTCGTTTCGCTCGCG | 4500 |
| QY | 4501 | GCTAAACAGCTCTCCCGCAGCCTATGTGCTCAGAGCGACGCTGACAGCGTGTCACT | 4560 |
| Db | 4501 | GCTAAACAGCTCTCCCGCAGCCTATGTGCTCAGAGCGACGCTGACAGCGTGTCACT | 4560 |
| QY | 4561 | CAGATCCTCTCTAGTCTTTACCATCACTCAGTGTCTGTAAGAGGCTTCCACAGTGGATCAAC | 4620 |
| Db | 4561 | CAGATCCTCTCTAGTCTTTACCATCACTCAGTGTCTGTAAGAGGCTTCCACAGTGGATCAAC | 4620 |
| QY | 4621 | GAGGACTGCTCCAGCCCATGCTCCGGCTGTGGCTTAAGAGATGTTGGGATGATATGC | 4680 |
| Db | 4621 | GAGGACTGCTCCAGCCCATGCTCCGGCTGTGGCTTAAGAGATGTTGGGATGATATGC | 4680 |
| QY | 4681 | ACGGTGTGACTGATTTCAAGACCTGCTCCAGTCCAGTCCAGCTCTCCCGCGGATTCGCGGA | 4740 |
| Db | 4681 | ACGGTGTGACTGATTTCAAGACCTGCTCCAGTCCAGTCCAGCTCTCCCGCGGATTCGCGGA | 4740 |
| QY | 4741 | GTCCCTCTCTCTCATGTCAACGCTGGGTCAAGGAGTCTGGCGGGCGACGGCATCATG | 4800 |
| Db | 4741 | GTCCCTCTCTCTCATGTCAACGCTGGGTCAAGGAGTCTGGCGGGCGACGGCATCATG | 4800 |
| QY | 4801 | CAAAACCACTGCTGAGTGTGAGCAGATCAACCGGATGTAAGAGATGTTGGGATGATATGC | 4860 |
| Db | 4801 | CAAAACCACTGCTGAGTGTGAGCAGATCAACCGGATGTAAGAGATGTTGGGATGATATGC | 4860 |
| QY | 4861 | ATCGTGGGGCTTAGGACTCTGTAGTAAACAGCTGCAATGGAACATTTCCCCATTAAGCGGTAC | 4920 |
| Db | 4861 | ATCGTGGGGCTTAGGACTCTGTAGTAAACAGCTGCAATGGAACATTTCCCCATTAAGCGGTAC | 4920 |
| QY | 4921 | ACCAACGCGCCCTGCAAGCTCTCCCGCGCCCAAAATTTATTTAGGGCGCTGTGGCGGGT | 4980 |
| Db | 4921 | ACCAACGCGCCCTGCAAGCTCTCCCGCGCCCAAAATTTATTTAGGGCGCTGTGGCGGGT | 4980 |
| QY | 4981 | GCTGCTGAGAGTACGTTGAGGTTTACCGGGTGGGGATTTCCACTACGTTGACGGGATG | 5040 |
| Db | 4981 | GCTGCTGAGAGTACGTTGAGGTTTACCGGGTGGGGATTTCCACTACGTTGACGGGATG | 5040 |
| QY | 5041 | ACCACTGACAACTAAAGTSCCGTGTCAAGTTCGGGCGCCCGAAATTTCTTTCAGAGATG | 5100 |
| Db | 5041 | ACCACTGACAACTAAAGTSCCGTGTCAAGTTCGGGCGCCCGAAATTTCTTTCAGAGATG | 5100 |
| QY | 5101 | GATGGGCTGGTTGACAGGTACGCTCCAGCGTGCAGAACCCCTCTTACGGGAGGAGTTC | 5160 |
| Db | 5101 | GATGGGCTGGTTGACAGGTACGCTCCAGCGTGCAGAACCCCTCTTACGGGAGGAGTTC | 5160 |
| QY | 5161 | ACATTTCTGCTGGCTCAATCAATACCTGTTGGGTTCACAGTCCCATGCGAGCGCGAA | 5220 |
| Db | 5161 | ACATTTCTGCTGGCTCAATCAATACCTGTTGGGTTCACAGTCCCATGCGAGCGCGAA | 5220 |
| QY | 5221 | CCGAGCTAGCAGTGTCTCTCCATGCTCACCGCCCTCCCTCCACATTAAGCGGAGACG | 5280 |
| Db | 5221 | CCGAGCTAGCAGTGTCTCTCCATGCTCACCGCCCTCCCTCCACATTAAGCGGAGACG | 5280 |
| QY | 5281 | GCTAAGCTAGGCTGCGCCAGGGGATCTCCCGCTCTTCCGCGAGCTCATCAGTACCCAG | 5340 |
| Db | 5281 | GCTAAGCTAGGCTGCGCCAGGGGATCTCCCGCTCTTCCGCGAGCTCATCAGTACCCAG | 5340 |
| QY | 5341 | CTGTCTGCGCTCTTCTTGAAGGCAATGCACTAACCCGCTATGACCTCCCGGACGCTGAC | 5400 |
| Db | 5341 | CTGTCTGCGCTCTTCTTGAAGGCAATGCACTAACCCGCTATGACCTCCCGGACGCTGAC | 5400 |
| QY | 5401 | CTCATCGAGCCCACTCTCTGTCGGGAGGAGATGGGCGGGAACATCATCCCGCTGGAG | 5460 |

[illegible]

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QY 7621 TTATCCAGTGGTTCCTGCTGTTTACAGCGGGGAGACATATATACAGCCTGCTCTGT 7680
Db 7621 TTATCCAGTGGTTCCTGCTGTTTACAGCGGGGAGACATATATACAGCCTGCTCTGT 7680
QY 7681 GCCCGACCCCGCTGGTTCATGTGGTGCCTTACTCTTCTGTAGGGGTAGGCATCTAT 7740
Db 7681 GCCCGACCCCGCTGGTTCATGTGGTGCCTTACTCTTCTGTAGGGGTAGGCATCTAT 7740
QY 7741 CTACTCCCCAACCCGATGAACGGGGAGCTAAACACATCCAGGCCAATAGGCCATCTGTTT 7800
Db 7741 CTACTCCCCAACCCGATGAACGGGGAGCTAAACACATCCAGGCCAATAGGCCATCTGTTT 7800
QY 7801 TTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
Db 7801 TTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
QY 7861 TTTTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
Db 7861 TTTTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
QY 7921 TAGCTGTGAAGGTCCTGAGCGGCTTGACCTGCAGAGAGTGTGTATCTGGCCTCTCTGC 7980
Db 7921 TAGCTGTGAAGGTCCTGAGCGGCTTGACCTGCAGAGAGTGTGTATCTGGCCTCTCTGC 7980
QY 7981 AGATCAAGTACT 7992
Db 7981 AGATCAAGTACT 7992

RESULT 8
ABK91243
ID ABK91243 standard; DNA; 10690 BP.
XX AC ABK91243;
XX AC
DT 15-NOV-2002 (first entry)
DE Hepatitis C virus vector construct pHCVNeo.17.m1.
XX KW HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;
KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
KW internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
XX OS Hepatitis C virus.
OS Encephalomyocarditis virus.
OS Escherichia coli.
OS Enterobacteria phage T7.
OS Synthetic.

FH Key Location/Qualifiers
FT 5'UTR 1..341
FT /*tag= a
FT CDS 342..1181
FT /*tag= b
FT /product= "Core-neo fusion protein"
FT misc_signal 1190..1800
FT /*tag= c
FT /label= IRES
FT 1801..7758
FT /*tag= d
FT /product= "Polyprotein"
FT /note= "Comprising NS3, NS4A, NS4B, NS5A and NS5B"
FT mutation replace(4847,A)
FT /*tag= e
FT 7759..7991
FT /*tag= f
FT misc_feature 7992..10690
FT /*tag= g
FT /note= "Plasmid derived sequences"
XX PN WO200259321-A2.

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XX 01-AUG-2002.
PD 16-JAN-2002; 2002WO-BF000526.
XX 23-JAN-2001; 2001US-0263479P.
XX (RICE-) IST RICERHE BIOL MOLECOLARE ANGELETTI.
XX De Francesco R, Migliaiaccio G, Paonessa G;
XX WPI; 2002-599793/64.
XX New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
XX NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
XX ribosome entry site (IRES) region, useful in studying HCV replication and
XX expression.
XX Example 1; Page; 69pp; English.
XX The invention relates to nucleic acid molecules comprising altered HCV
XX NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
XX internal ribosome entry site (IRES) region coding for one or more NS3,
XX NS5A, or EMCV IRES mutations, respectively. The location of the mutations
XX are detailed in the specification. Also included are (1) an expression
XX vector comprising a nucleotide sequence coding for the altered nucleic
XX acids, which is transcriptionally coupled to an exogenous promoter; (2) a
XX recombinant cell human hepatoma cell comprising the altered nucleic acids
XX ; (3) a recombinant cell produced by introducing into a human hepatoma
XX cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
XX replicon enhanced cell or which containing a functional HCV replicon; (5)
XX an HCV replicon enhanced cells made in the method; and (6) measuring the
XX ability of a compound to affect HCV activity. The HCV replicons and HCV
XX replicon enhanced cells are useful in studying HCV replication and
XX expression, and HCV and host cell interactions, producing HCV RNA and
XX proteins, and providing a system for measuring the ability of a compound
XX to modulate one or more HCV activities e.g. to discover drugs which may
XX treat HCV mediated diseases such as liver failure, cirrhosis and
XX hepatocellular carcinoma. The present sequence is an HCV based vector
XX pHCVNeo.17 mutant of the invention. Note: The present sequence is not
XX shown in the specification but was created by the indexer using the HCV
XX vector sequence appearing as ABK91412 and the information in example 1
XX SQ Sequence 10690 BP; 2333 A; 3046 C; 2908 G; 2403 T; 0 U; 0 Other;

Query Match 100.0%; Score 7990.4; DB 6; Length 10690;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCAGCCCCCGATTGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAACACTG 60
Db 1 GCCAGCCCCCGATTGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAACACTG 60
QY 61 TCTTTCAGCAGAAAGCGTCTAGCCATGGGTTAGTATGAGTGTGTCGACGCTCCAGGAC 120
Db 61 TCTTTCAGCAGAAAGCGTCTAGCCATGGGTTAGTATGAGTGTGTCGACGCTCCAGGAC 120
QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATTGCCAG 180
Db 121 CCCCCCTCCCGGAGAGCCATAGTGTCTCGGAAACCGGTGAGTACACCGGAATTGCCAG 180
QY 181 GAGACCGGGTCTTCTTTGGATCAACCCGCTCAATGCTGGAGATTGGGGCGTCCCCC 240
Db 181 GAGACCGGGTCTTCTTTGGATCAACCCGCTCAATGCTGGAGATTGGGGCGTCCCCC 240
QY 241 GCGAGACTCTAGCCGAGTAGTGTGGTTCGGAAGGCGCTTGTGTACTGCTGTAGG 300
Db 241 GCGAGACTCTAGCCGAGTAGTGTGGTTCGGAAGGCGCTTGTGTACTGCTGTAGG 300
QY 301 GTGCTTGGAGTCCCGGGAGGTCTCGTAGACCGGTGACCATGACGACGAATCTTAAC 360
Db 301 GTGCTTGGAGTCCCGGGAGGTCTCGTAGACCGGTGACCATGACGACGAATCTTAAC 360

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QY 361 CTCAAGAAACAAAGGGCGCCATGATTGAACAAGATGGATTGACGCGAGTTCTC 420
Db 361 CTCAAGAAACAAAGGGCGCCATGATTGAACAAGATGGATTGACGCGAGTTCTC 420
QY 421 CGGCGCTTGGGTGGAGAGGCTATTTCGGCTATGACTGGGCAACAAGCAATCGGCTGCT 480
Db 421 CGGCGCTTGGGTGGAGAGGCTATTTCGGCTATGACTGGGCAACAAGCAATCGGCTGCT 480
QY 481 CTGATGCGCGCTGTTCCGGCTGTCAGCGCAGGGGCGCCGGTCTCTTTTGTCAAGACCG 540
Db 481 CTGATGCGCGCTGTTCCGGCTGTCAGCGCAGGGGCGCCGGTCTCTTTTGTCAAGACCG 540
QY 541 ACCTGTCGGTGCCTCGAATGAATGCAGGACAGGCGCGGCTATCGTGGCTGGCCA 600
Db 541 ACCTGTCGGTGCCTCGAATGAATGCAGGACAGGCGCGGCTATCGTGGCTGGCCA 600
QY 601 CGACGGGGTTCCTTTCGGCAGCTGTGCTCGACGTTGTCACTGAAGCGGAAGGACTGGC 660
Db 601 CGACGGGGTTCCTTTCGGCAGCTGTGCTCGACGTTGTCACTGAAGCGGAAGGACTGGC 660
QY 661 TCGTATTGGGGAAGTCCGGGCGGAGGATCTCTGTCACTCTCACCTTGTCTCTGCGGAGA 720
Db 661 TCGTATTGGGGAAGTCCGGGCGGAGGATCTCTGTCACTCTCACCTTGTCTCTGCGGAGA 720
QY 721 AAGTATCCATATGCTGATGCAATGCGGCGGCTGCATACGCTTGTATCCGGCTACCTGCC 780
Db 721 AAGTATCCATATGCTGATGCAATGCGGCGGCTGCATACGCTTGTATCCGGCTACCTGCC 780
QY 781 CATTCGACCAACCAAGCGAACAATCGCATCGAGGAGCAGTACTCGGATGGAAGCGGTC 840
Db 781 CATTCGACCAACCAAGCGAACAATCGCATCGAGGAGCAGTACTCGGATGGAAGCGGTC 840
QY 841 TTGTCGATCAGATGATCTGGAGAGAGCATCAGGGGCTCGGCGCAGCGCACTCTTCG 900
Db 841 TTGTCGATCAGATGATCTGGAGAGAGCATCAGGGGCTCGGCGCAGCGCACTCTTCG 900
QY 901 CCAAGGCTCAAGGCGCGCATGCGGACGCGAGGATCTCGTGTGACCCATGGCGATGCCCT 960
Db 901 CCAAGGCTCAAGGCGCGCATGCGGACGCGAGGATCTCGTGTGACCCATGGCGATGCCCT 960
QY 961 GCTTGGCGGAATCATGTTGGAAATGGCGCTTTTCTGGATTCATCGACTGTGGCGGC 1020
Db 961 GCTTGGCGGAATCATGTTGGAAATGGCGCTTTTCTGGATTCATCGACTGTGGCGGC 1020
QY 1021 TGGGTGGCGGACCGCTATCAGACATACGTTGGCTACCGCTGATTTGCTGAAGAGC 1080
Db 1021 TGGGTGGCGGACCGCTATCAGACATACGTTGGCTACCGCTGATTTGCTGAAGAGC 1080
QY 1081 TTGGCGGCAATGGGCTGACCGCTTCTCGTGTCTTACGGTATCGCGCTCCCGATTCGC 1140
Db 1081 TTGGCGGCAATGGGCTGACCGCTTCTCGTGTCTTACGGTATCGCGCTCCCGATTCGC 1140
QY 1141 AGCGATPCGCTTCTATCGCTTCTTGAAGATTCGCTTGAATTCATCGACTGTGGCGGC 1200
Db 1141 AGCGATPCGCTTCTATCGCTTCTTGAAGATTCGCTTGAATTCATCGACTGTGGCGGC 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCTTCTCCCTCCCGCTTACGTTACTTGGC 1260
Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCTTCTCCCTCCCGCTTACGTTACTTGGC 1260
QY 1261 CGAAGCGCTTGAATGAAGCGGCTGTCGTTGCTCTATATGTTATTTTCCACATATG 1320
Db 1261 CGAAGCGCTTGAATGAAGCGGCTGTCGTTGCTCTATATGTTATTTTCCACATATG 1320
QY 1321 CCGTCTTTTGGCAATGAGGGCCGGAAACCTGGCCCTGCTCTTTCGACGAGCATTCCT 1380
Db 1321 CCGTCTTTTGGCAATGAGGGCCGGAAACCTGGCCCTGCTCTTTCGACGAGCATTCCT 1380
QY 1381 AGGGCTCTTCCCTCTCGCCAAAGGAATGCAAGGCTCTGTTGAATGCTGTAAGGAGCA 1440
Db 1381 AGGGCTCTTCCCTCTCGCCAAAGGAATGCAAGGCTCTGTTGAATGCTGTAAGGAGCA 1440
QY 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACAACGCTCTGTAGCGACCTTTTGCAGGCGCG 1500

Db 1441 GTTCTCTGGAAGCTTCTTGAAGACAAACAACGCTCTGTAGCGACCTTTTGCAGGCGCG 1500
QY 1501 AACCCCCCACCCTGGCGCAGGTGCTCTGCGGCAAAAGCCACGCTGTATAGATACACT 1560
Db 1501 AACCCCCCACCCTGGCGCAGGTGCTCTGCGGCAAAAGCCACGCTGTATAGATACACT 1560
QY 1561 GCAAAGGGGCAAAACCCAGTGCACGTTGTGAGTTGGATAGTTGTGGAAGAGTCAAA 1620
Db 1561 GCAAAGGGGCAAAACCCAGTGCACGTTGTGAGTTGGATAGTTGTGGAAGAGTCAAA 1620
QY 1621 TGGCTCTCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAAGAGTACCCCATGT 1680
Db 1621 TGGCTCTCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAAGAGTACCCCATGT 1680
QY 1681 ATGGGATCTGATCTGGGCTCGGTGCACTGCTTTAATGTTGTTAGTTCGAGGTTAAA 1740
Db 1681 ATGGGATCTGATCTGGGCTCGGTGCACTGCTTTAATGTTGTTAGTTCGAGGTTAAA 1740
QY 1741 AACGCTAGGCCCCCGGAAACACGCGGAGCGTGTTCCTTTGAAAACACCATATATCC 1800
Db 1741 AACGCTAGGCCCCCGGAAACACGCGGAGCGTGTTCCTTTGAAAACACCATATATCC 1800
QY 1801 ATGGCGCTTATTACGCTCTACTCCCAACAGACGCGAGGCTACTTGGCTGCAATCACT 1860
Db 1801 ATGGCGCTTATTACGCTCTACTCCCAACAGACGCGAGGCTACTTGGCTGCAATCACT 1860
QY 1861 AGCCTCACAGGCGGACAGGAAACAGGTCGAGGGGAGGTCGAAGTGTCTCCACCGCA 1920
Db 1861 AGCCTCACAGGCGGACAGGAAACAGGTCGAGGGGAGGTCGAAGTGTCTCCACCGCA 1920
QY 1921 ACAATATCTTCTCGGACCTCGCTCAATGCGGTGTGTTGAGCTGCTATCATGTGTC 1980
Db 1921 ACAATATCTTCTCGGACCTCGCTCAATGCGGTGTGTTGAGCTGCTATCATGTGTC 1980
QY 1981 GGCTCAAGACCTTTCGCGCCCAAGAGGCCAATCACCCAAATGTACACCAATGTGGAC 2040
Db 1981 GGCTCAAGACCTTTCGCGCCCAAGAGGCCAATCACCCAAATGTACACCAATGTGGAC 2040
QY 2041 CAGGACCTCGTGGCTGGCAAGCGCCCCCGGGCGGCTTCTTGAACCATGCACTGC 2100
Db 2041 CAGGACCTCGTGGCTGGCAAGCGCCCCCGGGCGGCTTCTTGAACCATGCACTGC 2100
QY 2101 GGCAGCTCGGACCTTTACTTGTGTCAAGGATCGCGATGTCATTCGGGTGCGCGCGG 2160
Db 2101 GGCAGCTCGGACCTTTACTTGTGTCAAGGATCGCGATGTCATTCGGGTGCGCGCGG 2160
QY 2161 GGCAGCAGCAGGCGGAGCTTCTCTCCCGCAGGCGCTCTCTTACTTGAAGGCTCTTCG 2220
Db 2161 GGCAGCAGCAGGCGGAGCTTCTCTCCCGCAGGCGCTCTCTTACTTGAAGGCTCTTCG 2220
QY 2221 GGCAGTCCACTGCTCTGCCCTCGGGGCAAGCTGTGGGCAATCTTTCGGGTGCGGTGTC 2280
Db 2221 GGCAGTCCACTGCTCTGCCCTCGGGGCAAGCTGTGGGCAATCTTTCGGGTGCGGTGTC 2280
QY 2281 ACCGAGGGGTTCGGAAGGCGGTGGACTTTGTACCCGTCAGTCTATGGAACACCACTATG 2340
Db 2281 ACCGAGGGGTTCGGAAGGCGGTGGACTTTGTACCCGTCAGTCTATGGAACACCACTATG 2340
QY 2341 CGGTCCCGGTCTTTCAGGACAACTCGTCCCTCGCGCCGCTACCGCAGACATTCAGAGTG 2400
Db 2341 CGGTCCCGGTCTTTCAGGACAACTCGTCCCTCGCGCCGCTACCGCAGACATTCAGAGTG 2400
QY 2401 GCGCATCTACAGCCCCCTACTGTTAGCGGCAAGAGCACTAAGGTGCGGCTGCGGTATGCA 2460
Db 2401 GCGCATCTACAGCCCCCTACTGTTAGCGGCAAGAGCACTAAGGTGCGGCTGCGGTATGCA 2460
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QY 2521 GCGTATATGCTAAGGACATGTTATCGACCTTAACATCAGAACCGGGGTGAGGACATC 2580

Db 2521 GCGTATATGCTAAGGCACATGATGATCGACCCCTAAACATCAGAAACCGGGGTAAAGCAATC 2580
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Db 2581 ACCACGGGTGCCCCATACAGTACTCCACCTATGCAAGTTTCTTGCCGACCGTGTGTGC 2640
QY 2641 TCTGGGGGGCGCTATACATCATATAATGTGATGATGCCACTCAACTGACTCGACCACT 2700
Db 2641 TCTGGGGGGCGCTATACATCATATAATGTGATGATGCCACTCAACTGACTCGACCACT 2700
QY 2701 ATCTGGGCATCGGCACAGTCTCTGACCAAGCGGAGACGGCTGGAGCGGACTCGTCGTG 2760
Db 2701 ATCTGGGCATCGGCACAGTCTCTGACCAAGCGGAGACGGCTGGAGCGGACTCGTCGTG 2760
QY 2761 CTGCGCACCGCTACGGCTCGGGATCGGTCAACGCTGCCACATCCAAACATCGAGAGGTG 2820
Db 2761 CTGCGCACCGCTACGGCTCGGGATCGGTCAACGCTGCCACATCCAAACATCGAGAGGTG 2820
QY 2821 GCTGTGTCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC 2880
Db 2821 GCTGTGTCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC 2880
QY 2881 AAGGGGGGAGGACCTCATTTTCTGCCATTCCAAAGAGAAATGTCAGAGCTCGCCGG 2940
Db 2881 AAGGGGGGAGGACCTCATTTTCTGCCATTCCAAAGAGAAATGTCAGAGCTCGCCGG 2940
QY 2941 AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTACCGGGGCTTGTATGATCCGTC 3000
Db 2941 AAGCTGTCCGGCTCGGACTCAATGCTGTAGCATATTACCGGGGCTTGTATGATCCGTC 3000
QY 3001 ATACCACTAGCGGAGAGCTCATTTGCTGTAGCAACGGAGCTCTAATGACGGGCTTTACC 3060
Db 3001 ATACCACTAGCGGAGAGCTCATTTGCTGTAGCAACGGAGCTCTAATGACGGGCTTTACC 3060
QY 3061 GCGGATTTGCACTCAGTGCATCGACTGCAATCATGTGTCACCCAGAGTGCATTCAGC 3120
Db 3061 GCGGATTTGCACTCAGTGCATCGACTGCAATCATGTGTCACCCAGAGTGCATTCAGC 3120
QY 3121 CTGACCCGACCTTACCAATTGACAGCAGCCGCTGCCAAGACCGGGTGTACGCTCG 3180
Db 3121 CTGACCCGACCTTACCAATTGACAGCAGCCGCTGCCAAGACCGGGTGTACGCTCG 3180
QY 3181 CAGCGGGGAGGACGCTGTAGGGGAGGATGGGCAATTAACGTTTGTGACTCCAGGA 3240
Db 3181 CAGCGGGGAGGACGCTGTAGGGGAGGATGGGCAATTAACGTTTGTGACTCCAGGA 3240
QY 3241 GAACGGCCCTCGGCGATGTTCCGATTCCTCGGTTCTGTGCGAGTCTATGACCGGGCTGT 3300
Db 3241 GAACGGCCCTCGGCGATGTTCCGATTCCTCGGTTCTGTGCGAGTCTATGACCGGGCTGT 3300
QY 3301 GCTTGTACAGGCTACGCGCGCGGAGACCTCAGTTAGGTTGCGGGCTTACCTAAACACA 3360
Db 3301 GCTTGTACAGGCTACGCGCGCGGAGACCTCAGTTAGGTTGCGGGCTTACCTAAACACA 3360
QY 3361 CCAGGTTGCGGCTGTCAGGACCATCTGGAGTTCTGGAGAGCGTCTTTACAGGCTC 3420
Db 3361 CCAGGTTGCGGCTGTCAGGACCATCTGGAGTTCTGGAGAGCGTCTTTACAGGCTC 3420
QY 3421 ACCACATAGACGCCATTTCTTGTCAGACTAAGCAGGACGAGACAACTTCCCTAC 3480
Db 3421 ACCACATAGACGCCATTTCTTGTCAGACTAAGCAGGACGAGACAACTTCCCTAC 3480
QY 3481 CTGGTAGCATACAGGCTACGGTGTGCGCGGAGGCTCAGGCTCCACCTCCATCGTGGAC 3540
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Db 3541 CAAATGTGAAGTGTCTCATACGGCTAAAGCTTACGCTGACGCGGCAACGCGCCCTGCTG 3600
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Db 3601 TATAGGCTGGAGCCGTTCAAAACGAGGTTTACTACACACACCCCATTAACCAATACATC 3660

QY 3661 ATGCGATGCTGTCGGCTGACCTGGAGGTGCTGCACGAGCACCTGGGTGCTGGTAGCGGA 3720
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Db 3781 ATCACTTGTCCGGAAGCCGCCATCAITTCGCGACAGGAAAGTCTTTTACCGGAGTTTC 3840
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Db 4021 TGGATTTTATCAGCGGAGTACAATATTTAGAGGCTTGTCCACTCTGCTGGCAACCCC 4080
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Db 4081 GCGATAGCATCACTGATGGCATTCACAGCCTTATCACAGCCTTATCACAGCCGCTCACCACCAACAT 4140
QY 4141 ACCCTCTGTTTAAACATCTCTGGGGGATGGTGGCGGCCAACTTGTCTTCCAGCGCT 4200
Db 4141 ACCCTCTGTTTAAACATCTCTGGGGGATGGTGGCGGCCAACTTGTCTTCCAGCGCT 4200
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Db 4201 GCTTCTGCTTCTGAGGCGCGGATGCTGAGAGGCTGTTGGCAGCATAGGCTTGGG 4260
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Db 4681 ACGGTGTGACTGATTTCAAGACCTGGCTCCAGTCCAGTCTCTGCGGATTTGCCGGA 4740

Db 6901 AAGCTCCAGGACTGCAGATGCTCGTATGCGGAGACGACCTGTCTGTTATCTGTGAAAGC 6960
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Db 7321 ATCTAGGGGCTGTACTCCATGAGCCACTGACCTACCTCAGATCATCAAGACTC 7380
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Db 7921 TAGCTGTAAGGTCCGTGAGCGCTGACTGACGAGAGTGTGATCTAGCTGCTCTCTG 7980
QY 7981 AGATCAAGTACT 7992
Db 7981 AGATCAAGTACT 7992

RESULT 9
ABK91434
ID ABK91434 standard; DNA; 10690 BP.
XX AC ABK91434;
XX AC ABK91434;
DT 15-NOV-2002 (first entry)
XX Hepatitis C virus vector construct pHCVNeo.17m0.
DE HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;
XX hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
KW internal ribosome entry site; IRES; NS5A; HCV replication; mutant.
XX Hepatitis C virus.
OS Encephalomyocarditis virus.
OS Escherichia coli.
OS Enterobacteria phage T7.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..341
FT /tag= a
FT CDS 342..1181
FT /tag= b
FT /product= "Core-neo fusion protein"
FT misc_signal 1190..1800
FT /tag= c
FT /label= IRES
FT /note= "Internal ribosome entry site from EMCV"
FT CDS 1801..7758
FT /tag= d
FT /product= "Polyprotein"
FT /note= "Comprising NS3, NS4A, NS4B, NS5A and NS5B"
FT mutation replace(5337,C)
FT /tag= e
FT 3'UTR 7759..7991
FT /tag= f
FT misc_feature 7992..10690
FT /tag= g
FT /note= "Plasmid derived sequences"
WO200259321-A2.
XX
PD 01-AUG-2002.
XX
PF 16-JAN-2002; 2002WO-EP000526.
XX
PR 23-JAN-2001; 2001US-0263479P.
XX
PA (RICE-) IST RICERHE BIOL MOLECOLARE ANGELETTI.
XX De Francesco R, Migliaccio G, Paonessa G;
PI
XX
DR WPI; 2002-599793/64.
XX
XX New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
PT NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
PT ribosome entry site (IRES) region, useful in studying HCV replication and
PT expression.
XX
PS Claim 16; Page; 69pp; English.
XX
CC The invention relates to nucleic acid molecules comprising altered HCV
CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
CC internal ribosome entry site (IRES) region coding for one or more NS3,
CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations
CC are detailed in the specification. Also included are (1) an expression
CC vector comprising a nucleotide sequence coding for the altered nucleic
CC acids, which is transcriptionally coupled to an exogenous promoter; (2) a
CC recombinant cell human hepatoma cell comprising the altered nucleic acids

CC ; (3) a recombinant cell produced by introducing into a human hepatoma
CC cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
CC replicon enhanced cell or which containing a functional HCV replicon; (5)
CC an HCV replicon enhanced cells made in the method; and (6) measuring the
CC ability of a compound to affect HCV activity. The HCV replicons and HCV
CC replicon enhanced cells are useful in studying HCV replication and
CC expression, and HCV and host cell interactions, producing HCV RNA and
CC proteins, and providing a system for measuring the ability of a compound
CC to modulate one or more HCV activities e.g. to discover drugs which may
CC treat HCV mediated diseases such as liver failure, cirrhosis and
CC hepatocellular carcinoma. The present sequence is an HCV based vector
CC pHCVneo.17 mutant of the invention. Note: The present sequence is not
CC shown in the specification but was created by the indexer using the HCV
CC vector sequence appearing as ABK91412 and the information in Claim 16
XX
SQ Sequence 10690 BP; 2335 A; 3044 C; 2908 G; 2403 T; 0 U; 0 Other;

Query Match 100.0%; Score 7990.4; DB 6; Length 10690;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCAGCCCCCGATTGGGGCGACACTCCACATAGATCACTCCCTGTGAGGAACACTG 60
DB |
QY 61 TCTTACGAGAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTGCGAGCCTCCAGGAC 120
DB |
QY 121 CCCCCCTCCCGGAGAGCCATAGTGGTCTCGGAAACCGGTGAGTACACCGGAATTCGCG 180
DB |
QY 181 GAGACCGGTCCTTCTTGGATCAACCCGCTCAATCCCTGAGATTTGGCGTGCCTCC 240
DB |
QY 241 GCGAGACTGTAGCCGAGTATGTGGTTCGGAAGGCTTGTGGTACTGCTGTATAGG 300
DB |
QY 301 GTGCTTGGAGTGTCCCGGAGGTCTCGTAGACCGTGCACCATGAGCAAGAACTCTAAC 360
DB |
QY 361 CTCAGAGAAAAACAAAGGGCGCGCATGATGAAACAGATGATGCAACGAGTCTC 420
DB |
QY 421 CCGCGGCTGGGTGGAGAGGCTATTGGGCTATGACTGGGCAACAGACAAATCGGCTGCT 480
DB |
QY 481 CTGATGCGCGGTGTTCGGGTGTGAGCGAGGGGCGCCGGTCTTTTGTCTAAGACCG 540
DB |
QY 541 ACCTGTCCGGTGCCTGAATGAATCTGAGGAGCGAGCGCGGTATCGTGGCTGGCCA 600
DB |
QY 601 CGACGGGCTTCTTGGCAGCTGTCTGAGCTGTGCTCACTGAAGCGGAAGGACTGCG 660
DB |
QY 661 TCGTATTGGGCGAAGTGC CGGGCGAGGATCTCTGTCTCATCTCACTTGTCTCGCGAGA 720
DB |
QY 721 AAGTATCCATCATGCGTGTATGCAATCGCGGGCTGCATACGCTTGTATCGGCTACCTGCC 780
DB |
QY 780 AAGTATCCATCATGCGTGTATGCAATCGCGGGCTGCATACGCTTGTATCGGCTACCTGCC 780
DB |

QY 781 CATTCGACCAACAGCGAAACATCGCATCGAGCGAGCAGTACTCGATGGAAGCGGTC 840
DB |
QY 841 TTGTCGATCAGGATGATCTGGACGAGAGCATCAGGGCTCGCGCAGCGAACTGTTCG 900
DB |
QY 901 CCAGGCTCAAGCGCGCATGTCGCCGAGGAGTCTGTCGTGACCCATCGCGATGCGCT 960
DB |
QY 961 GCTTCCGNAATATGTTGGAAATGCCGCTTTTCTCGATTCACTGACTGTGGCCGGC 1020
DB |
QY 1021 TGCGTGTGCGGACCGCTATCAGGACATAGCGTTGGTACCCTGATATGCTGAAGAGC 1080
DB |
QY 1081 TTGGCGGCGAAATGGGCTGACCGCTTCTTACGGTATCGCGCTCCCGATTTCG 1140
DB |
QY 1141 AGCGCATCGCTTCTATCGCTTCTTGAAGAGTCTTCTGAGTTTAAACAGACCAACAG 1200
DB |
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCCCCCCCTAACGTTACTGGC 1260
DB |
QY 1261 CGAAGCGCTTGAATAAGCGCGGTGTGCTTATATGTTTATATGTTTCCACCATATG 1320
DB |
QY 1321 CGGTCTTTGGCAATGTGAGGCGCGGAAACCTTGGCCCTCTCTTCTTGAAGAGCATTCCT 1380
DB |
QY 1381 AGGGTCTTTTCCCTCTCGCAAGAGAAATCAAGGTCTGTGATGTCTGTGAAGAGCA 1440
DB |
QY 1441 GTTCCTCTGAAAGCTTCTTGAAGCAAAACAGTCTGTAGCGCCCTTTCGAGCAGCGG 1500
DB |
QY 1501 AACCCCGCAGCTGGCGACAGTGTCTCTGCGGCCAAAGCCACCGTGTATAAGATACACT 1560
DB |
QY 1561 GCAAAGGCGCACAAACCCAGTGTGAGTGTGATGTGAGTGTGGAAGAGTCAAA 1620
DB |
QY 1621 TGGCTCTCTCAAGCGTATTCAACAAAGGGGTGAAGGATGCCAGAGGTACCCCATGT 1680
DB |
QY 1681 ATGGATCTGATCTGGGCTCGGTGACATGCTTACATGTTTGTAGTTCGAGGTAAAA 1740
DB |
QY 1741 AACGTCATAGGCCCCCGGAAACCAACGCGGACCTGCTTCTTTGAAAAACACGATATACC 1800
DB |
QY 1801 ATGGCGCTATTACGGCTCTATCCCAACAGACGCGAGGCTACTTGGCTGCATCATCT 1860
DB |
QY 1861 AGCTTACAGCGCGGACAGGAACAGGTCGAGGGGAGGTCCAAAGTGTCTCCACCGCA 1920
DB |

| | | | | |
|----|------|---|------|---|
| Db | 1861 | AGCCTCACAGGCGGGGACAGGAACAGGTTCGAGGGGGAGGTC | 1921 | AGCCTCACAGGCGGGGACAGGAACAGGTTCGAGGGGGAGGTC |
| QY | 1921 | ACACAATCTTTCTTGGCGACCTTGCGCTCAATGCGCTGTGTGGACTGTCTATCATGNGTGC | 1980 | ACACAATCTTTCTTGGCGACCTTGCGCTCAATGCGCTGTGTGGACTGTCTATCATGNGTGC |
| Db | 1921 | ACACAATCTTTCTTGGCGACCTTGCGCTCAATGCGCTGTGTGGACTGTCTATCATGNGTGC | 1980 | ACACAATCTTTCTTGGCGACCTTGCGCTCAATGCGCTGTGTGGACTGTCTATCATGNGTGC |
| QY | 1981 | GGCTCAAGACCCCTTTCGCGGCCCAAGGGCCCAATCACCCAAATGTATACCAATGTGCAC | 2040 | GGCTCAAGACCCCTTTCGCGGCCCAAGGGCCCAATCACCCAAATGTATACCAATGTGCAC |
| Db | 1981 | GGCTCAAGACCCCTTTCGCGGCCCAAGGGCCCAATCACCCAAATGTATACCAATGTGCAC | 2040 | GGCTCAAGACCCCTTTCGCGGCCCAAGGGCCCAATCACCCAAATGTATACCAATGTGCAC |
| QY | 2041 | CAGGACCTCGTGGCTGGCAAGCGCCCCCGGGGGCGGTTCCTTTGACACCATGCACTGC | 2100 | CAGGACCTCGTGGCTGGCAAGCGCCCCCGGGGGCGGTTCCTTTGACACCATGCACTGC |
| Db | 2041 | CAGGACCTCGTGGCTGGCAAGCGCCCCCGGGGGCGGTTCCTTTGACACCATGCACTGC | 2100 | CAGGACCTCGTGGCTGGCAAGCGCCCCCGGGGGCGGTTCCTTTGACACCATGCACTGC |
| QY | 2101 | GGCAGCTCGGACCTTTACTTGGTTCAGAGGCATCCGATGTCTTCCGCTGCGCGCGG | 2160 | GGCAGCTCGGACCTTTACTTGGTTCAGAGGCATCCGATGTCTTCCGCTGCGCGCGG |
| Db | 2101 | GGCAGCTCGGACCTTTACTTGGTTCAGAGGCATCCGATGTCTTCCGCTGCGCGCGG | 2160 | GGCAGCTCGGACCTTTACTTGGTTCAGAGGCATCCGATGTCTTCCGCTGCGCGCGG |
| QY | 2161 | GGCGACACAGGGGAGGACCTACTCTCCCGAGGGCCCGTCTCTTCTTGAAGGCTCTTGG | 2220 | GGCGACACAGGGGAGGACCTACTCTCCCGAGGGCCCGTCTCTTCTTGAAGGCTCTTGG |
| Db | 2161 | GGCGACACAGGGGAGGACCTACTCTCCCGAGGGCCCGTCTCTTCTTGAAGGCTCTTGG | 2220 | GGCGACACAGGGGAGGACCTACTCTCCCGAGGGCCCGTCTCTTCTTGAAGGCTCTTGG |
| QY | 2221 | GGCGTCCACTGCTCTGCGCCCTCGGGCAGGCTGTGGGCATCTTTGGGCTGCGGTGTC | 2280 | GGCGTCCACTGCTCTGCGCCCTCGGGCAGGCTGTGGGCATCTTTGGGCTGCGGTGTC |
| Db | 2221 | GGCGTCCACTGCTCTGCGCCCTCGGGCAGGCTGTGGGCATCTTTGGGCTGCGGTGTC | 2280 | GGCGTCCACTGCTCTGCGCCCTCGGGCAGGCTGTGGGCATCTTTGGGCTGCGGTGTC |
| QY | 2281 | ACCTGAGGGTTGCGAAGGGCGTGGACTTTGTACCCGTCGAGTCTATGAAACCACTATG | 2340 | ACCTGAGGGTTGCGAAGGGCGTGGACTTTGTACCCGTCGAGTCTATGAAACCACTATG |
| Db | 2281 | ACCTGAGGGTTGCGAAGGGCGTGGACTTTGTACCCGTCGAGTCTATGAAACCACTATG | 2340 | ACCTGAGGGTTGCGAAGGGCGTGGACTTTGTACCCGTCGAGTCTATGAAACCACTATG |
| QY | 2341 | CGGTCCCGGTCCTTTCAGGCAACTGTCCTCCCTCCCGCCGCTACCGCAGACATTCAGGTC | 2400 | CGGTCCCGGTCCTTTCAGGCAACTGTCCTCCCTCCCGCCGCTACCGCAGACATTCAGGTC |
| Db | 2341 | CGGTCCCGGTCCTTTCAGGCAACTGTCCTCCCTCCCGCCGCTACCGCAGACATTCAGGTC | 2400 | CGGTCCCGGTCCTTTCAGGCAACTGTCCTCCCTCCCGCCGCTACCGCAGACATTCAGGTC |
| QY | 2401 | GCCCATCTACACGCCCTTACTTGGTAGCGGCAAGACACTAAGGTGCGCGCTCGGTATGCA | 2460 | GCCCATCTACACGCCCTTACTTGGTAGCGGCAAGACACTAAGGTGCGCGCTCGGTATGCA |
| Db | 2401 | GCCCATCTACACGCCCTTACTTGGTAGCGGCAAGACACTAAGGTGCGCGCTCGGTATGCA | 2460 | GCCCATCTACACGCCCTTACTTGGTAGCGGCAAGACACTAAGGTGCGCGCTCGGTATGCA |
| QY | 2461 | GCCCAAGGGTATAAGGTGCTTGTCTTGAACCCCGTCCGCGCCACCCCTAGGTTTCGGG | 2520 | GCCCAAGGGTATAAGGTGCTTGTCTTGAACCCCGTCCGCGCCACCCCTAGGTTTCGGG |
| Db | 2461 | GCCCAAGGGTATAAGGTGCTTGTCTTGAACCCCGTCCGCGCCACCCCTAGGTTTCGGG | 2520 | GCCCAAGGGTATAAGGTGCTTGTCTTGAACCCCGTCCGCGCCACCCCTAGGTTTCGGG |
| QY | 2521 | CGGTATATGCTTAAGGCACATGTATCGACCTTAACATCAGAAACCGGGTAAGGACCATC | 2580 | CGGTATATGCTTAAGGCACATGTATCGACCTTAACATCAGAAACCGGGTAAGGACCATC |
| Db | 2521 | CGGTATATGCTTAAGGCACATGTATCGACCTTAACATCAGAAACCGGGTAAGGACCATC | 2580 | CGGTATATGCTTAAGGCACATGTATCGACCTTAACATCAGAAACCGGGTAAGGACCATC |
| QY | 2581 | ACCACGGGTGCCCGCCATCAGTACTCCACTATGGCAAGTTCCTTTCGCGACGGTGTTGC | 2640 | ACCACGGGTGCCCGCCATCAGTACTCCACTATGGCAAGTTCCTTTCGCGACGGTGTTGC |
| Db | 2581 | ACCACGGGTGCCCGCCATCAGTACTCCACTATGGCAAGTTCCTTTCGCGACGGTGTTGC | 2640 | ACCACGGGTGCCCGCCATCAGTACTCCACTATGGCAAGTTCCTTTCGCGACGGTGTTGC |
| QY | 2641 | TCTGGGGCGCCCTATGACATCAPAATATGATGAGTGCCACTCAACTGACTCGACCACT | 2700 | TCTGGGGCGCCCTATGACATCAPAATATGATGAGTGCCACTCAACTGACTCGACCACT |
| Db | 2641 | TCTGGGGCGCCCTATGACATCAPAATATGATGAGTGCCACTCAACTGACTCGACCACT | 2700 | TCTGGGGCGCCCTATGACATCAPAATATGATGAGTGCCACTCAACTGACTCGACCACT |
| QY | 2701 | ATCTCGGGCATCGGCACAGTCTTGACCAAGCGGAGAGCGGTGGAGCGCGACTCGTGTC | 2760 | ATCTCGGGCATCGGCACAGTCTTGACCAAGCGGAGAGCGGTGGAGCGCGACTCGTGTC |
| Db | 2701 | ATCTCGGGCATCGGCACAGTCTTGACCAAGCGGAGAGCGGTGGAGCGCGACTCGTGTC | 2760 | ATCTCGGGCATCGGCACAGTCTTGACCAAGCGGAGAGCGGTGGAGCGCGACTCGTGTC |
| QY | 2761 | CTCGCCACCGCTACGGCTCGGGATCGGTCACCGTGCCACATCCAAACATCGAGGAGTG | 2820 | CTCGCCACCGCTACGGCTCGGGATCGGTCACCGTGCCACATCCAAACATCGAGGAGTG |
| Db | 2761 | CTCGCCACCGCTACGGCTCGGGATCGGTCACCGTGCCACATCCAAACATCGAGGAGTG | 2820 | CTCGCCACCGCTACGGCTCGGGATCGGTCACCGTGCCACATCCAAACATCGAGGAGTG |
| QY | 2821 | GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC | 2880 | GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC |
| Db | 2821 | GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC | 2880 | GCTCTGTCCAGCACTGGAGAAATCCCTTTTATGGCAAGCCATCCCATCGAGACCATC |
| QY | 2881 | AAGGGGGGAGGACCTCATTTTCTGCCATCCAAAGAAATGTATGAGCTCGCGCG | 2940 | AAGGGGGGAGGACCTCATTTTCTGCCATCCAAAGAAATGTATGAGCTCGCGCG |
| Db | 2881 | AAGGGGGGAGGACCTCATTTTCTGCCATCCAAAGAAATGTATGAGCTCGCGCG | 2940 | AAGGGGGGAGGACCTCATTTTCTGCCATCCAAAGAAATGTATGAGCTCGCGCG |
| QY | 2941 | AAGCTGTCGGGCTCGGACTCAATGCTAGCATATTACCGGGCGCTTGATATCCGTC | 3000 | AAGCTGTCGGGCTCGGACTCAATGCTAGCATATTACCGGGCGCTTGATATCCGTC |

| | | | |
|----|------|--|------|
| Db | 2941 | AAGCTGTCCGGCCCTCGGACTCAATGCTGTAGCATATATTACCGGGCCCTTGATGTATCCGTC | 3000 |
| QY | 3001 | ATACCAACTTAGCGGAGACGCTCATTTGCTGTAGCAACGAGCGCTCTAATGACGGGCTTTTACC | 3060 |
| Db | 3001 | ATACCAACTTAGCGGAGACGCTCATTTGCTGTAGCAACGAGCGCTCTAATGACGGGCTTTTACC | 3060 |
| QY | 3061 | GGCGATTTTCGACTTCAGTGATCGACTGCAATACATGTGTCAACGACAGAGTCGACTTCAGC | 3120 |
| Db | 3061 | GGCGATTTTCGACTTCAGTGATCGACTGCAATACATGTGTCAACGACAGAGTCGACTTCAGC | 3120 |
| QY | 3121 | CTGGACCCGACCTTTCACCAATTGAGACGACGACCGTGCCCAAGACGCGGTGTCAACGCTCG | 3180 |
| Db | 3121 | CTGGACCCGACCTTTCACCAATTGAGACGACGACCGTGCCCAAGACGCGGTGTCAACGCTCG | 3180 |
| QY | 3181 | CAGCGCGAGGACGAGACTGGTATGGGCGAGGATGGGCATTTACAGGTTTGTGACTCCAGCA | 3240 |
| Db | 3181 | CAGCGCGAGGACGAGACTGGTATGGGCGAGGATGGGCATTTACAGGTTTGTGACTCCAGCA | 3240 |
| QY | 3241 | GAACGGCCCTCGGGCATGTTTCGATTCCTCGGTTCTGTGCGAGTGTATGACGCGGGCTGT | 3300 |
| Db | 3241 | GAACGGCCCTCGGGCATGTTTCGATTCCTCGGTTCTGTGCGAGTGTATGACGCGGGCTGT | 3300 |
| QY | 3301 | GCTTGATCGAGCTCACGCCGCCCGAGACCTCAGTTAGTTGCGGGCTTACCTTAACACA | 3360 |
| Db | 3301 | GCTTGATCGAGCTCACGCCGCCCGAGACCTCAGTTAGTTGCGGGCTTACCTTAACACA | 3360 |
| QY | 3361 | CCAGGGTTGCCGCTGTGCCAGGACCATCTGGAGTTCTGGGAGAGCGTCTTTACAGGCCTC | 3420 |
| Db | 3361 | CCAGGGTTGCCGCTGTGCCAGGACCATCTGGAGTTCTGGGAGAGCGTCTTTACAGGCCTC | 3420 |
| QY | 3421 | ACCCACATAGACGCCATTTCTGTGCCAGACTAGCAGGACGAGAGACAACTTCCCTTAC | 3480 |
| Db | 3421 | ACCCACATAGACGCCATTTCTGTGCCAGACTAGCAGGAGGAGAGACAACTTCCCTTAC | 3480 |
| QY | 3481 | CTGTTAGCATACAGGCTACGGTGTGCCAGGGCTCAGGCTCCACCTTCATCTCGTGGGAC | 3540 |
| Db | 3481 | CTGTTAGCATACAGGCTACGGTGTGCCAGGGCTCAGGCTCCACCTTCATCTCGTGGGAC | 3540 |
| QY | 3541 | CAAAATGTGAAGTGTCTCATACGGCTAAAGCTACGCTGCAACGGGCGCAACGCCCTCTGTC | 3600 |
| Db | 3541 | CAAAATGTGAAGTGTCTCATACGGCTAAAGCTACGCTGCAACGGGCGCAACGCCCTCTGTC | 3600 |
| QY | 3601 | TATAGGCTGGAGCGGTTTCAAAACGAGGTACTACCAACACGCCCATTAACCAATATC | 3660 |
| Db | 3601 | TATAGGCTGGAGCGGTTTCAAAACGAGGTACTACCAACACGCCCATTAACCAATATC | 3660 |
| QY | 3661 | ATGCATGTCATGTCCGCTGACCTCGAGGTGTGTACAGAGCAGCTGGGTGTGGTAGGGCGGA | 3720 |
| Db | 3661 | ATGCATGTCATGTCCGCTGACCTCGAGGTGTGTACAGAGCAGCTGGGTGTGGTAGGGCGGA | 3720 |
| QY | 3721 | GTCTTAGCAGCTGTGGCGGGTATTTGCTTGACAAACAGGACGCGTGTGTCATTGTGGGAGG | 3780 |
| Db | 3721 | GTCTTAGCAGCTGTGGCGGGTATTTGCTTGACAAACAGGACGCGTGTGTCATTGTGGGAGG | 3780 |
| QY | 3781 | ATCATCTTGTCCGAAGCCGGCCATCATTCCTCGGACAGGGAAGTCTTTTACCGGGAGTTC | 3840 |
| Db | 3781 | ATCATCTTGTCCGAAGCCGGCCATCATTCCTCGGACAGGGAAGTCTTTTACCGGGAGTTC | 3840 |
| QY | 3841 | GATGAGATGAAGAGTGCAGCTCACACCTCCCTTACATCGAACAGGGAATGCAAGCTCGCC | 3900 |
| Db | 3841 | GATGAGATGAAGAGTGCAGCTCACACCTCCCTTACATCGAACAGGGAATGCAAGCTCGCC | 3900 |
| QY | 3901 | GAACAATTCACAGAGGCAATTCGGGTTGTCGAACAGCCCAAGCAAGCGGAGGCT | 3960 |
| Db | 3901 | GAACAATTCACAGAGGCAATTCGGGTTGTCGAACAGCCCAAGCAAGCGGAGGCT | 3960 |
| QY | 3961 | GCTGCTCCGCTGGTGAATCCAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG | 4020 |
| Db | 3961 | GCTGCTCCGCTGGTGAATCCAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG | 4020 |
| QY | 4021 | TGGAATTTTCATCAGCGGGATACAATATTTAGCAGGCTTCTGCATCTGCTGGCAACCCC | 4080 |
| Db | 4021 | TGGAATTTTCATCAGCGGGATACAATATTTAGCAGGCTTCTGCATCTGCTGGCAACCCC | 4080 |

| | | | | | | | |
|----|------|---|------|----|------|--|------|
| QY | 4081 | GGATAGCATCACTGATGCAATTCACAGCTCTATCACAGCCGCTCACACCCAAAT | 4140 | QY | 5161 | ACATTCCTGGTGGGCTCAATCAATACCTGGTGGGTACAGCTCCCATGGAGCCGAA | 5220 |
| DB | 4081 | GGATAGCATCACTGATGCAATTCACAGCTCTATCACAGCCGCTCACACCCAAAT | 4140 | DB | 5161 | ACATTCCTGGTGGGCTCAATCAATACCTGGTGGGTACAGCTCCCATGGAGCCGAA | 5220 |
| QY | 4141 | ACCTTCCTGTTTAAATCTCTGGGGGATGGGTGGCGCCAACTTGCTCTCCAGCGCT | 4200 | QY | 5221 | CGGAGGTAGAGTCTCACTTCCATGTCAACGACCCCTCCCAATACGCGGAGAGG | 5280 |
| DB | 4141 | ACCTTCCTGTTTAAATCTCTGGGGGATGGGTGGCGCCAACTTGCTCTCCAGCGCT | 4200 | DB | 5221 | CGGAGGTAGAGTCTCACTTCCATGTCAACGACCCCTCCCAATACGCGGAGAGG | 5280 |
| QY | 4201 | GCTTCGTCTTTCGTAGCGCCGCGCATCGCTGGAGCGGTGTGGAGCATAGGCTTGGG | 4260 | QY | 5281 | GCTAAGCGTAGGCTGGCCAGGGGATCTCCCTCTCTTGGCCAGCTCATCAGTAGCCAG | 5340 |
| DB | 4201 | GCTTCGTCTTTCGTAGCGCCGCGCATCGCTGGAGCGGTGTGGAGCATAGGCTTGGG | 4260 | DB | 5281 | GCTAAGCGTAGGCTGGCCAGGGGATCTCCCTCTCTTGGCCAGCTCATCAGTAGCCAG | 5340 |
| QY | 4261 | AAGGTCTGTGGATATTTGGAGGTTATGAGCAGGGGTGCGAGCGCTCGTGGCC | 4320 | QY | 5341 | CTGTCTGCGCTTCTTGAAGCAATGCACTACCCGTCATGCTCCCGGACGCTGAC | 5400 |
| DB | 4261 | AAGGTCTGTGGATATTTGGAGGTTATGAGCAGGGGTGCGAGCGCTCGTGGCC | 4320 | DB | 5341 | CTGTCTGCGCTTCTTGAAGCAATGCACTACCCGTCATGCTCCCGGACGCTGAC | 5400 |
| QY | 4321 | TTTAAAGTATGAGCGCGGATGCCCTCCACGAGGACCTGGTTAACTTCTCCCTGCT | 4380 | QY | 5401 | CTCATCGAGCCAACTCTGTGGCGGAGGATGGGCGGGAACATCAACCGCGTGGAG | 5460 |
| DB | 4321 | TTTAAAGTATGAGCGCGGATGCCCTCCACGAGGACCTGGTTAACTTCTCCCTGCT | 4380 | DB | 5401 | CTCATCGAGCCAACTCTGTGGCGGAGGATGGGCGGGAACATCAACCGCGTGGAG | 5460 |
| QY | 4381 | ATCCTCTCCCTCGCGCCCTAGTCGTGGGTCTGTGGCGACGATATCTGCTCGGCAC | 4440 | QY | 5461 | TCAGAAATTAAGGTAGTAAATTTGGACTCTTTTCGAGCGCTTCAAGGGAGGATGAG | 5520 |
| DB | 4381 | ATCCTCTCCCTCGCGCCCTAGTCGTGGGTCTGTGGCGACGATATCTGCTCGGCAC | 4440 | DB | 5461 | TCAGAAATTAAGGTAGTAAATTTGGACTCTTTTCGAGCGCTTCAAGGGAGGATGAG | 5520 |
| QY | 4441 | GTGGGCCAGGGAGGGGGTGTGCAGTGGATGAACCGGCTGATAGCGTTCGGCTCGCGG | 4500 | QY | 5521 | AGGAAAGTATCCGTTCCGCGGAGATCTCGGAGGTTCAGGAAATTTCCCTCGAGCGATG | 5580 |
| DB | 4441 | GTGGGCCAGGGAGGGGGTGTGCAGTGGATGAACCGGCTGATAGCGTTCGGCTCGCGG | 4500 | DB | 5521 | AGGAAAGTATCCGTTCCGCGGAGATCTCGGAGGTTCAGGAAATTTCCCTCGAGCGATG | 5580 |
| QY | 4501 | GTTAAACACGCTCCCGCACGACTATGTGCTGAGAGCAGCTGCGAGCACGTGTCACT | 4560 | QY | 5581 | CCCATATGGCAGCGCCGATTAACACCTTCCACTGTTAGAGTCTTGAAAGGACCCGAC | 5640 |
| DB | 4501 | GTTAAACACGCTCCCGCACGACTATGTGCTGAGAGCAGCTGCGAGCACGTGTCACT | 4560 | DB | 5581 | CCCATATGGCAGCGCCGATTAACACCTTCCACTGTTAGAGTCTTGAAAGGACCCGAC | 5640 |
| QY | 4561 | CAGATCCTCTAGTCTTACCATCACTCAGTGTGTAAGAGGCTTCCACAGTGGATCAAC | 4620 | QY | 5641 | TAGTCTCCTCCAGTGTGTACACGGGTGTCAATTCGCGCTTCCAGGCCCCCTCGATACCA | 5700 |
| DB | 4561 | CAGATCCTCTAGTCTTACCATCACTCAGTGTGTAAGAGGCTTCCACAGTGGATCAAC | 4620 | DB | 5641 | TAGTCTCCTCCAGTGTGTACACGGGTGTCAATTCGCGCTTCCAGGCCCCCTCGATACCA | 5700 |
| QY | 4621 | GAGACTGTCCAGCCATGCTCGGCTCTGGCTTAGAGATGTTTCGGATGATATGC | 4680 | QY | 5701 | CTTCCAGGAGGAGGAGGAGCGGTGTCTCTCAGAACTTACCGGTCTTCTCGCTTGGCG | 5760 |
| DB | 4621 | GAGACTGTCCAGCCATGCTCGGCTCTGGCTTAGAGATGTTTCGGATGATATGC | 4680 | DB | 5701 | CTTCCAGGAGGAGGAGGAGCGGTGTCTCTCAGAACTTACCGGTCTTCTCGCTTGGCG | 5760 |
| QY | 4681 | ACGGTGTGACTGATTTCAAGACCTGCTCCAGTCCAGCTCTCTGCGCGATTCGCGGA | 4740 | QY | 5761 | GAGCTCCCAAGAGCTTTCGCGAGCTCCGAAATCGTCCGCGCTGACAGCGGACGCA | 5820 |
| DB | 4681 | ACGGTGTGACTGATTTCAAGACCTGCTCCAGTCCAGCTCTCTGCGCGATTCGCGGA | 4740 | DB | 5761 | GAGCTCCCAAGAGCTTTCGCGAGCTCCGAAATCGTCCGCGCTGACAGCGGACGCA | 5820 |
| QY | 4741 | GTCCCTCTTCTCATGTCAACGTGGGTACAAGGAGTCTGGCGGGGACGGCATCATG | 4800 | QY | 5821 | ACGSCCTCTCTGTACACAGCCCTCCGACGAGCGCGGATCCCGATCTCAGCGAGCGGTCTTGG | 5880 |
| DB | 4741 | GTCCCTCTTCTCATGTCAACGTGGGTACAAGGAGTCTGGCGGGGACGGCATCATG | 4800 | DB | 5821 | ACGSCCTCTCTGTACACAGCCCTCCGACGAGCGCGGATCCCGATCTCAGCGAGCGGTCTTGG | 5880 |
| QY | 4801 | CAAAACACCTGCTGAGGACAGATCACCGACATGTGAATAACGGTTTCCATGAGG | 4860 | QY | 5881 | TCCTCCATGCCCCCTTGGGGGAGCGGGGGATCCCGATCTCAGCGAGCGGTCTTGG | 5940 |
| DB | 4801 | CAAAACACCTGCTGAGGACAGATCACCGACATGTGAATAACGGTTTCCATGAGG | 4860 | DB | 5881 | TCCTCCATGCCCCCTTGGGGGAGCGGGGGATCCCGATCTCAGCGAGCGGTCTTGG | 5940 |
| QY | 4861 | ATCGTGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTCCTCCATTAACCGTAC | 4920 | QY | 5941 | TCTACCGTAAAGGAGGCTAGTGAAGACGCTCTGCTCTCGATCTCGATCTTACATGAG | 6000 |
| DB | 4861 | ATCGTGGGCTTAGGACCTGTAGTAAACAGTGGCATGGAACATTCCTCCATTAACCGTAC | 4920 | DB | 5941 | TCTACCGTAAAGGAGGCTAGTGAAGACGCTCTGCTCTCGATCTCGATCTTACATGAG | 6000 |
| QY | 4921 | ACCAGGCGCTGCAACGCTTCCCGGGGCAAAATTTATCTAGGCGCTGTGGCGGGT | 4980 | QY | 6001 | ACAGCGCCTTGATCACGCCATGCGCTCGGAGGAAACCAAGTCCCATCAATGCACTG | 6060 |
| DB | 4921 | ACCAGGCGCTGCAACGCTTCCCGGGGCAAAATTTATCTAGGCGCTGTGGCGGGT | 4980 | DB | 6001 | ACAGCGCCTTGATCACGCCATGCGCTCGGAGGAAACCAAGTCCCATCAATGCACTG | 6060 |
| QY | 4981 | GCTGTGAGGATGCTGAGGATGAGGAGTACCGGGTGGGGATTTCCATGAGCGGCGATG | 5040 | QY | 6061 | AGCAACTCTTGTCTCCGTCAACCACTTGTGTATGTCAACATCTCGAGCGCAAGC | 6120 |
| DB | 4981 | GCTGTGAGGATGCTGAGGATGAGGAGTACCGGGTGGGGATTTCCATGAGCGGCGATG | 5040 | DB | 6061 | AGCAACTCTTGTCTCCGTCAACCACTTGTGTATGTCAACATCTCGAGCGCAAGC | 6120 |
| QY | 5041 | ACCACTGACAAAGTAAAGTCCCGGTTCAGGTTCGCGGCCCGAAATTTCTCAAGAGTG | 5100 | QY | 6121 | CTGCGGCAAGAAAGGTCACTTTGACAGACTGAGGTCTTGGAGCGACACTACCGGAC | 6180 |
| DB | 5041 | ACCACTGACAAAGTAAAGTCCCGGTTCAGGTTCGCGGCCCGAAATTTCTCAAGAGTG | 5100 | DB | 6121 | CTGCGGCAAGAAAGGTCACTTTGACAGACTGAGGTCTTGGAGCGACACTACCGGAC | 6180 |
| QY | 5101 | GATGGGTGCGGTTCACAGGTACGCTCAGCGTGCACACCTCTCAGGAGGAGGTC | 5160 | QY | 6181 | GTGCTCAAGGAGTGAAGCGGAGCGTCCACAGTTAAGGCTTAACTTCTATCCGTGGAG | 6240 |
| DB | 5101 | GATGGGTGCGGTTCACAGGTACGCTCAGCGTGCACACCTCTCAGGAGGAGGTC | 5160 | DB | 6181 | GTGCTCAAGGAGTGAAGCGGAGCGTCCACAGTTAAGGCTTAACTTCTATCCGTGGAG | 6240 |
| | | | | QY | 6241 | GAAGCTGTAGCTGACGCGCCCACTTCGCGCCAGATCTAAATTTTGGCTATGCGGCAAG | 6300 |

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Db 6241 GAAAGCTGTGAAGCTGACGCCCCACATTCGGCCAGATCTAAATTTTGGCTATGGGGCAAG 6300
QY 6301 GACGTCGGGAACCTATCCAGCAGGCGGTTAACACATCGCTCCGCTGTGGAGGACTTG 6360
Db 6301 GACGTCGGGAACCTATCCAGCAGGCGGTTAACACATCGCTCCGCTGTGGAGGACTTG 6360
QY 6361 CTGGGAAGACATGAGACACAAATTGACACCAACCATCATGGCAAAAATGAGGTTTCTGC 6420
Db 6361 CTGGGAAGACATGAGACACAAATTGACACCAACCATCATGGCAAAAATGAGGTTTCTGC 6420
QY 6421 GTCCAAACAGAGAGGGGGCGCAGCCAGCTCGCTTATCGTATTCACAGATTGGGG 6480
Db 6421 GTCCAAACAGAGAGGGGGCGCAGCCAGCTCGCTTATCGTATTCACAGATTGGGG 6480
QY 6481 GTTCGTGTGTGCGAGAAATGCCCCCTTTACGATGTGCTCCACCTCCCTCAGGCCGTTG 6540
Db 6481 GTTCGTGTGTGCGAGAAATGCCCCCTTTACGATGTGCTCCACCTCCCTCAGGCCGTTG 6540
QY 6541 ATGGGCTCTTCATACGGATTCCAATCTCTCTGACACAGCGGTGAGTTCTGTTGAAT 6600
Db 6541 ATGGGCTCTTCATACGGATTCCAATCTCTCTGACACAGCGGTGAGTTCTGTTGAAT 6600
QY 6601 GCCTGGAAGCGAAGAAATGCCCTATGGCTTCGCATATGACACCCGCTGTTTGACTCA 6660
Db 6601 GCCTGGAAGCGAAGAAATGCCCTATGGCTTCGCATATGACACCCGCTGTTTGACTCA 6660
QY 6661 ACGGCTACTGAGATGACATCCGTTGTCAGGAGTCAATCTACCAATGTGTGACTTGACC 6720
Db 6661 ACGGCTACTGAGATGACATCCGTTGTCAGGAGTCAATCTACCAATGTGTGACTTGACC 6720
QY 6721 CCCGAAGCAGACAGGCGCATTAAGTTCGCTCAGAGCGGCTTTTACATCGGGGGCCCCCTG 6780
Db 6721 CCCGAAGCAGACAGGCGCATTAAGTTCGCTCAGAGCGGCTTTTACATCGGGGGCCCCCTG 6780
QY 6781 ACTAATTTCTAAGGCGAGAACTGGGCTATCGCGGTGCCGCGAGCGGTGTACTGACG 6840
Db 6781 ACTAATTTCTAAGGCGAGAACTGGGCTATCGCGGTGCCGCGAGCGGTGTACTGACG 6840
QY 6841 ACCAGCTCGCGTAATACCTTCACATGTACTTGAAGCGCGCTGCGGCTGTGCGAGCTGCG 6900
Db 6841 ACCAGCTCGCGTAATACCTTCACATGTACTTGAAGCGCGCTGCGGCTGTGCGAGCTGCG 6900
QY 6901 AAGCTCAGAGCTGCAAGTCTCGATGTCGAGAGACGACCTTGTCTTATCTGTGAAGC 6960
Db 6901 AAGCTCAGAGCTGCAAGTCTCGATGTCGAGAGACGACCTTGTCTTATCTGTGAAGC 6960
QY 6961 GCGGGACCCCAAGAGGACGAGCGAGCTAGGGCTTTCACGGAGGCTATGACTAGATAC 7020
Db 6961 GCGGGACCCCAAGAGGACGAGCGAGCTAGGGCTTTCACGGAGGCTATGACTAGATAC 7020
QY 7021 TCTGCCCCCTCTGGGACCCGCCCCAACCAAGATAACGACTTGGAGTTGATAACATCATGC 7080
Db 7021 TCTGCCCCCTCTGGGACCCGCCCCAACCAAGATAACGACTTGGAGTTGATAACATCATGC 7080
QY 7081 TCTTCAATGTGTAGTTCGGGCGAGTGCATCTGGCAAAAAGGTTACTATCACCCTG 7140
Db 7081 TCTTCAATGTGTAGTTCGGGCGAGTGCATCTGGCAAAAAGGTTACTATCACCCTG 7140
QY 7141 GACCCACCAACCCCTTGGCGGGCTGCGTGGAGACAGCTAGACACATCCAGTCAAT 7200
Db 7141 GACCCACCAACCCCTTGGCGGGCTGCGTGGAGACAGCTAGACACATCCAGTCAAT 7200
QY 7201 TCTTGGCTAGGCAACATCATCATGTATGCGCCACCTTGTGGCAAGGATGATCCTGATG 7260
Db 7201 TCTTGGCTAGGCAACATCATCATGTATGCGCCACCTTGTGGCAAGGATGATCCTGATG 7260
QY 7261 ACTCATTTCTTCPCATCTTCTAGCTCAGGAACAACTTGAAAAAGCCCTAGATTCTCAG 7320
Db 7261 ACTCATTTCTTCPCATCTTCTAGCTCAGGAACAACTTGAAAAAGCCCTAGATTCTCAG 7320
QY 7321 ATCTACGGGCGCTGTACTCCATTGAGCCACTTGACCTACCTCAGATCAATCAACGACTC 7380
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Db 7321 ATCTACGGGCGCTGTACTCCATTGAGCCACTTGACCTACCTCAGATCAATCAACGACTC 7380
QY 7381 CATGGCTTTAGCGCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGTTGGCT 7440
Db 7381 CATGGCTTTAGCGCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGTTGGCT 7440
QY 7441 TCATGCTCTCAGAAACTTGGGTACCGCCTTGGCGAGTCTGGAGACATCGGCGCAGAAGT 7500
Db 7441 TCATGCTCTCAGAAACTTGGGTACCGCCTTGGCGAGTCTGGAGACATCGGCGCAGAAGT 7500
QY 7501 GTCCGCGCTAGGCTACTGTCCAGGGGGGAGGCTGCCACTTGTGGCAAGTACCTCTTC 7560
Db 7501 GTCCGCGCTAGGCTACTGTCCAGGGGGGAGGCTGCCACTTGTGGCAAGTACCTCTTC 7560
QY 7561 AACTGGGAGTAAAGACCAAGCTCAAACTCACTCCCAATCCCGGCTGCGTCCAGTTGGAT 7620
Db 7561 AACTGGGAGTAAAGACCAAGCTCAAACTCACTCCCAATCCCGGCTGCGTCCAGTTGGAT 7620
QY 7621 TTATCCAGCTGGTTGGTTGCTGTTTACAGCGGGGAGACATATATCACAGCCTGTCTCGT 7680
Db 7621 TTATCCAGCTGGTTGGTTGCTGTTTACAGCGGGGAGACATATATCACAGCCTGTCTCGT 7680
QY 7681 GCCGACCCCGCTGTTTCATGTGTGCTACTCTCTACTTTCTGTAGGGGTAGGCATCTAT 7740
Db 7681 GCCGACCCCGCTGTTTCATGTGTGCTACTCTCTACTTTCTGTAGGGGTAGGCATCTAT 7740
QY 7741 CTACTCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTTT 7800
Db 7741 CTACTCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTCTGTTTT 7800
QY 7801 TTTCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 7860
Db 7801 TTTCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 7860
QY 7861 TTTTCTCTTTTTTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
Db 7861 TTTTCTCTTTTTTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
QY 7921 TAGCTGTGAAGGTCCTGTAGCGCTTGAAGTGCAGAGAGTCTGATCTACTGSCCTCTCTGC 7980
Db 7921 TAGCTGTGAAGGTCCTGTAGCGCTTGAAGTGCAGAGAGTCTGATCTACTGSCCTCTCTGC 7980
QY 7981 AGATCAAGTACT 7992
Db 7981 AGATCAAGTACT 7992
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RESULT 10

ID ADP86264 standard; DNA; 11313 BP.

XX AC ADP86264;

XX XX 23-SEP-2004 (first entry)

XX Hepatitis C virus Con-1 replicon I377/NS-3', plasmid DNA.

XX Hepatitis C virus; HCV; anti-HCV agent; HCV infection; therapy; plasmid; ds.

XX Hepatitis C virus.

XX WO2004055216-A2.

XX 01-JUL-2004.

XX 12-DEC-2003; 2003WO-US039722.

XX 13-DEC-2002; 2002US-0433303P.

XX (FOXC-) FOX CHASE CANCER CENT.

PI Zhu Q, Guo J, Seeger C;

XX WPI; 2004-498079/46.
DR GENBANK; AJ242652.
XX
XX
PT New cell-line that replicates hepatitis C virus (HCV), where the cell
line is selected from a non-human cell line and a human non-hepatic cell
PT line, useful for identifying anti-HCV agents for treating HCV infections.
XX
XX Example III; SEQ ID NO 1; 130pp; English.
XX
XX The present invention provides hepatitis C virus (HCV) replication cells
CC and cell lines derived from human non-hepatic cells or non-human cells.
CC The invention is useful for identifying anti-HCV agents for treating HCV
CC infections. The present sequence is hepatitis C virus Con-1 replicon
CC I377/NS3-3' plasmid DNA.
XX
XX Sequence 11313 BP; 2347 A; 3334 C; 3152 G; 2480 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 7990.4; DB 12; Length 11313;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7991; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCCAGCCCCCGATTGGGGCGGCACTCCACCATAGATCACTCCCTGTGAGAACTACTG 60
Db 1 GCCAGCCCCCGATTGGGGCGGCACTCCACCATAGATCACTCCCTGTGAGAACTACTG 60
QY 61 TCTTACGAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTCAGCCCTCCAGGAC 120
Db 61 TCTTACGAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTCAGCCCTCCAGGAC 120
QY 121 CCCCCCTCCGGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATGCCAG 180
Db 121 CCCCCCTCCGGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGGAATGCCAG 180
QY 181 GACGACCGGTCCTTTCTTGATCAACCCGCTCAATGCTGAGATTTGGCGTGGCCCC 240
Db 181 GACGACCGGTCCTTTCTTGATCAACCCGCTCAATGCTGAGATTTGGCGTGGCCCC 240
QY 241 GCAGAGCTGTAGCGAGTAGTGTGGGTGCGGAAGGCGCTTGTGCTGCTGATAGG 300
Db 241 GCAGAGCTGTAGCGAGTAGTGTGGGTGCGGAAGGCGCTTGTGCTGCTGATAGG 300
QY 301 GTGCTTCGAGTGTCCCGGAGGTCTCGTAGACCGTGCACCAAGCAATCTTAAC 360
Db 301 GTGCTTCGAGTGTCCCGGAGGTCTCGTAGACCGTGCACCAAGCAATCTTAAC 360
QY 361 CTCAGAGAAACCAAGAGGCGGCCATGATTTGAACAAAGATGGATTCACGAGTTCTC 420
Db 361 CTCAGAGAAACCAAGAGGCGGCCATGATTTGAACAAAGATGGATTCACGAGTTCTC 420
QY 421 CGGCGCTTGGGTGAGAGGCTATTTCGGCTATGACTGGGACACAGACATCGCTGCT 480
Db 421 CGGCGCTTGGGTGAGAGGCTATTTCGGCTATGACTGGGACACAGACATCGCTGCT 480
QY 481 CTGATGCGCGCTGTTCGGGTGTGAGCGGCGCGCCGGTTCTTTTGTCAAGACCG 540
Db 481 CTGATGCGCGCTGTTCGGGTGTGAGCGGCGCGCCGGTTCTTTTGTCAAGACCG 540
QY 541 ACCTGTCCGGTGCCTGAATGAATGCAAGAGGAGCGCGCGCTATCGTGGCTGGCA 600
Db 541 ACCTGTCCGGTGCCTGAATGAATGCAAGAGGAGCGCGCGCTATCGTGGCTGGCA 600
QY 601 CGAGGGGCTTCTTGGCGAGCTGTGCTGAGCTGTGCTGAGCGGAAGGAGTGGC 660
Db 601 CGAGGGGCTTCTTGGCGAGCTGTGCTGAGCTGTGCTGAGCGGAAGGAGTGGC 660
QY 661 TGCTATTGGCGAAGTGGCGGCGAGGATCTCTGTCACTCACTTGTCTGCTCGCGAGA 720
Db 661 TGCTATTGGCGAAGTGGCGGCGAGGATCTCTGTCACTCACTTGTCTGCTCGCGAGA 720
QY 721 AAGTATCATATGCTGATGCAATGCGGCGCTGCATACGCTGATCCGGTACCTGCC 780
Db 721 AAGTATCATATGCTGATGCAATGCGGCGCTGCATACGCTGATCCGGTACCTGCC 780

QY 781 CATTGACCAACAGCGAAACATCGATCGAGCGAGCAGCTACTCGATGGAAGCGGTC 840
Db 781 CATTGACCAACAGCGAAACATCGATCGAGCGAGCAGCTACTCGATGGAAGCGGTC 840
QY 841 TTGTGATCAGATGATCTGACGAAGAGCATCAGGGGCTCGCGCCAGCGAATGTTTCG 900
Db 841 TTGTGATCAGATGATCTGACGAAGAGCATCAGGGGCTCGCGCCAGCGAATGTTTCG 900
QY 901 CCAGGCTCAAGCGCGCATGCGCGAGCGAGGATCTCGTGTGACCCATGCGATGCT 960
Db 901 CCAGGCTCAAGCGCGCATGCGCGAGCGAGGATCTCGTGTGACCCATGCGATGCT 960
QY 961 GCTTCCGGAATATCATGTGGAATGCGCGTTTCTGGATCATGCACTGTGCGCGG 1020
Db 961 GCTTCCGGAATATCATGTGGAATGCGCGTTTCTGGATCATGCACTGTGCGCGG 1020
QY 1021 TGGGTGCGGACCGCTATCAGGACATAGCGTTGCTACCGCTGATATTGCTGAAGAGC 1080
Db 1021 TGGGTGCGGACCGCTATCAGGACATAGCGTTGCTACCGCTGATATTGCTGAAGAGC 1080
QY 1081 TTGGCGGGAATGGGCTGACCGCTTCTGCTGCTTACGGTATCGCGCTCCCGATTCCG 1140
Db 1081 TTGGCGGGAATGGGCTGACCGCTTCTGCTGCTTACGGTATCGCGCTCCCGATTCCG 1140
QY 1141 AGCGATGCGCTTCTATCGCTTCTTACGAGTCTTCTGAGTTTAAACAGACCAACAG 1200
Db 1141 AGCGATGCGCTTCTATCGCTTCTTACGAGTCTTCTGAGTTTAAACAGACCAACAG 1200
QY 1201 GTTTCCTCTAGCGGATCAATTTCCGCGCTTCTCCCTCCCGCGCTTAACTGCTGGC 1260
Db 1201 GTTTCCTCTAGCGGATCAATTTCCGCGCTTCTCCCTCCCGCGCTTAACTGCTGGC 1260
QY 1261 CGAAGCGCTTGAATGAAGCGGCTGTGCTTATATGTTTATTTTCCACATATTG 1320
Db 1261 CGAAGCGCTTGAATGAAGCGGCTGTGCTTATATGTTTATTTTCCACATATTG 1320
QY 1321 CGGTCTTTGGCAATGTGAGGCGCGGAAACCTGCGCTTCTTCTTGAAGAGATTCCT 1380
Db 1321 CGGTCTTTGGCAATGTGAGGCGCGGAAACCTGCGCTTCTTCTTGAAGAGATTCCT 1380
QY 1381 AGGGGTCTTTCCTCTCGCAAGGAATGCAAGGTCTGTTGAATGCTGTAAGAGAGCA 1440
Db 1381 AGGGGTCTTTCCTCTCGCAAGGAATGCAAGGTCTGTTGAATGCTGTAAGAGAGCA 1440
QY 1441 GTTCTCTGGAAGCTTCTTGAAGCAAAACAAAGTCTGCTAGCAGCCCTTTCAGCAGCGG 1500
Db 1441 GTTCTCTGGAAGCTTCTTGAAGCAAAACAAAGTCTGCTAGCAGCCCTTTCAGCAGCGG 1500
QY 1501 AACCCCGCTTGGCGAGCTGCTGCGGCGCAAGGCGCTGCTGTAAGATACACCT 1560
Db 1501 AACCCCGCTTGGCGAGCTGCTGCGGCGCAAGGCGCTGCTGTAAGATACACCT 1560
QY 1561 GCAAGCGGCAACAAACCGAGTGCAGTGTGAGTTGAGTGTGGAAGAGTCAAA 1620
Db 1561 GCAAGCGGCAACAAACCGAGTGCAGTGTGAGTTGAGTGTGGAAGAGTCAAA 1620
QY 1621 TGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGATGCGGAGAGTACCCCATGT 1680
Db 1621 TGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGATGCGGAGAGTACCCCATGT 1680
QY 1681 ATGGATCTGATCTGGGCGCTCGGTGACATGCTTTTACATGTTTGTAGTTCGAGTTAAA 1740
Db 1681 ATGGATCTGATCTGGGCGCTCGGTGACATGCTTTTACATGTTTGTAGTTCGAGTTAAA 1740
QY 1741 AACGTCTAGGCGCGCAACCAACCGGGAAGTGTGCTTTCCTTTGAAAAACAGATATACC 1800
Db 1741 AACGTCTAGGCGCGCAACCAACCGGGAAGTGTGCTTTCCTTTGAAAAACAGATATACC 1800
QY 1801 ATGGCGCTATTAAGCGCTACTCCCAAGAGCGGAGGCTTCTGCTGATCATCACT 1860
Db 1801 ATGGCGCTATTAAGCGCTACTCCCAAGAGCGGAGGCTTCTGCTGATCATCACT 1860

| | | | | | | | | | |
|----|------|-----------|-----------------|-----------------|----------------|----------------|---------------------------|--------|------|
| Qy | 1861 | AGCCTCA | AGCGCGGACAGGAAC | CAGGTCC | GAGGGGAGGTC | CAAGTGGTCT | CTCCACCGCA | 1921 | |
| Db | 1861 | AGCCTCA | AGCGCGGACAGGAAC | CAGGTCC | GAGGGGAGGTC | CAAGTGGTCT | CTCCACCGCA | 1920 | |
| Qy | 1921 | ACACAATCT | TTCTTCTGCGAC | CTTGCGTCA | ATGTCGCTGT | GTGTGACTGT | CTATCATSGTGCC | 1980 | |
| Db | 1921 | ACACAATCT | TTCTTCTGCGAC | CTTGCGTCA | ATGTCGCTGT | GTGTGACTGT | CTATCATSGTGCC | 1980 | |
| Qy | 1981 | GGCTCA | AAGACCTTCCCGG | CCCAAGGGCCCA | TCACCCCAATGT | TACACCAATGTGAC | 2040 | | |
| Db | 1981 | GGCTCA | AAGACCTTCCCGG | CCCAAGGGCCCA | TCACCCCAATGT | TACACCAATGTGAC | 2040 | | |
| Qy | 2041 | CAGGACT | CGTGGGTGGCAAG | CGCCCCCGGGCGCGT | TCCTTGA | CACATGCACTGC | 2100 | | |
| Db | 2041 | CAGGACT | CGTGGGTGGCAAG | CGCCCCCGGGCGCGT | TCCTTGA | CACATGCACTGC | 2100 | | |
| Qy | 2101 | GGCAGCT | CGGACCTTTACT | TGTGACAGGAC | GTGCGGATG | TCATTCGGTGC | CGCGCGG | 2160 | |
| Db | 2101 | GGCAGCT | CGGACCTTTACT | TGTGACAGGAC | GTGCGGATG | TCATTCGGTGC | CGCGCGG | 2160 | |
| Qy | 2161 | GGCGAC | GAGGAGGAGCTACT | CTCTCCCGCAGG | CGCGTCTCTACT | TGAAAGGCTCTTCG | 2220 | | |
| Db | 2161 | GGCGAC | GAGGAGGAGCTACT | CTCTCCCGCAGG | CGCGTCTCTACT | TGAAAGGCTCTTCG | 2220 | | |
| Qy | 2221 | GGCGGT | CCACTGCTG | CCCCCTCGGG | GCAGCTGTGGGCAT | CTTTCCGGGTGC | CGGTGTGC | 2280 | |
| Db | 2221 | GGCGGT | CCACTGCTG | CCCCCTCGGG | GCAGCTGTGGGCAT | CTTTCCGGGTGC | CGGTGTGC | 2280 | |
| Qy | 2281 | ACCCGAG | GGGTGCGAAGG | CGGTGGA | CTTTGTACCCGT | CGAGTCTATG | GAAACCACTATG | 2340 | |
| Db | 2281 | ACCCGAG | GGGTGCGAAGG | CGGTGGA | CTTTGTACCCGT | CGAGTCTATG | GAAACCACTATG | 2340 | |
| Qy | 2341 | CGGTCCC | CGGTCTTAC | CGGCAAACTCGT | CCCCCTCGG | CCGTACCGGAC | ATTGAAACCACTATG | 2400 | |
| Db | 2341 | CGGTCCC | CGGTCTTAC | CGGCAAACTCGT | CCCCCTCGG | CCGTACCGGAC | ATTGAAACCACTATG | 2400 | |
| Qy | 2401 | GCCCAT | CTACAGG | CCCTACTG | TGTAGCGG | CAAGACATAAGGT | CGCGTGCATATGCA | 2460 | |
| Db | 2401 | GCCCAT | CTACAGG | CCCTACTG | TGTAGCGG | CAAGACATAAGGT | CGCGTGCATATGCA | 2460 | |
| Qy | 2461 | GCCCAAG | GGGTATAG | GTGTTG | TCTGAA | CCCGTCCG | CGCCACCCCTAGGTTTCGGG | 2520 | |
| Db | 2461 | GCCCAAG | GGGTATAG | GTGTTG | TCTGAA | CCCGTCCG | CGCCACCCCTAGGTTTCGGG | 2520 | |
| Qy | 2521 | CGGTAT | TATGCTAAGG | CACATG | TATCGAC | CCCTAA | CATCAGAACCGGGTAAAGGACCATC | 2580 | |
| Db | 2521 | CGGTAT | TATGCTAAGG | CACATG | TATCGAC | CCCTAA | CATCAGAACCGGGTAAAGGACCATC | 2580 | |
| Qy | 2581 | ACCAGGG | TGCCCCCAT | CAGTACTCA | CTATGGCAAG | TTTCTTCG | CGACGGTGGTTGC | 2640 | |
| Db | 2581 | ACCAGGG | TGCCCCCAT | CAGTACTCA | CTATGGCAAG | TTTCTTCG | CGACGGTGGTTGC | 2640 | |
| Qy | 2641 | TCTGGGG | CGCCTATG | ACATATA | TATGTAGT | GCCATCA | CTCACTGCACTCGACCACT | 2700 | |
| Db | 2641 | TCTGGGG | CGCCTATG | ACATATA | TATGTAGT | GCCATCA | CTCACTGCACTCGACCACT | 2700 | |
| Qy | 2701 | ATCTTGG | GCATCGG | CAAGTCTT | GCAAGG | CGGACCGG | CTGAGCGCACTCGTCTG | 2760 | |
| Db | 2701 | ATCTTGG | GCATCGG | CAAGTCTT | GCAAGG | CGGACCGG | CTGAGCGCACTCGTCTG | 2760 | |
| Qy | 2761 | CTGCCAC | CGCTAG | CGCTCGG | ATCGGTCA | CCGTGCCA | ATCCAAACATCGAGAGGTG | 2820 | |
| Db | 2761 | CTGCCAC | CGCTAG | CGCTCGG | ATCGGTCA | CCGTGCCA | ATCCAAACATCGAGAGGTG | 2820 | |
| Qy | 2821 | GCTCTGT | CCAGCACTG | GAAATCCC | CTTTATG | GCAAGG | CAATCCCAACATCGAGAGGTG | 2880 | |
| Db | 2821 | GCTCTGT | CCAGCACTG | GAAATCCC | CTTTATG | GCAAGG | CAATCCCAACATCGAGAGGTG | 2880 | |
| Qy | 2881 | AAGGGGG | GAGGAC | CTCATTTT | CTGCCAT | TCGCAAG | AAATGTGATGAC | TCGCGG | 2940 |
| Db | 2881 | AAGGGGG | GAGGAC | CTCATTTT | CTGCCAT | TCGCAAG | AAATGTGATGAC | TCGCGG | 2940 |
| Qy | 2941 | AAGCTGT | CGGCTCG | ACTCAAT | GCTGTAG | CATATT | ATACCGGGGCTTTGATGATCGCTC | 3000 | |

| | | | | | |
|---|---|--|------|--|------|
| D | b | | 2941 | AAGCTGTCCGGCCTCGGACTCAATGTCTAGCATATTACCGGGGCTTGATGATCCGTC | 3000 |
| Q | y | | 3001 | ATACCAACTAGCGAGAGCTCATTTGTCTAGCAACGAGCGTCTTAATGACGGCTTTACC | 3060 |
| D | b | | 3001 | ATACCAACACTAGCGAGAGCTCATTTGTCTAGCAACGAGCGTCTTAATGACGGCTTTACC | 3060 |
| Q | y | | 3061 | GGCGAATTCGAATCAGTGATCGCATGCGAATACATGTGTACCCAGACAGTCGACTTCAGC | 3120 |
| D | b | | 3061 | GGCGAATTCGAATCAGTGATCGCATGCGAATACATGTGTACCCAGACAGTCGACTTCAGC | 3120 |
| Q | y | | 3121 | CTGAAACCCGACTTCAACAATTGACAGCACGCCGTGCCAACAGACGCAGTGTCAAGCTCG | 3180 |
| D | b | | 3121 | CTGAAACCCGACTTCAACAATTGACAGCACGCCGTGCCAACAGACGCAGTGTCAAGCTCG | 3180 |
| Q | y | | 3181 | CAGCGGAGGACGAGACTGGTAGGGGACAGATGGGCATTACAGTTTGTGACTCCAGA | 3240 |
| D | b | | 3181 | CAGCGGAGGACGAGACTGGTAGGGGACAGATGGGCATTACAGTTTGTGACTCCAGA | 3240 |
| Q | y | | 3241 | GAAACGGCCCTCGGGCATTGTCGATTCCTCGGTTCTGTGCGAGTGCATGACGCGGGCTGT | 3300 |
| D | b | | 3241 | GAAACGGCCCTCGGGCATTGTCGATTCCTCGGTTCTGTGCGAGTGCATGACGCGGGCTGT | 3300 |
| Q | y | | 3301 | GCTTGTGTACGAGTCAAGCCCGCCGAGACCTCAGTTAGTTTCCGGGTACTCTAAACACA | 3360 |
| D | b | | 3301 | GCTTGTGTACGAGTCAAGCCCGCCGAGACCTCAGTTAGTTTCCGGGTACTCTAAACACA | 3360 |
| Q | y | | 3361 | CCAGGGTTCGCCCTCTGCCAGGACCATCTGGAGTTTGGGAGAGCGTCTTACAGGGCTC | 3420 |
| D | b | | 3361 | CCAGGGTTCGCCCTCTGCCAGGACCATCTGGAGTTTGGGAGAGCGTCTTACAGGGCTC | 3420 |
| Q | y | | 3421 | ACCACATAGACGCCCATTTCTTTGTCCCAGACTAAGCAGCAGCAGAGACAATTCCTCCCTAC | 3480 |
| D | b | | 3421 | ACCACATAGACGCCCATTTCTTTGTCCCAGACTAAGCAGCAGCAGAGACAATTCCTCCCTAC | 3480 |
| Q | y | | 3481 | CTGGTAGCATACGAGCTACGGTGTGCGCAGGGCTCAGGCTCCACCTCCATCGTGGGAC | 3540 |
| D | b | | 3481 | CTGGTAGCATACGAGCTACGGTGTGCGCAGGGCTCAGGCTCCACCTCCATCGTGGGAC | 3540 |
| Q | y | | 3541 | CAAATGTGAAGTGTCTCATAGCGCTAAAGCCTACGCTGCAGGGCCACGCCCTCTGCTG | 3600 |
| D | b | | 3541 | CAAATGTGAAGTGTCTCATAGCGCTAAAGCCTACGCTGCAGGGCCACGCCCTCTGCTG | 3600 |
| Q | y | | 3601 | TATAGCTGGGAGCCGTTCAAACAGAGTTACTACACACACCCCCATACCAATACATC | 3660 |
| D | b | | 3601 | TATAGCTGGGAGCCGTTCAAACAGAGTTACTACACACACCCCCATACCAATACATC | 3660 |
| Q | y | | 3661 | ATGGCATGATGTCCGTGACCTCGAGGTTCGTACGAGCACCTGGGTGCTGTAGGCGGA | 3720 |
| D | b | | 3661 | ATGGCATGATGTCCGTGACCTCGAGGTTCGTACGAGCACCTGGGTGCTGTAGGCGGA | 3720 |
| Q | y | | 3721 | GTCTTAGCAGCTCTGGCGCGATTTCCTGTGACAAAGCAGCGTGTGTATGTGGGAGG | 3780 |
| D | b | | 3721 | GTCTTAGCAGCTCTGGCGCGATTTCCTGTGACAAAGCAGCGTGTGTATGTGGGAGG | 3780 |
| Q | y | | 3781 | ATCATCTTGTCCGAAAAGCCGCCATCATTCGCCGACAGGGAAGTCTTTACCGGGAGTTC | 3840 |
| D | b | | 3781 | ATCATCTTGTCCGAAAAGCCGCCATCATTCGCCGACAGGGAAGTCTTTACCGGGAGTTC | 3840 |
| Q | y | | 3841 | GATGAGATGGAAGATGCGCCTCACACCTCCCTTACATCGAACAGGGAATCAGACTCGCC | 3900 |
| D | b | | 3841 | GATGAGATGGAAGATGCGCCTCACACCTCCCTTACATCGAACAGGGAATCAGACTCGCC | 3900 |
| Q | y | | 3901 | GAAACAATTCAAACAGAGGCAATCGGTTGTGTGMAACAGCCACCAAGCGGAGGCT | 3960 |
| D | b | | 3901 | GAAACAATTCAAACAGAGGCAATCGGTTGTGTGMAACAGCCACCAAGCGGAGGCT | 3960 |
| Q | y | | 3961 | GCTGCTCCCGTGTGGAAATCAAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG | 4020 |
| D | b | | 3961 | GCTGCTCCCGTGTGGAAATCAAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG | 4020 |
| Q | y | | 4021 | TGGAATTTTCATACGCGGATACAAATATTAGCAGGCTTGTCCACTCTGCTGGCAACCCC | 4080 |

QY 6241 GAAGCTGTAGCTGACGCGCCCAATTCGCGCAGATCTAAATTTGGCTATGGGCAAG 6300
Db |||||
QY 6241 GAAGCTGTAGCTGACGCGCCCAATTCGCGCAGATCTAAATTTGGCTATGGGCAAG 6300
Db |||||
QY 6301 GAGCTCCGGAACCTATCCAGCAAGCGCGTTAAACACATCCGCTCCGCTGCGAGGACTTG 6360
Db |||||
QY 6301 GAGCTCCGGAACCTATCCAGCAAGCGCGTTAAACACATCCGCTCCGCTGCGAGGACTTG 6360
Db |||||
QY 6361 CTGGAAGACACTGAGACACCAATTGACACCAATATGACACCAATATGAGGTTTCTGC 6420
Db |||||
QY 6361 CTGGAAGACACTGAGACACCAATTGACACCAATATGACACCAATATGAGGTTTCTGC 6420
Db |||||
QY 6421 GTCCAAACAGAGAAGGGGCGCGCAAGCAGCTGCTTACCACTATGAGGTTTCTGC 6480
Db |||||
QY 6421 GTCCAAACAGAGAAGGGGCGCGCAAGCAGCTGCTTACCACTATGAGGTTTCTGC 6480
Db |||||
QY 6481 GTTCGCTGTGCGAGAAATGGCCCTTTACGATGTGCTTCCACCTCCCTCAGGCGCTG 6540
Db |||||
QY 6481 GTTCGCTGTGCGAGAAATGGCCCTTTACGATGTGCTTCCACCTCCCTCAGGCGCTG 6540
Db |||||
QY 6541 ATGGGCTCTTACCGGATTCGAATCTCTCTGCGACAGCGGTGAGTTTCTGTTGAAT 6600
Db |||||
QY 6541 ATGGGCTCTTACCGGATTCGAATCTCTCTGCGACAGCGGTGAGTTTCTGTTGAAT 6600
Db |||||
QY 6601 GCCTGGAAGCGAAGAAATGCCCTATGGGCTTCGCATATGACACCGCTGTTGACTCA 6660
Db |||||
QY 6601 GCCTGGAAGCGAAGAAATGCCCTATGGGCTTCGCATATGACACCGCTGTTGACTCA 6660
Db |||||
QY 6661 AGGTCACGTAGAAATGACATCCGCTGTGAGGAGTCAATCTACCAATGTTGACTTGGCC 6720
Db |||||
QY 6661 AGGTCACGTAGAAATGACATCCGCTGTGAGGAGTCAATCTACCAATGTTGACTTGGCC 6720
Db |||||
QY 6721 CCCGAAGCCAGACAGGCCATAGGTCGCTCAAGAGCGCTTTTACATCGGGGCGCCCTG 6780
Db |||||
QY 6721 CCCGAAGCCAGACAGGCCATAGGTCGCTCAAGAGCGCTTTTACATCGGGGCGCCCTG 6780
Db |||||
QY 6781 ACTAATTTAAAGGCGAAGAACTCGCGCTATCGCGGTGCGCGCGAGCGGTGACTGACG 6840
Db |||||
QY 6781 ACTAATTTAAAGGCGAAGAACTCGCGGTGCGCGGTGCGCGCGAGCGGTGACTGACG 6840
Db |||||
QY 6841 ACCAGCTCGGTAATACCTTACATGTTACTTGAAGCGCGCTGCGCGCTGTCGAGCTCG 6900
Db |||||
QY 6841 ACCAGCTCGGTAATACCTTACATGTTACTTGAAGCGCGCTGCGCGCTGTCGAGCTCG 6900
Db |||||
QY 6901 AAGCTCCAGGACTCAGATCTGATGCGGAGCAGCACTTGTGTTATCTGTGAAGC 6960
Db |||||
QY 6901 AAGCTCCAGGACTCAGATCTGATGCGGAGCAGCACTTGTGTTATCTGTGAAGC 6960
Db |||||
QY 6961 GCGGGGACCCAAAGAGGAGCGAGCGCTACGGGCTTACGGAGGCTATGACTAGATAC 7020
Db |||||
QY 6961 GCGGGGACCCAAAGAGGAGCGAGCGCTACGGGCTTACGGAGGCTATGACTAGATAC 7020
Db |||||
QY 7021 TCTGCGCCCTCGGGACCCGCCAAACACAGATACGACTTGGAGTTGATAACATATGC 7080
Db |||||
QY 7021 TCTGCGCCCTCGGGACCCGCCAAACACAGATACGACTTGGAGTTGATAACATATGC 7080
Db |||||
QY 7081 TCTTCCAAATGTCAGTCGCGCAGATGATCTGGGCAAGGCTGTAATCTATCCACCGT 7140
Db |||||
QY 7081 TCTTCCAAATGTCAGTCGCGCAGATGATCTGGGCAAGGCTGTAATCTATCCACCGT 7140
Db |||||
QY 7141 GACCCCAACACCCCTTGGCGGCTGCGGCGAGCTGAGGAGTGTGATAACATATGC 7200
Db |||||
QY 7141 GACCCCAACACCCCTTGGCGGCTGCGGCGAGCTGAGGAGTGTGATAACATATGC 7200
Db |||||
QY 7201 TCTTGGCTAGGCAACATCATGATGTATGCGCCACCTTGGGCAAGGATGATCTGATG 7260
Db |||||
QY 7201 TCTTGGCTAGGCAACATCATGATGTATGCGCCACCTTGGGCAAGGATGATCTGATG 7260
Db |||||
QY 7261 ACTCATTTCTTCCATCTTCTAGTCTAGGAAACAACTTGAAAGCCCTAGATTTCTAG 7320
Db |||||
QY 7261 ACTCATTTCTTCCATCTTCTAGTCTAGGAAACAACTTGAAAGCCCTAGATTTCTAG 7320
Db |||||
QY 7321 ATCTACGGGCGCTGTTACTCCATTTGAGCCACTTGACCTACCTCAGATCATCAACGACTC 7380

Db |||||
QY 7321 ATCTACGGGCGCTGTTACTCCATTTAGCCACTTGACACTCCTCAGATCATTTCAACGACTC 7380
Db |||||
QY 7381 CATGGCCTTAGCGCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGCTGCT 7440
Db |||||
QY 7381 CATGGCCTTAGCGCAATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGCTGCT 7440
Db |||||
QY 7441 TCATGCTCAGGAAACTTGGGGTACCGCTTCCGAGTCTGGAGACATCGGGCCAGAGT 7500
Db |||||
QY 7441 TCATGCTCAGGAAACTTGGGGTACCGCTTCCGAGTCTGGAGACATCGGGCCAGAGT 7500
Db |||||
QY 7501 GTCCGCGCTAGGCTACTGTCCAGGGGGAGGCTGCCACTTGTGGCAAGTACTCTTC 7560
Db |||||
QY 7501 GTCCGCGCTAGGCTACTGTCCAGGGGGAGGCTGCCACTTGTGGCAAGTACTCTTC 7560
Db |||||
QY 7561 AACTGGGAGTAAAGCAAGCTCAAACTCACTCCCAATCCCGCTGCTGCCAGTTGGAT 7620
Db |||||
QY 7621 TTATCCAGCTGGTTCGTTCTGCTGTTACAGGGGGAGACATATCACAGCCTGTCTCGT 7680
Db |||||
QY 7621 TTATCCAGCTGGTTCGTTCTGCTGTTACAGGGGGAGACATATCACAGCCTGTCTCGT 7680
Db |||||
QY 7681 GCCGACCCCGCTGGTTCATGTGTGCTTCTACTCTCTCTCTCTCTCTCTCTCTCTCT 7740
Db |||||
QY 7681 GCCGACCCCGCTGGTTCATGTGTGCTTCTACTCTCTCTCTCTCTCTCTCTCTCTCT 7740
Db |||||
QY 7741 CTACTCCCAACCGATGAACGGGGAGCTAAACACATCCAGGCCAATAGGCCATCTCTGTTT 7800
Db |||||
QY 7741 CTACTCCCAACCGATGAACGGGGAGCTAAACACATCCAGGCCAATAGGCCATCTCTGTTT 7800
Db |||||
QY 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
Db |||||
QY 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
Db |||||
QY 7861 TTTTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 7920
Db |||||
QY 7861 TTTTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 7920
Db |||||
QY 7921 TAGCTGAAAGGTCGCTGAGCCGCTTGAAGTCTGAGAGTCTGATCTAGCCCTCTCTGC 7980
Db |||||
QY 7921 TAGCTGAAAGGTCGCTGAGCCGCTTGAAGTCTGAGAGTCTGATCTAGCCCTCTCTGC 7980
Db |||||
QY 7981 AGATCAAGTACT 7992
Db |||||
QY 7981 AGATCAAGTACT 7992
Db |||||

RESULT 11

AAA98968
ID AAA98968 standard; DNA; 7989 BP.
XX
AC AAA98968;
XX
DT 08-FEB-2001 (first entry)
XX
DE Hepatitis C virus DNA fragment SEQ ID NO: 4.
XX
KW Cell culture; therapy; infection; vaccine; diagnosis; gene therapy; ds.
XX
OS Hepatitis C virus.
XX
PN DE19915178-Al.
XX
PD 05-OCT-2000.
XX
PF 03-APR-1999; 99DE-01015178.
XX
PR 03-APR-1999; 99DE-01015178.
XX
PA (UYMA-) UNIV MAINZ GUTENBERG JOHANNES.
XX
PI Bartenschlager R;

XX WPI; 2000-629140/61.
XX Cell culture system for hepatitis C virus, useful e.g. in screening for
XX therapeutic agents, comprises human hepatoma cells containing a viral RNA
XX construct that includes a selectable gene.
XX
XX Claim 8; Page 37-43; 58pp; German.
XX
XX This invention describes a novel Hepatitis C virus (HCV) cell culture
XX system comprising human hepatoma cells that contain an integrated HCV-RNA
XX construct (I). (I) contains the HCV-specific RNA segments 5'-NTR (non-
XX translated region), NS (non-structural), NS4B, NS4B, NS5A, NS5B and 3'-
XX NTR, and a selectable (marker) gene (II). The cell cultures, and/or (I),
XX are used to prepare, evaluate and/or test therapeutic and/or diagnostic
XX agents for HCV infections, and to prepare vaccines against HCV infection
XX (particularly preparation of attenuated HCV). The can also be used for
XX preparation of a liver-specific delivery system for gene therapy, and to
XX identify cells permissive for HCV replication. Virus RNA replicates
XX autonomously and with high efficiency in this cellular system, so that
XX variations in replication rates can be measured (for screening antiviral
XX agents) quantitatively or qualitatively, using standard laboratory
XX equipment. Efficient replication of HCV RNA is only achieved when the
XX specified RNA segments are present and when the transfected cells are
XX maintained under permanent selection pressure
XX
XX Sequence 7989 BP; 1647 A; 2368 C; 2243 G; 1731 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 7989; DB 3; Length 7989;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 7989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 601 CGACGGCGGTTCCTTGGCGAGCTGTGCTCGACGTTGTCTACTGAAGCGGAAAGGAGCTG 660

Db CGACGGCGGTTCCTTGGCGAGCTGTGCTCGACGTTGTCTACTGAAGCGGAAAGGAGCTGC 660
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Qy TTGTCGATCAGGATGATCGGACGAGGATCATGAGGCTCGGCGGCGGCGGCGGCGGCTTCG 900
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1741 AACCTCTAGGCCCCCGAACAACACGGGACGTGGTTTCTTTTGAAAAACAGATAATACC 1800
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RESULT 12

ADJ57845
 ID ADJ57845 standard; DNA; 7989 BP.
 XX
 AC ADJ57845;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE HCV replicon encoding sequence.
 XX
 KW hepatitis C virus; HCV; Antiinflammatory; Hepatotropic; Virucide; ds;
 KW HCV replicon.
 XX
 OS Unidentified.
 XX

Key Location/Qualifiers
 CDS 1801..7759
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 /product= "HCV replicon"
 WO2004015131-A2.
 19-FEB-2004.
 12-AUG-2003; 2003WO-US025260.
 12-AUG-2002; 2002US-0402661P.
 (BRIM) BRISTOL-MYERS SQUIBB CO.
 Gao M, Lemm JA, O'boyle DR, Nower P, Rigat K, Sun J;
 WPI; 2004-180685/17.
 P-PSDB; ADJ57846.
 XX
 PT Use of hepatitis C virus assays or reporter assays, e.g. identifying a
 PT compound that inhibits hepatitis C virus RNA replication or identifying a
 PT compound that modulates the activity of a gene of interest.
 XX
 PS Claim 3; SEQ ID NO 1; 45pp; English.
 XX
 CC The present invention relates to the use of hepatitis C virus (HCV)
 CC assays for identifying a compound that inhibits HCV RNA replication and
 CC reporter assays for identifying a compound that modulates the activity of
 CC a gene of interest. The assays are useful for identifying a compound that
 CC inhibits HCV RNA replication or for identifying a compound that modulates
 CC the activity of a gene of interest. The HCV assay is useful for high
 CC throughput screening that quantifies both the amount of HCV RNA
 CC replication and inhibitory activity associated with a test compound and the
 CC amount of cytotoxicity associated with the test compound. The compound is
 CC useful for treating hepatitis C infection. Assays of the invention have
 CC distinct advantages when compared to qRT-PCR or other methods in that
 CC assays of the invention may take place in situ in a detergent based crude
 CC cell lysate, which requires no further preparation prior to performing
 CC the assays. The assays do not also involve numerous manipulations to add
 CC or subtract reagents after addition of test compounds and are desirably
 CC based on a viral protein which is required by the HCV replicon for
 CC replication. The present sequence represents a HCV replicon encoding
 CC sequence used in the assay of the invention.
 XX
 SQ Sequence 7989 BP; 1647 A; 2368 C; 2243 G; 1731 T; 0 U; 0 Other;
 Query Match 100.0%; Score 7989; DB 12; Length 7989;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 7989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCACGCCCGGATGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAACCTACTG 60
 DB 1 GCACGCCCGGATGGGGCGACACTCCACCATAGATCACTCCCTGTGAGGAACCTACTG 60
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 DB 121 CCCCCCTCCCGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAG 180
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 DB 181 GACGACCGGGTCTTTCTTGGATCAACCGCTCAATGCTGAGATTTGGCGGTGCCCC 240
 QY 241 GCGAGCTGTAGCCGAGTAGTGTGGTTCGGAAGCGCTTGTGCTACTGCTGATAGG 300
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 QY 901 CCAGGCTCAAGCGCGCATGCGCGAGCGAGATCTCGTGTGAGCCCATGGGATGCTT 960
 Db 901 CCAGGCTCAAGCGCGCATGCGCGAGCGAGATCTCGTGTGAGCCCATGGGATGCTT 960
 QY 961 GTTTCGGAATATCATGTTGGTGAATAATGGCGCTTTTCTGGATTCATCGACTGTGGCGGCG 1020
 Db 961 GTTTCGGAATATCATGTTGGTGAATAATGGCGCTTTTCTGGATTCATCGACTGTGGCGGCG 1020
 QY 1021 TGGGTGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCGCTGATATTCGTGAAGAGC 1080
 Db 1021 TGGGTGTGCGGACCGCTATCAGGACATAGCGTTGGCTACCGCTGATATTCGTGAAGAGC 1080
 QY 1081 TTGGCGGCGAATGGGCTGACCGCTTCTCGTCTTTACGGTATCGCGCTCCCGATTGCG 1140
 Db 1081 TTGGCGGCGAATGGGCTGACCGCTTCTCGTCTTTACGGTATCGCGCTCCCGATTGCG 1140
 QY 1141 AGCGCATCGCTTCTATCGCTTCTTGAAGAGTCTTCTGAGTTTAAACAGACCAACAG 1200
 Db 1141 AGCGCATCGCTTCTATCGCTTCTTGAAGAGTCTTCTGAGTTTAAACAGACCAACAG 1200
 QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCCCTTAACTTACTGGC 1260
 Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCCCGCCCCCTTAACTTACTGGC 1260
 QY 1261 CGAAGCCCTTGGAAATAAGCGCGGTGTGCTTGTCTATGTTTATTTTCCACCATATG 1320
 Db 1261 CGAAGCCCTTGGAAATAAGCGCGGTGTGCTTGTCTATGTTTATTTTCCACCATATG 1320
 QY 1321 CGGCTTTTGGCAATGTAGGCGCGGAAACCTGGCCCTGTCTTCTTGAAGAGCATTCCT 1380
 Db 1321 CGGCTTTTGGCAATGTAGGCGCGGAAACCTGGCCCTGTCTTCTTGAAGAGCATTCCT 1380
 QY 1381 AGGGGTCTTCCCTCTCGCCCAAGGATGCAAGGTCTGTTGAATGTGTGAGGAGCA 1440
 Db 1381 AGGGGTCTTCCCTCTCGCCCAAGGATGCAAGGTCTGTTGAATGTGTGAGGAGCA 1440

1441 GTTCCTCTGGAAGCTTCTTGAAGCAAAACAACGTCGTGTAGCAACCTTTGAGGAGCGG 1500
1441 GTTCCTCTGGAAGCTTCTTGAAGCAAAACAACGTCGTGTAGCAACCTTTGAGGAGCGG 1500
1501 AACCCCCACCTGCGGACAGGTGCTCTGCGGCCAAAGACCAACGTCGTGTATAGATACACCT 1560
1501 AACCCCCACCTGCGGACAGGTGCTCTGCGGCCAAAGACCAACGTCGTGTATAGATACACCT 1560
1561 GCAAAGCGGCACAAACCCAGTGCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAA 1620
1561 GCAAAGCGGCACAAACCCAGTGCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAA 1620
1621 TGCTCTCTCTCAAGCGTATTCAACAAGGGCTGAAGGATGCCAGAGGTACCCCAATTGT 1680
1621 TGCTCTCTCTCAAGCGTATTCAACAAGGGCTGAAGGATGCCAGAGGTACCCCAATTGT 1680
1681 ATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTTGTAGTCAAGTTAAAA 1740
1681 ATGGGATCTGATCTGGGGCTCGGTGCACATGCTTTACATGTTGTAGTCAAGTTAAAA 1740
1741 AAGCTTAGGCCCCCGGAACCCAGGGACGTGGTTCCTTTGAAAAACAGATAATACC 1800
1741 AAGCTTAGGCCCCCGGAACCCAGGGACGTGGTTCCTTTGAAAAACAGATAATACC 1800
1801 ATGGCGCTATTACGGCTACTTCCCAACAGACGGAGGCTCACTTGGCTGCATCATCACT 1860
1801 ATGGCGCTATTACGGCTACTTCCCAACAGACGGAGGCTCACTTGGCTGCATCATCACT 1860
1861 AGCTCACAGGGCGGACAGAACACAGTGCAGGGGAGGTCCAAAGTGTCTCCACGGCA 1920
1861 AGCTCACAGGGCGGACAGAACACAGTGCAGGGGAGGTCCAAAGTGTCTCCACGGCA 1920
1921 ACACAACTTTCTGCGGACCTGCGTCAATGGCGTGTGTGGACTGTCTATCATGTGCG 1980
1921 ACACAACTTTCTGCGGACCTGCGTCAATGGCGTGTGTGGACTGTCTATCATGTGCGC 1980
1981 GGCTCAAGACCCCTTCCCGGCCCAAGGGCCCAATCACCACAAATGTACCAATGTGGAC 2040
1981 GGCTCAAGACCCCTTCCCGGCCCAAGGGCCCAATCACCACAAATGTACCAATGTGGAC 2040
2041 CAGGACCTCGTGGCTGCAAGCGCCCCCGGGCGCGTTCCTTGACACCATGCACTGCG 2100
2041 CAGGACCTCGTGGCTGCAAGCGCCCCCGGGCGCGTTCCTTGACACCATGCACTGCG 2100
2101 GGCAGCTCGGACCTTTACTTGTGTACAGAGCATGCGGATGTCATTCGGGTGCGCGCGG 2160
2101 GGCAGCTCGGACCTTTACTTGTGTACAGAGCATGCGGATGTCATTCGGGTGCGCGCGG 2160
2161 GSCGACAGAGGGAGGCTACTCTCCCGCAGGCGCGTGTGAGTGTGATTCGGGTGCGCGG 2220
2161 GSCGACAGAGGGAGGCTACTCTCCCGCAGGCGCGTGTGAGTGTGATTCGGGTGCGCGG 2220
2221 GCGGTCCACTGCTCTGCCCTCGGGGACGCTGTGGGCTGCTCTCTCTGAGGGCTCTTCG 2280
2221 GCGGTCCACTGCTCTGCCCTCGGGGACGCTGTGGGCTGCTCTCTCTGAGGGCTCTTCG 2280
2281 ACCGAGGGTTGGAAGCGGTGACTTTGTATCCCGTTCGAGTCTATGGAACCACTATG 2340
2281 ACCGAGGGTTGGAAGCGGTGACTTTGTATCCCGTTCGAGTCTATGGAACCACTATG 2340
2341 CGGTCCCGGTCTTACCGGACAACTGCTCCCTCCGCGGTACCGCAGACATTCAGGTG 2400
2341 CGGTCCCGGTCTTACCGGACAACTGCTCCCTCCGCGGTACCGCAGACATTCAGGTG 2400
2401 GCGCATCTACAGCCCTTACTGGTAGCGGACAGACTAAGTGCAGGCTCGGTGATGCA 2460
2401 GCGCATCTACAGCCCTTACTGGTAGCGGACAGACTAAGTGCAGGCTCGGTGATGCA 2460
2461 GCCCAAGGGTATAAGGTGCTTGTCTGTAAACCGTCCGTCGCGGCCACCCCTAGTTTCGG 2520
2461 GCCCAAGGGTATAAGGTGCTTGTCTGTAAACCGTCCGTCGCGGCCACCCCTAGTTTCGG 2520

2521 GCCTATATGCTTAAGGCACATGGTATCGACCCCTAACATCAGAACCGGGGTAAAGCAATC 2580
2521 GCCTATATGCTTAAGGCACATGGTATCGACCCCTAACATCAGAACCGGGGTAAAGCAATC 2580
2581 ACCACGGGTGCCCCCATCAGTACTCCACCTATGCAAGTTTCTTGCCGAGGTGGTTCG 2640
2581 ACCACGGGTGCCCCCATCAGTACTCCACCTATGCAAGTTTCTTGCCGAGGTGGTTCG 2640
2641 TCTGGGGCGCTTATGACATCATATATGTGATGAGTGCACCTCAACTGACTCGACCACT 2700
2641 TCTGGGGCGCTTATGACATCATATATGTGATGAGTGCACCTCAACTGACTCGACCACT 2700
2701 ATCTCGGCGATCGGACAGTCTCGGACCAAGCGGAGACGGCTGAGGCGGACTCGTGGTG 2760
2701 ATCTCGGCGATCGGACAGTCTCGGACCAAGCGGAGACGGCTGAGGCGGACTCGTGGTG 2760
2761 CTCGCCACCGCTACGCTCCGGGATCGGTCAACGTCGACATCCAAACATCGAGGAGGTG 2820
2761 CTCGCCACCGCTACGCTCCGGGATCGGTCAACGTCGACATCCAAACATCGAGGAGGTG 2820
2821 GCTCTGTCTAGGACTGAGGAAATCCCTTTTATGGCAAAACCCATCCCATCGAGCAATC 2880
2821 GCTCTGTCTAGGACTGAGGAAATCCCTTTTATGGCAAAACCCATCCCATCGAGCAATC 2880
2881 AAGGGGGGAGGACACCTCAATTTCTGCCATTTCCAAAGAAATGTGATGAGCTCGCGCG 2940
2881 AAGGGGGGAGGACACCTCAATTTCTGCCATTTCCAAAGAAATGTGATGAGCTCGCGCG 2940
2941 AAGCTGTCCGGCTCCGACTCAATGCTGTAGCATATTTACCGGGGCTTGTATGATCCGTC 3000
2941 AAGCTGTCCGGCTCCGACTCAATGCTGTAGCATATTTACCGGGGCTTGTATGATCCGTC 3000
3001 ATACCAACTAGCGGAGACGTCTATGTCGCAACCGACGCTCTAATGAGGCTTTTACC 3060
3001 ATACCAACTAGCGGAGACGTCTATGTCGCAACCGACGCTCTAATGAGGCTTTTACC 3060
3061 GCGATTTTCGACTCGAGTGCATGATCATGTCATGTCATGTCATGTCATGTCATGTCATG 3120
3061 GCGATTTTCGACTCGAGTGCATGATCATGTCATGTCATGTCATGTCATGTCATGTCATG 3120
3121 CTGGACCGGACCTTCAACATTTGAGACGACGACGCTGCCAACAGACGCGGTGTCAGCTCG 3180
3121 CTGGACCGGACCTTCAACATTTGAGACGACGACGCTGCCAACAGACGCGGTGTCAGCTCG 3180
3181 CAGCGCGGAGGACGAGTGTGAGGGGAGGATGGGCAATTAAGGTTTGTGACTCCAGG 3240
3181 CAGCGCGGAGGACGAGTGTGAGGGGAGGATGGGCAATTAAGGTTTGTGACTCCAGG 3240
3241 GAAACCGGCTCGGGCATGTTGATTCCTCGGTTCTGTGGAGTGTATGACGCGGGCTGT 3300
3241 GAAACCGGCTCGGGCATGTTGATTCCTCGGTTCTGTGGAGTGTATGACGCGGGCTGT 3300
3301 GCTTGGTACGAGCTCACCGCGCCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACA 3360
3301 GCTTGGTACGAGCTCACCGCGCCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACA 3360
3361 CCAGGTTGCCGCTGTCAGGACCATCTGGAGTTCTGGAGAGGCTCTTTACAGGCTC 3420
3361 CCAGGTTGCCGCTGTCAGGACCATCTGGAGTTCTGGAGAGGCTCTTTACAGGCTC 3420
3421 ACCCAGATAGACGCTTCTTGTCCAGACTAAGCAGGAGGAGACAATTCCTCCCTAC 3480
3421 ACCCAGATAGACGCTTCTTGTCCAGACTAAGCAGGAGGAGACAATTCCTCCCTAC 3480
3481 CTGTTAGCATACAGGCTTCTGTCGCGGAGGCTCAGGCTCCACCTCCATCGTGGAC 3540
3481 CTGTTAGCATACAGGCTTCTGTCGCGGAGGCTCAGGCTCCACCTCCATCGTGGAC 3540
3541 CAATGTGGAAGTGTCTCATACGCTTAAAGCTACGCTGACGCGGCAACCGCCCTGCTG 3600
3541 CAATGTGGAAGTGTCTCATACGCTTAAAGCTACGCTGACGCGGCAACCGCCCTGCTG 3600
3601 TATAGGCTGGAGCGGTTCAAAACGAGGTTTACTACACACACCCCTTAAACCAATATC 3660

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|----|------|---|------|------|--|------|
| Db | 3601 | TATAGCTGGAGCCGTTCAAAACGAGGTTACTACACACACCCCAATCAATACATC | 3660 | 4681 | ACGGTGTGACTGATTTAAAGACCTGGCTCCAGTCCAGCTCTCTGCGCGGATTCGCGGA | 4740 |
| Qy | 3661 | ATGGCATGATGTCGGCTGACCTGGAGTCTGTCACAGACACCTGGGTGCTGGTAGCGGA | 3720 | 4741 | GTCCCCCTTCTCATGTCAAGTGGGTACAAAGGAGTCTGGGGGGGACGACATCATG | 4800 |
| Db | 3661 | ATGGCATGATGTCGGCTGACCTGGAGTCTGTCACAGACACCTGGGTGCTGGTAGCGGA | 3720 | 4741 | GTCCCCCTTCTCATGTCAAGTGGGTACAAAGGAGTCTGGGGGGGACGACATCATG | 4800 |
| Qy | 3721 | GTCCATAGACCTCTGGCGGCTATTGCTGACACAGGAGCGTGTCAATGTGGCAGG | 3780 | 4801 | CAAAACACCTGCGCCATGTGGAGCAGATCACCGGACATGTGAACACGGTTCATGAGG | 4860 |
| Db | 3721 | GTCCATAGACCTCTGGCGGCTATTGCTGACACAGGAGCGTGTCAATGTGGCAGG | 3780 | 4801 | CAAAACACCTGCGCCATGTGGAGCAGATCACCGGACATGTGAACACGGTTCATGAGG | 4860 |
| Qy | 3781 | ATCATCTGTGCGGAAGCCGGCATCATTTCCGACAGGAAGTCTCTTACCGGAGTTC | 3840 | 4861 | ATCGTGGGCTAGGACCTGTAGTAAACAGTGCATGGAACATTCGCCATTAACCGGTAC | 4920 |
| Db | 3781 | ATCATCTGTGCGGAAGCCGGCATCATTTCCGACAGGAAGTCTCTTACCGGAGTTC | 3840 | 4861 | ATCGTGGGCTAGGACCTGTAGTAAACAGTGCATGGAACATTCGCCATTAACCGGTAC | 4920 |
| Qy | 3841 | GATGAGATGAAGAGTGGCTCACACCTCCCTTACATGAAACAGGAATGCGAGTCCG | 3900 | 4921 | ACCAAGGCGCCCTGACGCGCTCCCGGCGCCAAATPATTTCTAGGGGCTGTGGCGGGT | 4980 |
| Db | 3841 | GATGAGATGAAGAGTGGCTCACACCTCCCTTACATGAAACAGGAATGCGAGTCCG | 3900 | 4921 | ACCAAGGCGCCCTGACGCGCTCCCGGCGCCAAATPATTTCTAGGGGCTGTGGCGGGT | 4980 |
| Qy | 3901 | GAACAATTAACAGAGGCAATCGGTTGCTGCAACAGCCACCAAGCAGCGAGGCT | 3960 | 4981 | GCTGCTGAGGAGTACGTGGAGGTTACCGGGTGGGGATTTCCACTACGTGACGGGCATG | 5040 |
| Db | 3901 | GAACAATTAACAGAGGCAATCGGTTGCTGCAACAGCCACCAAGCAGCGAGGCT | 3960 | 4981 | GCTGCTGAGGAGTACGTGGAGGTTACCGGGTGGGGATTTCCACTACGTGACGGGCATG | 5040 |
| Qy | 3961 | GCTGCTCCGTTGGTGAATCAAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG | 4020 | 5041 | ACCACTACACAACTAAAGTCCCGTGTACAGTTCGGGCGCCCGAAATTTCTTACAGAAAGT | 5100 |
| Db | 3961 | GCTGCTCCGTTGGTGAATCAAGTGGCGGACCTCGAAGCCTTCTGGGCGAAGCATATG | 4020 | 5041 | ACCACTACACAACTAAAGTCCCGTGTACAGTTCGGGCGCCCGAAATTTCTTACAGAAAGT | 5100 |
| Qy | 4021 | TGGAATTTTATCAGCGGATCAATATTTAGCAGGTTGTCCACTGCTGGCGCAACCC | 4080 | 5101 | GATGGGTGGGTTGACAGGTACGCTCCAGCGTGCAAAACCCCTCTTACCGGAGGAGT | 5160 |
| Db | 4021 | TGGAATTTTATCAGCGGATCAATATTTAGCAGGTTGTCCACTGCTGGCGCAACCC | 4080 | 5101 | GATGGGTGGGTTGACAGGTACGCTCCAGCGTGCAAAACCCCTCTTACCGGAGGAGT | 5160 |
| Qy | 4081 | CGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT | 4140 | 5161 | ACATTCCTGCTGGGCTCAATCAATACCTGGTGGGTACAGTCCCATGCGAGCCCGAA | 5220 |
| Db | 4081 | CGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT | 4140 | 5161 | ACATTCCTGCTGGGCTCAATCAATACCTGGTGGGTACAGTCCCATGCGAGCCCGAA | 5220 |
| Qy | 4141 | ACCTCTCTGTTTAAATCTCTGGGGGATGGGTGGCGGCCCAACTTGTCTTCCAGCGCT | 4200 | 5221 | CCGACGTAGCAGTGTCACTTCCATGCTCACCGACCCCTCCCATTTACCGCGGAGACG | 5280 |
| Db | 4141 | ACCTCTCTGTTTAAATCTCTGGGGGATGGGTGGCGGCCCAACTTGTCTTCCAGCGCT | 4200 | 5221 | CCGACGTAGCAGTGTCACTTCCATGCTCACCGACCCCTCCCATTTACCGCGGAGACG | 5280 |
| Qy | 4201 | GCTTCTGCTTTTGGTAGGCGCGGCATCGCTGGAGCGGTGTGGCAGATAGGCTTGGG | 4260 | 5281 | GCTAAGCGTAGGCTGGCGAGGGGATCTCCCGCTCTTGGGCGAGCTATCATAGTAGCCAG | 5340 |
| Db | 4201 | GCTTCTGCTTTTGGTAGGCGCGGCATCGCTGGAGCGGTGTGGCAGATAGGCTTGGG | 4260 | 5281 | GCTAAGCGTAGGCTGGCGAGGGGATCTCCCGCTCTTGGGCGAGCTATCATAGTAGCCAG | 5340 |
| Qy | 4261 | AAGTGTCTTGGATATTTTGGCAGGTTATGGAGCAGGGTGGAGCGCGCTCGTGCC | 4320 | 5341 | CTGTCTGGCGCTTCTTGAAGGCAACATGCACTACCGTCTATGCTCCCGGAGCCTGAC | 5400 |
| Db | 4261 | AAGTGTCTTGGATATTTTGGCAGGTTATGGAGCAGGGTGGAGCGCGCTCGTGCC | 4320 | 5341 | CTGTCTGGCGCTTCTTGAAGGCAACATGCACTACCGTCTATGCTCCCGGAGCCTGAC | 5400 |
| Qy | 4321 | TTTAAAGTTCATGAGCGGAGATGCCCTCCACCGAGGACCTGGTTAACTCTCCCTGCT | 4380 | 5401 | CTCATCGAGGCAACCTCTCTGTGGCGCAGGAGATGGCGGGGAAATCATCCCGCTGGAG | 5460 |
| Db | 4321 | TTTAAAGTTCATGAGCGGAGATGCCCTCCACCGAGGACCTGGTTAACTCTCCCTGCT | 4380 | 5401 | CTCATCGAGGCAACCTCTCTGTGGCGCAGGAGATGGCGGGGAAATCATCCCGCTGGAG | 5460 |
| Qy | 4381 | ATCCCTCTCCCTGGCGCCCTAGTGTGGGGTGTGGGAGCGATAGTGGTGGG | 4440 | 5461 | TCAGAAAATAAGGTAGTAAATTTTGGACTCTTTCGAGCGCTCCAAAGCGAGGAGATGAG | 5520 |
| Db | 4381 | ATCCCTCTCCCTGGCGCCCTAGTGTGGGGTGTGGGAGCGATAGTGGTGGG | 4440 | 5461 | TCAGAAAATAAGGTAGTAAATTTTGGACTCTTTCGAGCGCTCCAAAGCGAGGAGATGAG | 5520 |
| Qy | 4441 | GTGGGCGCAGGGAGGGGCTGTGAGTGAAGAACCGGCTCATAGCGTTCTGCTCGCG | 4500 | 5521 | AGGGAAGTATCGGTTCCCGCGGAGATCTCGGAGGTCCAGGAATTCCTCGAGCGATG | 5580 |
| Db | 4441 | GTGGGCGCAGGGAGGGGCTGTGAGTGAAGAACCGGCTCATAGCGTTCTGCTCGCG | 4500 | 5521 | AGGGAAGTATCGGTTCCCGCGGAGATCTCGGAGGTCCAGGAATTCCTCGAGCGATG | 5580 |
| Qy | 4501 | GGTAAACACGCTCTCCCGCAGCATATGTCCTGAGAGCGACGCTGACGACGTGTCACT | 4560 | 5581 | CCCATATGGGACGCGCGGATTAACACCCCTCCACTGTTAGAGTCTCTGGAAGAACCGGAC | 5640 |
| Db | 4501 | GGTAAACACGCTCTCCCGCAGCATATGTCCTGAGAGCGACGCTGACGACGTGTCACT | 4560 | 5581 | CCCATATGGGACGCGCGGATTAACACCCCTCCACTGTTAGAGTCTCTGGAAGAACCGGAC | 5640 |
| Qy | 4561 | CAGATCCTCTAGTCTTACCATCTAGCTGTGAGAGGCTTACCAAGGCTTACCAAGTGAATCAAC | 4620 | 5641 | TACGTCCCTCCAGTGGTACACGGGTGTCCATTTCCGCTCCAGGCCCTCCGATACCA | 5700 |
| Db | 4561 | CAGATCCTCTAGTCTTACCATCTAGCTGTGAGAGGCTTACCAAGGCTTACCAAGTGAATCAAC | 4620 | 5641 | TACGTCCCTCCAGTGGTACACGGGTGTCCATTTCCGCTCCAGGCCCTCCGATACCA | 5700 |
| Qy | 4621 | GAGGATGCTCCACGCGCATGCTCCGCTCGTGGCTAAGAGATGTTTGGGATGGATATGC | 4680 | 5701 | CCTCCACGGAGAGAGGAGCGGTGTCTGTGTCAGAAATCTACCGTGTCTTCTGCTTGGCG | 5760 |
| Db | 4621 | GAGGATGCTCCACGCGCATGCTCCGCTCGTGGCTAAGAGATGTTTGGGATGGATATGC | 4680 | 5701 | CCTCCACGGAGAGAGGAGCGGTGTCTGTGTCAGAAATCTACCGTGTCTTCTGCTTGGCG | 5760 |
| Qy | 4681 | ACGGTGTGATGATTTCAAGACCTGCTCCAGTCCAGTCTCTGCGGAGTTGCGGGA | 4740 | 5761 | GAGCTCGCCACAAAGACCTTCCGAGCTCCGAATCTGTCGCGCTCGACAGCGCACGGCA | 5820 |
| Db | 4681 | ACGGTGTGATGATTTCAAGACCTGCTCCAGTCCAGTCTCTGCGGAGTTGCGGGA | 4740 | 5761 | GAGCTCGCCACAAAGACCTTCCGAGCTCCGAATCTGTCGCGCTCGACAGCGCACGGCA | 5820 |

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| QY | 5821 | ACGGCTCTCTCTGACACAGCCCTCCGACGACGCGGATCCGAGCTTGAGTCGTAC | 5880 |
| Db | 5821 | ACGGCTCTCTGACACAGCCCTCCGACGACGCGGATCCGAGCTTGAGTCGTAC | 5880 |
| QY | 5881 | TCCTCATGCCCCCTTTGAGGGGAGCGGGGATCCCGATCTCAGCGACGGTCTTGG | 5940 |
| Db | 5881 | TCCTCATGCCCCCTTTGAGGGGAGCGGGGATCCCGATCTCAGCGACGGTCTTGG | 5940 |
| QY | 5941 | TCCTACCGTAAGCGAGGAGCTAGTGAGAGCGTCTGCTCTCTCGATGCTCAACATGG | 6000 |
| Db | 5941 | TCCTACCGTAAGCGAGGAGCTAGTGAGAGCGTCTGCTCTCTCGATGCTCAACATGG | 6000 |
| QY | 6001 | ACAGCGCCCTGATCACGCCATCGCTCGGAGGAAACCAAGCTGCCCATCAATGCACTG | 6060 |
| Db | 6001 | ACAGCGCCCTGATCACGCCATCGCTCGGAGGAAACCAAGCTGCCCATCAATGCACTG | 6060 |
| QY | 6061 | AGCAACTCTTTGCTCCGTCACCACTTTGTCTATGCTCAACATCTCGCAGCGCAAGC | 6120 |
| Db | 6061 | AGCAACTCTTTGCTCCGTCACCACTTTGTCTATGCTCAACATCTCGCAGCGCAAGC | 6120 |
| QY | 6121 | CTGCGGCAGAGAAGGTCACCTTTGACAGACTGCAAGTCTGTGAGACACACTACCGGAC | 6180 |
| Db | 6121 | CTGCGGCAGAGAAGGTCACCTTTGACAGACTGCAAGTCTGTGAGACACACTACCGGAC | 6180 |
| QY | 6181 | GTGCTCAAGGAGATGAAGCGCAAGCGCTCCACAGCTTAAGGCTAACTTCTATCCGTGGAG | 6240 |
| Db | 6181 | GTGCTCAAGGAGATGAAGCGCAAGCGCTCCACAGCTTAAGGCTAACTTCTATCCGTGGAG | 6240 |
| QY | 6241 | GAAGCTCTTAGCTGACGCCCCCACTTCGCGCAGATCTAAATTTGCTATGGGCAAAAG | 6300 |
| Db | 6241 | GAAGCTCTTAGCTGACGCCCCCACTTCGCGCAGATCTAAATTTGCTATGGGCAAAAG | 6300 |
| QY | 6301 | GACGTCGGAACCTATCCAGCAAGCGCTTAAACACATCCGCTCCGTGTGGAGAGACTTG | 6360 |
| Db | 6301 | GACGTCGGAACCTATCCAGCAAGCGCTTAAACACATCCGCTCCGTGTGGAGAGACTTG | 6360 |
| QY | 6361 | CTGGAAGACACTGAGACACCAATTTGACACCACTCATGTGCAAAAATGAGTTTCTGC | 6420 |
| Db | 6361 | CTGGAAGACACTGAGACACCAATTTGACACCACTCATGTGCAAAAATGAGTTTCTGC | 6420 |
| QY | 6421 | GTCCAAACGAGAAAGGGGGCGCAAGCTCGCTTATCGTATTTCCAGATTTGGGG | 6480 |
| Db | 6421 | GTCCAAACGAGAAAGGGGGCGCAAGCTCGCTTATCGTATTTCCAGATTTGGGG | 6480 |
| QY | 6481 | GTTTCGTGTGTGCGAGAAATGGCCCTTACGATGTGTCTCCACCTCCCTCAGGCCGTG | 6540 |
| Db | 6481 | GTTTCGTGTGTGCGAGAAATGGCCCTTACGATGTGTCTCCACCTCCCTCAGGCCGTG | 6540 |
| QY | 6541 | ATGGGCTCTTCAATACGGAATCCAAATCTCTCTCGGACAGCGGTCCAGTTCTCTGTGAAT | 6600 |
| Db | 6541 | ATGGGCTCTTCAATACGGAATCCAAATCTCTCTCGGACAGCGGTCCAGTTCTCTGTGAAT | 6600 |
| QY | 6601 | GCGTGAAGACGGAAGAAATGCCCTATGTGGCTTCGCATATGACACCGCTGTTTGACTCA | 6660 |
| Db | 6601 | GCGTGAAGACGGAAGAAATGCCCTATGTGGCTTCGCATATGACACCGCTGTTTGACTCA | 6660 |
| QY | 6661 | ACGGTCACTGAGAAATGACATCCGCTGTGAGGAGTCAATCTCAATGTTGTGACTGGCC | 6720 |
| Db | 6661 | ACGGTCACTGAGAAATGACATCCGCTGTGAGGAGTCAATCTCAATGTTGTGACTGGCC | 6720 |
| QY | 6721 | CCGGAAGCCAGACAGGCCATAAGGTCGCTCAAGAGCGGCTTACATCGGGGGCCCCCTG | 6780 |
| Db | 6721 | CCGGAAGCCAGACAGGCCATAAGGTCGCTCAAGAGCGGCTTACATCGGGGGCCCCCTG | 6780 |
| QY | 6781 | ACTAATTTAAAGGGCAGAACTGCGGCTATCGCCGTCGCCGCGAGCGGTGTACTGACG | 6840 |
| Db | 6781 | ACTAATTTAAAGGGCAGAACTGCGGCTATCGCCGTCGCCGCGAGCGGTGTACTGACG | 6840 |
| QY | 6841 | ACCAGCTGCGGTAAATACCCCTCACTGTTACTTAAAGCCCGCTGCGGCTGTGAGCTGCG | 6900 |
| Db | 6841 | ACCAGCTGCGGTAAATACCCCTCACTGTTACTTAAAGCCCGCTGCGGCTGTGAGCTGCG | 6900 |

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| Qy | 6901 | AAGCTCCAGGACTGCACGATGCTCGTATGTCGGAGACGACCTTGTCTGTTATCTGTGAAGC | 6961 |
| Db | 6901 | AAGCTCCAGGACTGCACGATGCTCGTATGTCGGAGACGACCTTGTCTGTTATCTGTGAAGC | 6961 |
| Qy | 6961 | GCGGGGACCCAAAGAGGACGAGCGAGCCTACGCGGCTTCACGGAGGCTATGACTAGATAC | 7020 |
| Db | 6961 | GCGGGGACCCAAAGAGGACGAGCGAGCCTACGCGGCTTCACGGAGGCTATGACTAGATAC | 7020 |
| Qy | 7021 | TCTGCCCCCTCTGGGACCCGCCAAACACAGAAATACGACTTCGAGTTGATATACATCATGC | 7080 |
| Db | 7021 | TCTGCCCCCTCTGGGACCCGCCAAACACAGAAATACGACTTCGAGTTGATATACATCATGC | 7080 |
| Qy | 7081 | TCCTCCAAATGTCAGTCGCGCACGATGCACTCTGGCAAAAGGCTGACTATCTCACCCGT | 7140 |
| Db | 7081 | TCCTCCAAATGTCAGTCGCGCACGATGCACTCTGGCAAAAGGCTGACTATCTCACCCGT | 7140 |
| Qy | 7141 | GACCCACCAACCCCTTCGCGGGCTGCTGGGAGACAGCTAGACACACTCCAGTCAAT | 7200 |
| Db | 7141 | GACCCACCAACCCCTTCGCGGGCTGCTGGGAGACAGCTAGACACACTCCAGTCAAT | 7200 |
| Qy | 7201 | TCCTGGCTAGGCAACATCATCATGTCATGTCGCCCACTTCGCGCAAGGATGATCCTGATG | 7260 |
| Db | 7201 | TCCTGGCTAGGCAACATCATCATGTCATGTCGCCCACTTCGCGCAAGGATGATCCTGATG | 7260 |
| Qy | 7261 | ACTCATTTCTTCTCCATCTCTAGCTCAGGAAACAACTTGAAAAAGCCCTAGATTGTCAAG | 7320 |
| Db | 7261 | ACTCATTTCTTCTCCATCTCTAGCTCAGGAAACAACTTGAAAAAGCCCTAGATTGTCAAG | 7320 |
| Qy | 7321 | ATCTACGGGGCCTGTTACTCCATTGAGCGACTTGACCTACCTCAGATCAATTCACGACTC | 7380 |
| Db | 7321 | ATCTACGGGGCCTGTTACTCCATTGAGCGCACTTGACCTACCTCAGATCAATTCACGACTC | 7380 |
| Qy | 7381 | CATGGGCTTAGCGCATTTTCACCTCCATAGTTTACTCTCCAGTGTAGATCAATAGGGTGGCT | 7440 |
| Db | 7381 | CATGGGCTTAGCGCATTTTCACCTCCATAGTTTACTCTCCAGTGTAGATCAATAGGGTGGCT | 7440 |
| Qy | 7441 | TCATGGCTCAGGAAACTTGGGGTACCGCCCTTCGAGTCTGGAGACATCGCGGCCAGAAAGT | 7500 |
| Db | 7441 | TCATGGCTCAGGAAACTTGGGGTACCGCCCTTCGAGTCTGGAGACATCGCGGCCAGAAAGT | 7500 |
| Qy | 7501 | GTCCGGCTTAGGCTACTGTCTCCAGGGGGAGGGCTGCGCACTTGCGCAAGTACCTCTTC | 7560 |
| Db | 7501 | GTCCGGCTTAGGCTACTGTCTCCAGGGGGAGGGCTGCGCACTTGCGCAAGTACCTCTTC | 7560 |
| Qy | 7561 | AACCTGGCAGTAAAGGACCAAGCTCAAACTCACCTCCAATCCGGCTGCGTCCAGTTGAT | 7620 |
| Db | 7561 | AACCTGGCAGTAAAGGACCAAGCTCAAACTCACCTCCAATCCGGCTGCGTCCAGTTGAT | 7620 |
| Qy | 7621 | TTATCCAGCTGGTTCGTTGTTGTATACAGCGGGGAGACATATATACAGGCTGTCTCGT | 7680 |
| Db | 7621 | TTATCCAGCTGGTTCGTTGTTGTATACAGCGGGGAGACATATATACAGGCTGTCTCGT | 7680 |
| Qy | 7681 | GCCGACCCCGCTGGTTCAATGTTGCTCCTACTCTTCTGTAGGGGTAGGCACTCTAT | 7740 |
| Db | 7681 | GCCGACCCCGCTGGTTCAATGTTGCTCCTACTCTTCTGTAGGGGTAGGCACTCTAT | 7740 |
| Qy | 7741 | CTACTCCCCAACCGATGAACGGGAGCTAAACACTCCAGCCCAATAGGCCATCTGTTTT | 7800 |
| Db | 7741 | CTACTCCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTTT | 7800 |
| Qy | 7801 | TTTCCCTTTTTTTTTTTCTTT | 7860 |
| Db | 7801 | TTTCCCTTTTTTTTTTTCTTT | 7860 |
| Qy | 7861 | TTTTTCTCTTTTTTTTCTTTTTCTTTCCTTTGGTGGCTCCATCTTAGCCCTTAGTCACGGC | 7920 |
| Db | 7861 | TTTTTCTCTTTTTTTTCTTTTTCTTTCCTTTGGTGGCTCCATCTTAGCCCTTAGTCACGGC | 7920 |
| Qy | 7921 | TAGCTGTCAAAAGGTCGGTAGGCGCTTGACTGCAGAGAGTGCTGTAATGCGCTCTCTGC | 7980 |
| Db | 7921 | TAGCTGTCAAAAGGTCGGTAGGCGCTTGACTGCAGAGAGTGCTGTAATGCGCTCTCTGC | 7980 |
| Qy | 7981 | AGATCAAGT | 7989 |

|||||||
7981 AGATCAAGT 7989

RESULT 13

ABK91440
ID ABK91440 standard; DNA; 10690 BP.

AC ABK91440;

XX 15-NOV-2002 (first entry)

XX Hepatitis C virus vector construct pHCVNeo.17m7.

XX HCV; ss; pHCVNeo.17m2; adaptive mutation; liver failure; cirrhosis;
KW hepatocellular carcinoma; NS3; NS5; encephalomyocarditis virus; EMCV;
XX internal ribosome entry site; IRES; NS5A; HCV replication; mutant.

XX Hepatitis C virus.

OS Encephalomyocarditis virus.

OS Escherichia coli.

OS Enterobacteria phage T7.

OS Synthetic.

XX Key Location/Qualifiers

FT 5'UTR 1..341

FT /*tag= a

FT CDS 342..1181

FT /*tag= b

FT /product= "Core-neo fusion protein"

FT misc_signal 1190..1800

FT /*tag= c

FT /label= IRES

FT /note= "Internal ribosome entry site from EMCV"

FT CDS 1801..7758

FT /*tag= d

FT /product= "Polyprotein"

FT /note= "Comprising NS3, NS4A, NS4B, NS5A and NS5B"

FT mutation replace(4847,A)

FT /*tag= e

FT mutation replace(5243,C)

FT /*tag= f

FT 3'UTR 7759..7991

FT /*tag= g

FT misc_feature 7992..10690

FT /*tag= h

FT /note= "Plasmid derived sequences"

XX WO200259321-A2.

XX 01-AUG-2002.

XX 16-JAN-2002; 2002MO-EP000526.

XX 23-JAN-2001; 2001US-0263479P.

XX (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.

XX De Francesco R, Migliaccio G, Paonessa G;

XX WPI; 2002-599793/64.

XX New Hepatitis C virus (HCV) replicons comprising altered HCV NS3 or HCV
PT NS5 encoding region, or encephalomyocarditis virus (EMCV) internal
PT ribosome entry site (IRES) region, useful in studying HCV replication and
PT expression.

XX Claim 16; Page; 69pp; English.

XX The invention relates to nucleic acid molecules comprising altered HCV
CC NS3 or HCV NS5 encoding region, or encephalomyocarditis virus (EMCV)
CC internal ribosome entry site (IRES) region coding for one or more NS3,
CC NS5A, or EMCV IRES mutations, respectively. The location of the mutations

CC are detailed in the specification. Also included are (1) an expression
CC vector comprising a nucleotide sequence coding for the altered nucleic
CC acids, which is transcriptionally coupled to an exogenous promoter; (2) a
CC recombinant cell human hepatoma cell comprising the altered nucleic acids
CC ; (3) a recombinant cell produced by introducing into a human hepatoma
CC cell the altered nucleic acids; (4) producing an HCV (hepatitis C virus)
CC replicon enhanced cell or which containing a functional HCV replicon; (5)
CC an HCV replicon enhanced cells made in the method; and (6) measuring the
CC ability of a compound to affect HCV activity. The HCV replicons and HCV
CC replicon enhanced cells are useful in studying HCV replication and
CC expression, and HCV and host cell interactions, producing HCV RNA and
CC proteins, and providing a system for measuring the ability of a compound
CC to modulate one or more HCV activities e.g. to discover drugs which may
CC treat HCV mediated diseases such as liver failure, cirrhosis and
CC hepatocellular carcinoma. The present sequence is an HCV based vector
CC pHCVNeo.17 mutant of the invention. Note: The present sequence is not
CC shown in the specification but was created by the indexer using the HCV
CC vector sequence appearing as ABK91412 and the information in Claim 16
XX

XX Sequence 10690 BP; 2333 A; 3045 C; 2908 G; 2404 T; 0 U; 0 Other;

Query Match 100.0%; Score 7988.8; DB 6; Length 10690;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 7990; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCCAGCCCCCGATTGGGGCGACACTCCACATAGATCACTCCCTGTGAGAACTACTG 60

DB 1 GCCAGCCCCCGATTGGGGCGACACTCCACATAGATCACTCCCTGTGAGAACTACTG 60

QY 61 TCTTCAGCAGAAAGCGTCTAGCCATGGCTAGTATGATGCTGCTGCAGCTCCAGGAC 120

DB 61 TCTTCAGCAGAAAGCGTCTAGCCATGGCTAGTATGATGCTGCTGCAGCTCCAGGAC 120

QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGAATGCCAG 180

DB 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGAATGCCAG 180

QY 181 GACGACCGGTCTTTCTTGGATCAACCCGCTCAATGCTGAGATTTGGCGTGCCTCC 240

DB 181 GACGACCGGTCTTTCTTGGATCAACCCGCTCAATGCTGAGATTTGGCGTGCCTCC 240

QY 241 GCGAGACTGCTAGCCGAGTAGTGTGGTCCGGAAGCCCTTGTGTAATCGCTGATAGG 300

DB 241 GCGAGACTGCTAGCCGAGTAGTGTGGTCCGGAAGCCCTTGTGTAATCGCTGATAGG 300

QY 301 GTGCTTGGAGTGCCTCCGCGAGGTCTCGTAGACCGTGCACATGAGGACGAATCCTAAAC 360

DB 301 GTGCTTGGAGTGCCTCCGCGAGGTCTCGTAGACCGTGCACATGAGGACGAATCCTAAAC 360

QY 361 CTCAGAGAAAACCAAGGGCGCGCCATGATTGACAGATGGATTGCACGAGTCTTC 420

DB 361 CTCAGAGAAAACCAAGGGCGCGCCATGATTGACAGATGGATTGCACGAGTCTTC 420

QY 421 CGGCGCTTGGGTGAGAGGCTATTTCGGCTATGACTGGGCGACAAACAGCAATTCGCTGCT 480

DB 421 CGGCGCTTGGGTGAGAGGCTATTTCGGCTATGACTGGGCGACAAACAGCAATTCGCTGCT 480

QY 481 CTGATGCGCGCTGTTCCGGCTGTACGCGAGGGCGCGCGTCTTTTTCAGACCG 540

DB 481 CTGATGCGCGCTGTTCCGGCTGTACGCGAGGGCGCGCGTCTTTTTCAGACCG 540

QY 541 ACCTGTCGGTGCCTTGAATGAATGACGAGGCGAGGCGCGCTATCGTGGCTGGCCA 600

DB 541 ACCTGTCGGTGCCTTGAATGAATGACGAGGCGAGGCGCGCTATCGTGGCTGGCCA 600

QY 601 CGACGGGCTTCTTTCGCGAGCTGTGCTCGAGTGTGTCACTGAAGCGGGAAGGACTGCG 660

DB 601 CGACGGGCTTCTTTCGCGAGCTGTGCTCGAGTGTGTCACTGAAGCGGGAAGGACTGCG 660

QY 661 TGCTATTGGCGGAAGTGCCTGCTATCTCCTGTCTATCTACCTTGTCTCTCGCGAGA 720

DB 661 TGCTATTGGCGGAAGTGCCTGCTATCTCCTGTCTATCTACCTTGTCTCTCGCGAGA 720

QY 721 AAGTATCCATCATGGCTGATGCAATGCGCGGTGTCATACGCTTGATCCGCTACCTGCC 780
 Db 721 AAGTATCCATCATGGCTGATGCAATGCGCGGTGTCATACGCTTGATCCGCTACCTGCC 780
 QY 781 CATTTCAGACCAAGCGAAATCGATCCAGCGAGCACATGCTCGATGGAAGCCGGTC 840
 Db 781 CATTTCAGACCAAGCGAAATCGATCCAGCGAGCACATGCTCGATGGAAGCCGGTC 840
 QY 841 TTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGC 900
 Db 841 TTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTGC 900
 QY 901 CAGGGCTCAAGGCGCGATGCCCGAGCGAGGATCTCGTCGTGACCCATGGCGATGCTT 960
 Db 901 CAGGGCTCAAGGCGCGATGCCCGAGCGAGGATCTCGTCGTGACCCATGGCGATGCTT 960
 QY 961 GCTTGGCGGAATATCATGGTGGAAATGCGCGCTTTCTGGATTCATCGACTGTGGCGGC 1020
 Db 961 GCTTGGCGGAATATCATGGTGGAAATGCGCGCTTTCTGGATTCATCGACTGTGGCGGC 1020
 QY 1021 TGGGTGTGGCGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGC 1080
 Db 1021 TGGGTGTGGCGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGC 1080
 QY 1081 TTGGCGCGAANTGGGCTGACCGCTTCTCGTCTTTACGGTATPCGCGCTCCGATTTGC 1140
 Db 1081 TTGGCGCGAANTGGGCTGACCGCTTCTCGTCTTTACGGTATPCGCGCTCCGATTTGC 1140
 QY 1141 AGCGCATCGCCTTCTATCGCCTTTCTGACGAGTCTCTGAGTTTAAACAGACCAACAG 1200
 Db 1141 AGCGCATCGCCTTCTATCGCCTTTCTGACGAGTCTCTGAGTTTAAACAGACCAACAG 1200
 QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAACGTTACTGGC 1260
 Db 1201 GTTTCCTCTAGCGGATCAATTCGCGCCCTCTCCCTCCCGCCCTTAACGTTACTGGC 1260
 QY 1261 CGAAGCGCTTGGATAGGCGCGTGTGGTTTGTCTATATGTTATTTTCCACCATATTG 1320
 Db 1261 CGAAGCGCTTGGATAGGCGCGTGTGGTTTGTCTATATGTTATTTTCCACCATATTG 1320
 QY 1321 CCGTCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGTCTGTAAGTCTGTAAGGAAGCA 1440
 Db 1321 CCGTCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGTCTGTAAGTCTGTAAGGAAGCA 1440
 QY 1381 AGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGCTGTAAGGAAGCA 1500
 Db 1381 AGGGTCTTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGCTGTAAGGAAGCA 1500
 QY 1441 GTTCTCTGGAAGCTTCTTGAGACAAACAGCTCTGAGGACCCCTTTGCAAGGAGTTCCT 1560
 Db 1441 GTTCTCTGGAAGCTTCTTGAGACAAACAGCTCTGAGGACCCCTTTGCAAGGAGTTCCT 1560
 QY 1501 AACCCCCACCTGGCGACAGTGTCTGCGGCCAAAGGACCAAGGATGATAGATACACT 1560
 Db 1501 AACCCCCACCTGGCGACAGTGTCTGCGGCCAAAGGACCAAGGATGATAGATACACT 1560
 QY 1561 GCAAGGCGGCAACCCAGTCCACGCTGTGAGTTGATAGTTGTAAGGAGTCAAA 1620
 Db 1561 GCAAGGCGGCAACCCAGTCCACGCTGTGAGTTGATAGTTGTAAGGAGTCAAA 1620
 QY 1621 TGGCTCTCTCAAGGATTTCAACAGGGGCTGAAGGATGCCAGAGGTACCCCATTTG 1680
 Db 1621 TGGCTCTCTCAAGGATTTCAACAGGGGCTGAAGGATGCCAGAGGTACCCCATTTG 1680
 QY 1681 ATGGGATCTGATCTGGGCGCTCGGTGACATGCTTTTACATGTTTGTAGTCGAGTTAAA 1740
 Db 1681 ATGGGATCTGATCTGGGCGCTCGGTGACATGCTTTTACATGTTTGTAGTCGAGTTAAA 1740
 QY 1741 AACGTCTAGGCCCCGGAACCAACAGGGGAGCTGGTTTCTTTGAAACACGATAATACC 1800
 Db 1741 AACGTCTAGGCCCCGGAACCAACAGGGGAGCTGGTTTCTTTGAAACACGATAATACC 1800
 QY 1801 ATGGCGCTATTAGCGGCTACTCCCAACAGACGCGAGGCGCTACTTGGCTGCATCATCACT 1860

Db 1801 ATGGCGCTATTAGCGGCTACTCCCAACAGACGCGAGGCGCTACTTGGCTGCATCATCACT 1860
 QY 1861 AGCCTCACAGGCGCGGACAGAAACAGAGTCCAGGGGAGGTCCAAAGTGTCTCCACCGCA 1920
 Db 1861 AGCCTCACAGGCGCGGACAGAAACAGAGTCCAGGGGAGGTCCAAAGTGTCTCCACCGCA 1920
 QY 1921 ACACAATCTTTCTCGGCGACCTCGCTCAATGCGGTGTGTTGGACTGTCTATCATGTTGCC 1980
 Db 1921 ACACAATCTTTCTCGGCGACCTCGCTCAATGCGGTGTGTTGGACTGTCTATCATGTTGCC 1980
 QY 1981 GGCTCAAGACCCCTTCCCGGCCCAAGGCGCCCAATCACCAGATGTACACCAATGTGGAC 2040
 Db 1981 GGCTCAAGACCCCTTCCCGGCCCAAGGCGCCCAATCACCAGATGTACACCAATGTGGAC 2040
 QY 2041 CAGGACCTCGTGGCTGGCAAGCGCCCGGGGCGCTTCTTGAACACCATCACTGC 2100
 Db 2041 CAGGACCTCGTGGCTGGCAAGCGCCCGGGGCGCTTCTTGAACACCATCACTGC 2100
 QY 2101 GCGAGCTCGGACCTTTACTTGTGTACAGGCGATGCCGATGTCAATCCGTTGCCCGCGG 2160
 Db 2101 GCGAGCTCGGACCTTTACTTGTGTACAGGCGATGCCGATGTCAATCCGTTGCCCGCGG 2160
 QY 2161 GCGGACAGCAGGGGAGGCTTCTCTCCCGGAGCGCTCTCTTGAAGGGCTCTTGC 2220
 Db 2161 GCGGACAGCAGGGGAGGCTTCTCTCCCGGAGCGCTCTCTTGAAGGGCTCTTGC 2220
 QY 2221 GCGGTGTCACTCTCTGCGGCGAGCTGTGGGCTTTCGCGGCTGCGGTGTC 2280
 Db 2221 GCGGTGTCACTCTCTGCGGCGAGCTGTGGGCTTTCGCGGCTGCGGTGTC 2280
 QY 2281 ACCCGAGGGGTTGCAAGGCGGTGTGACTTTGACCCGTGAGTCTATGTAAGAACCACTATG 2340
 Db 2281 ACCCGAGGGGTTGCAAGGCGGTGTGACTTTGACCCGTGAGTCTATGTAAGAACCACTATG 2340
 QY 2341 CCGTCCCGGCTTCTCACGCAAACTCGTCCCTCCCGCGGTACCGGAGACATTCAGGTC 2400
 Db 2341 CCGTCCCGGCTTCTCACGCAAACTCGTCCCTCCCGCGGTACCGGAGACATTCAGGTC 2400
 QY 2401 GCCCATCTACAGCGCCCTTACTGGTAGCGGCAAGAGCACTAAGGTGCGGCTGCTATGCA 2460
 Db 2401 GCCCATCTACAGCGCCCTTACTGGTAGCGGCAAGAGCACTAAGGTGCGGCTGCTATGCA 2460
 QY 2461 GCCCAAGGGTATAGGTGCTTGTCTGAAACCGTCCGTGCGGCCCAACCTAGGTTTCGG 2520
 Db 2461 GCCCAAGGGTATAGGTGCTTGTCTGAAACCGTCCGTGCGGCCCAACCTAGGTTTCGG 2520
 QY 2521 GCGTATATGTAAAGGACATGCTATCGACCTTAACATCAGAACCGGGGTAAAGGACCATC 2580
 Db 2521 GCGTATATGTAAAGGACATGCTATCGACCTTAACATCAGAACCGGGGTAAAGGACCATC 2580
 QY 2581 ACCAGGGTGGCCCATCACGTACTTCCACCTATGCAAGTTTCTTGGCGAGGTTTGC 2640
 Db 2581 ACCAGGGTGGCCCATCACGTACTTCCACCTATGCAAGTTTCTTGGCGAGGTTTGC 2640
 QY 2641 TCTGGGCGGCTATGACATCATTAATATGATGAGTGCCACTCAACTGACCTCGACCAT 2700
 Db 2641 TCTGGGCGGCTATGACATCATTAATATGATGAGTGCCACTCAACTGACCTCGACCAT 2700
 QY 2701 ATCTCGGCGCATCGGACAGTCTCGACCAAGCGAGACGGTGGAGCGGACTCGTGTG 2760
 Db 2701 ATCTCGGCGCATCGGACAGTCTCGACCAAGCGAGACGGTGGAGCGGACTCGTGTG 2760
 QY 2761 CTGCCACCGCTAGCCTCCGGGATCGGTCAACCGTGCACATCCAAACATCGAGGAGTG 2820
 Db 2761 CTGCCACCGCTAGCCTCCGGGATCGGTCAACCGTGCACATCCAAACATCGAGGAGTG 2820
 QY 2821 GCTCTGTCCAGACTGAGAAATCCCTTTTATGGAAAGCCATCCCATCGAGACCATC 2880
 Db 2821 GCTCTGTCCAGACTGAGAAATCCCTTTTATGGAAAGCCATCCCATCGAGACCATC 2880
 QY 2881 AAGGGGAGGACCATCTTCTGCTGCAATTCGCAAGAAAGAAATGTGATGAGTCTGCGCG 2940

Db 2881 AAGGGGGGAGGACCTCATTTTCTGCCATTCCAAGAGAAATGTGATGAGCTGCGCGG 2940
Qy 2941 AAGCTGTCCGGCTCCGACTCAATGCTGTAGCATATTAACGGGGCCCTTCAATGATCCGTC 3000
Db 2941 AAGCTGTCCGGCTCCGACTCAATGCTGTAGCATATTAACGGGGCCCTTCAATGATCCGTC 3000
Qy 3001 ATACCAACTAGCGGAGAGCTCATTTGCTGTAGCAACGAGCGCTCTAATGACGGGCTTTAC 3060
Db 3001 ATACCAACTAGCGGAGAGCTCATTTGCTGTAGCAACGAGCGCTCTAATGACGGGCTTTAC 3060
Qy 3061 GCGATTTGACCTCAGTGTACGACTGCAATACATATGTGTCAACCCAGACAGTCGACTTCAG 3120
Db 3061 GCGATTTGACCTCAGTGTACGACTGCAATACATATGTGTCAACCCAGACAGTCGACTTCAG 3120
Qy 3121 CTGAGCCGACCTTCAATGAGAGAGCAACCGTGTGCAACAGCGGGGTGTCAACGCTG 3180
Db 3121 CTGAGCCGACCTTCAATGAGAGAGCAACCGTGTGCAACAGCGGGGTGTCAACGCTG 3180
Qy 3181 CAGCGGAGGAGGAGTGTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA 3240
Db 3181 CAGCGGAGGAGGAGTGTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA 3240
Qy 3241 GAACGGCCCTCGGCGATGTTGCAATTCCTCGGTTCTGTGCGAGTGTATGACGGGGCTGT 3300
Db 3241 GAACGGCCCTCGGCGATGTTGCAATTCCTCGGTTCTGTGCGAGTGTATGACGGGGCTGT 3300
Qy 3301 GCTTGTGACGAGTCAACCGCGCGAGACCTCAGTTAGGTTGGGGCTTACCTAAACACA 3360
Db 3301 GCTTGTGACGAGTCAACCGCGCGAGACCTCAGTTAGGTTGGGGCTTACCTAAACACA 3360
Qy 3361 CAGGGTTCCGCTCGGAGGACCTTGGAGTTCGGGAGAGCGTCTTTACAGGCTC 3420
Db 3361 CAGGGTTCCGCTCGGAGGACCTTGGAGTTCGGGAGAGCGTCTTTACAGGCTC 3420
Qy 3421 ACCACATAGACGCCCTTTCTTGTCCAGACTAAGCAGGAGGAGCAACTCCCTCTAC 3480
Db 3421 ACCACATAGACGCCCTTTCTTGTCCAGACTAAGCAGGAGGAGCAACTCCCTCTAC 3480
Qy 3481 CTGTTAGATACGAGGTACGGTGTGGCGGAGGCTCAGGCTCCACCTCCATCTGTGGAC 3540
Db 3481 CTGTTAGATACGAGGTACGGTGTGGCGGAGGCTCAGGCTCCACCTCCATCTGTGGAC 3540
Qy 3541 CAATGTGGAGTGTCTCATAGGCTAAGCTACGCTGACGGGCGCAACGCCCTCGTG 3600
Db 3541 CAATGTGGAGTGTCTCATAGGCTAAGCTACGCTGACGGGCGCAACGCCCTCGTG 3600
Qy 3601 TATAGGCTGGAGCGGTTCAAAACGAGGTTACTACACACACCCCATTAACCAATACATC 3660
Db 3601 TATAGGCTGGAGCGGTTCAAAACGAGGTTACTACACACACCCCATTAACCAATACATC 3660
Qy 3661 ATGGATGATGTGCGGTGACCTGGAGTGTGTGACGAGACCTGGGTGCTGGTAGGCGGA 3720
Db 3661 ATGGATGATGTGCGGTGACCTGGAGTGTGTGACGAGACCTGGGTGCTGGTAGGCGGA 3720
Qy 3721 GTCCTAGAGTCTGTGGCGGCTATTGCTGTGACACAGGAGCGTGTCAATTGTGGGAGG 3780
Db 3721 GTCCTAGAGTCTGTGGCGGCTATTGCTGTGACACAGGAGCGTGTCAATTGTGGGAGG 3780
Qy 3781 ATCATCTTTGTCGGAAAGCGGCGCATCATTCOCGACAGGAGTCTTTTACCGGAGTTC 3840
Db 3781 ATCATCTTTGTCGGAAAGCGGCGCATCATTCOCGACAGGAGTCTTTTACCGGAGTTC 3840
Qy 3841 GATGATGGAAGTGTGGCTCACACCTCCCTTACATCGAACAGGGAATGAGTCCGCG 3900
Db 3841 GATGATGGAAGTGTGGCTCACACCTCCCTTACATCGAACAGGGAATGAGTCCGCG 3900
Qy 3901 GAAACAATTCAACAGAGAGCAATCGGGTTGTGCAAAACAGCCACCAAGCAAGCGAGGCT 3960
Db 3901 GAAACAATTCAACAGAGAGCAATCGGGTTGTGCAAAACAGCCACCAAGCAAGCGAGGCT 3960
Qy 3961 GCTGTCCCGTGTGGAATCCAAAGTGGGAGCCCTCGAAGCCCTTCTGGCGGAGCATATG 4020
Db 3961 GCTGTCCCGTGTGGAATCCAAAGTGGGAGCCCTCGAAGCCCTTCTGGCGGAGCATATG 4020

Qy 4021 TGGAAATTTTCATCAGGGGATACAATATTTAGCAGGCTTTCACCTCTGCTGGCAACCCC 4080
Db 4021 TGGAAATTTTCATCAGGGGATACAATATTTAGCAGGCTTTCACCTCTGCTGGCAACCCC 4080
Qy 4081 GGGATAGCATCATGTGATGCAATTCACAGCTCTATCACCAGCCGCTACACCCCAACAT 4140
Db 4081 GGGATAGCATCATGTGATGCAATTCACAGCTCTATCACCAGCCGCTACACCCCAACAT 4140
Qy 4141 ACCCTCTCTTTAAACATCTGGGGGATGGTGGCGGCCCAACTTGTCTCTCCACAGGCT 4200
Db 4141 ACCCTCTCTTTAAACATCTGGGGGATGGTGGCGGCCCAACTTGTCTCTCCACAGGCT 4200
Qy 4201 GCTTCTGCTTTTGTAGCGCGCATCGTGTGAGCGGCTGTGAGCAGTGTGGCAGCAT 4260
Db 4201 GCTTCTGCTTTTGTAGCGCGCATCGTGTGAGCGGCTGTGAGCAGTGTGGCAGCAT 4260
Qy 4261 AAGTGTGCTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGGCTGTGGCC 4320
Db 4261 AAGTGTGCTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGGCTGTGGCC 4320
Qy 4321 TTTAAGGTATGAGCGCGGATGCGCTCCACCGAGGACCTGTGTTAACTTCTCCCTGCT 4380
Db 4321 TTTAAGGTATGAGCGCGGATGCGCTCCACCGAGGACCTGTGTTAACTTCTCCCTGCT 4380
Qy 4381 ATCTCTCTCCCTTGGCGGCTTGTGCTGGGTGTGTCGCGAGGATGTGCTGCGCAC 4440
Db 4381 ATCTCTCTCCCTTGGCGGCTTGTGCTGGGTGTGTCGCGAGGATGTGCTGCGCAC 4440
Qy 4441 GTGGGCCAGGAGGGGGCTGTGAGTGAACCGGCTGTAGCGTTTGGCTTCCGG 4500
Db 4441 GTGGGCCAGGAGGGGGCTGTGAGTGAACCGGCTGTAGCGTTTGGCTTCCGG 4500
Qy 4501 GGTAAACCACTCTCTCCCGACGCACTATGTGCTGAGAGCGAGCTGCGAGCACTGTC 4560
Db 4501 GGTAAACCACTCTCTCCCGACGCACTATGTGCTGAGAGCGAGCTGCGAGCACTGTC 4560
Qy 4561 CAGATCTCTCTAGTCTTACATCACTCAGTGTCTGAGAGGCTTCCACGATGTGATCAAC 4620
Db 4561 CAGATCTCTCTAGTCTTACATCACTCAGTGTCTGAGAGGCTTCCACGATGTGATCAAC 4620
Qy 4621 GAGGACTCTCCAGCCATCTCGGCTGTGAGTGAACCGGCTGTAGCGTGTGATGTC 4680
Db 4621 GAGGACTCTCCAGCCATCTCGGCTGTGAGTGAACCGGCTGTAGCGTGTGATGTC 4680
Qy 4681 ACAGTGTGATGATTTCAAGACCTGCTCCAGTCCAGTCTCTGCGCGATGTCGGGA 4740
Db 4681 ACAGTGTGATGATTTCAAGACCTGCTCCAGTCCAGTCTCTGCGCGATGTCGGGA 4740
Qy 4741 GTCCCTCTTCTCATGTCAACGTTGAGTGAACGATGGAACATTTCCCATTAACCGGTC 4800
Db 4741 GTCCCTCTTCTCATGTCAACGTTGAGTGAACGATGGAACATTTCCCATTAACCGGTC 4800
Qy 4801 CAACACCTCTCCAGTGTGAGCAGATCAACCGGACATGTGAAAAACGTTTCCATGAGG 4860
Db 4801 CAACACCTCTCCAGTGTGAGCAGATCAACCGGACATGTGAAAAACGTTTCCATGAGG 4860
Qy 4861 ATCTGCGGCTTAGGACCTGTAGTAAACGTTGGAACATTTCCCATTAACCGGTC 4920
Db 4861 ATCTGCGGCTTAGGACCTGTAGTAAACGTTGGAACATTTCCCATTAACCGGTC 4920
Qy 4921 ACCAGGCGCTTGTGACGCGCTTCCCGGCGCAATTTATTTAGGCGCTGTGGCGGGTG 4980
Db 4921 ACCAGGCGCTTGTGACGCGCTTCCCGGCGCAATTTATTTAGGCGCTGTGGCGGGTG 4980
Qy 4981 GCTGTGAGGAGTACGTTGAGGTTACGCGGTTGGGGGATTTCCACTAGTGAACGGCATG 5040
Db 4981 GCTGTGAGGAGTACGTTGAGGTTACGCGGTTGGGGGATTTCCACTAGTGAACGGCATG 5040
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Db 5041 ACCACTGACAAAGTAAAGTGGCGGCTGAGTTCGGGCGCGCAATTTCTTCAAGAGTG 5100

| | | | | |
|------|----|--|---|------|
| 6181 | DB | | GTGCTCAAGGAGATGAAGCGGAAGCGCTCCACAGTTAAAGCTAACTTCTATCCGTGGAG | 6240 |
| 6241 | QY | | GAAGCCTGTAACTGACGCCCCACATATTCGGCGAGATCTAAATTTTGGCTATGGGCAAAAG | 6300 |
| 6241 | DB | | GAAGCCTGTAACTGACGCCCCACATATTCGGCGAGATCTAAATTTTGGCTATGGGCAAAAG | 6300 |
| 6301 | QY | | GACGTCGGGAACCTATCCAGCAAGCGCGTTAAACCATCCGCTCCGCTGGGAAGGACTTGG | 6360 |
| 6301 | DB | | GACGTCGGGAACCTATCCAGCAAGCGCGTTAAACCATCCGCTCCGCTGGGAAGGACTTGG | 6360 |
| 6361 | QY | | CTGGAAGACACTGAGACACCAATTTGACCAACCACCATATGGCAAAAAATGAGGTTTTCTGC | 6420 |
| 6361 | DB | | CTGGAAGACACTGAGACACCAATTTGACCAACCACCATATGGCAAAAAATGAGGTTTTCTGC | 6420 |
| 6421 | QY | | GTTCCAAACGAGAAAGGGGGCGGAAGCCAGCTCGCTTATCGTATPTCCAGATTTGGGG | 6480 |
| 6421 | DB | | GTTCCAAACGAGAAAGGGGGCGGAAGCCAGCTCGCTTATCGTATPTCCAGATTTGGGG | 6480 |
| 6481 | QY | | GTTTCGTGTGTGGAGAAAAATGGCCCTTTACGATGTGGTCTCCACCCCTCCCTCAGGCCGTG | 6540 |
| 6481 | DB | | GTTTCGTGTGTGGAGAAAAATGGCCCTTTACGATGTGGTCTCCACCCCTCCCTCAGGCCGTG | 6540 |
| 6541 | QY | | ATGGGCTCTTTATACCGGATTTCCAAATACTCTCTCTGGACAGCGGTGAGTTCTCTGGTGAAT | 6600 |
| 6541 | DB | | ATGGGCTCTTTATACCGGATTTCCAAATACTCTCTCTGGACAGCGGTGAGTTCTCTGGTGAAT | 6600 |
| 6601 | QY | | GCTTGGAAACGGAAGAAATGCCCTATGGGCTTCGCATATGACACCGCGTGTTTTGACTCA | 6660 |
| 6601 | DB | | GCTTGGAAACGGAAGAAATGCCCTATGGGCTTCGCATATGACACCGCGTGTTTTGACTCA | 6660 |
| 6661 | QY | | ACGCTCACTCAGAAATGACATCCGCTGTGGAGGTCAATCTACCAATGTTGTGACTTTGGCC | 6720 |
| 6661 | DB | | ACGCTCACTCAGAAATGACATCCGCTGTGGAGGTCAATCTACCAATGTTGTGACTTTGGCC | 6720 |
| 6721 | QY | | CCGGAAGCCAGACAGGCCCATTAAGGTCGCTCACAGAGCGGCTTTACATCGGGGGCCCCCTG | 6780 |
| 6721 | DB | | CCGGAAGCCAGACAGGCCCATTAAGGTCGCTCACAGAGCGGCTTTACATCGGGGGCCCCCTG | 6780 |
| 6781 | QY | | ACTAAATTTAAAGGGCAGAACTGCGGCTATTCGCGGTTCGCGCGAGCGGTGTACTGACG | 6840 |
| 6781 | DB | | ACTAAATTTAAAGGGCAGAACTGCGGCTATTCGCGGTTCGCGCGAGCGGTGTACTGACG | 6840 |
| 6841 | QY | | ACCAGCTCGGTTAATACCTTCACATGTTACTTTGAAGCGCGCTGCGGCGCTGTGACGTGG | 6900 |
| 6841 | DB | | ACCAGCTCGGTTAATACCTTCACATGTTACTTTGAAGCGCGCTGCGGCGCTGTGACGTGG | 6900 |
| 6901 | QY | | AAGCTCCAGACTGCGACGATGCTCGTATCGGAGACGACCTTGTGCTTATCTGTCAAAGC | 6960 |
| 6901 | DB | | AAGCTCCAGACTGCGACGATGCTCGTATCGGAGACGACCTTGTGCTTATCTGTCAAAGC | 6960 |
| 6961 | QY | | GCGGGACCCAGAGACGAGCGAGCCTTACGGGCTTCAAGAGGCTATGACTAGATAC | 7020 |
| 6961 | DB | | GCGGGACCCAGAGACGAGCGAGCCTTACGGGCTTCAAGAGGCTATGACTAGATAC | 7020 |
| 7021 | QY | | TCTGCCCCCTCGGGGACCCGCCAAACAGAAATACGACTTGGAGTTGATAACATCATGC | 7080 |
| 7021 | DB | | TCTGCCCCCTCGGGGACCCGCCAAACAGAAATACGACTTGGAGTTGATAACATCATGC | 7080 |
| 7081 | QY | | TCTTCCAAATGTGTCACTGCTCGCGACGATGCTATCGGCAAAAGGGTGTACTTCTCACCCGT | 7140 |
| 7081 | DB | | TCTTCCAAATGTGTCACTGCTCGCGACGATGCTATCGGCAAAAGGGTGTACTTCTCACCCGT | 7140 |
| 7141 | QY | | GACCCCAACACCCCTTTCGCGGCGCTCGTGGGAGACAGCTAGACACACTCCAGTCAAT | 7200 |
| 7141 | DB | | GACCCCAACACCCCTTTCGCGGCGCTCGTGGGAGACAGCTAGACACACTCCAGTCAAT | 7200 |
| 7201 | QY | | TCTTGGCTAGGCAACATCATATGATCGGCCACCTTGTGGGCAAGATGATCCTGATG | 7260 |
| 7201 | DB | | TCTTGGCTAGGCAACATCATATGATCGGCCACCTTGTGGGCAAGATGATCCTGATG | 7260 |
| 7261 | QY | | ACTCATTTCTTCTCCATCCTTCTAGCTCAGGAAACAACTTGAAGAGCCCTAGATTGACG | 7320 |

Db 7261 ACTCATTTCTTCTCCATCTTCTAGCTCAGGAACAACTTGAAGAGCCCTAGATTGTCTAG 7320
QY 7321 ATCTAGGGGGCTGTGTACTTCCATTTAGGACCACTTGACCTACCTCAGATCAATCAAGACTC 7380
Db 7321 ATCTAGGGGGCTGTGTACTTCCATTTAGGACCACTTGACCTACCTCAGATCAATCAAGACTC 7380
QY 7381 CATGGCTTAGGGCAATTTTCACTCCCATAGTACTCTCCAGGTGAGATCAATAGGGTGGCT 7440
Db 7381 CATGGCTTAGGGCAATTTTCACTCCCATAGTACTCTCCAGGTGAGATCAATAGGGTGGCT 7440
QY 7441 TCATGGCTCAGGAAACTTGGGGTACCCGCTTGCAGTCTGGAGACATCGGGCCAGAACT 7500
Db 7441 TCATGGCTCAGGAAACTTGGGGTACCCGCTTGCAGTCTGGAGACATCGGGCCAGAACT 7500
QY 7501 GTCCGGCTAGGTACTGTCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTC 7560
Db 7501 GTCCGGCTAGGTACTGTCCAGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTC 7560
QY 7561 AACTGGGAGTAAAGCAACCAAGCTCAAACTCACTCCCAATCCCGGCTGCTGCCAGTTGGAT 7620
Db 7561 AACTGGGAGTAAAGCAACCAAGCTCAAACTCACTCCCAATCCCGGCTGCTGCCAGTTGGAT 7620
QY 7621 TTATCCAGCTGGTTCGTGTCTGTGTACAGCGGGGAGACATATCACAGCCCTGTCTCGT 7680
Db 7621 TTATCCAGCTGGTTCGTGTCTGTGTACAGCGGGGAGACATATCACAGCCCTGTCTCGT 7680
QY 7681 GCGGACCCGCTGGTTCATGTGGTCTACTCTACTTCTCTAGGGGTAGGCATCTAT 7740
Db 7681 GCGGACCCGCTGGTTCATGTGGTCTACTCTACTTCTCTAGGGGTAGGCATCTAT 7740
QY 7741 CTACTCCCAACCGATGAACGGGGAGCTAAACACTCCAGGCCCAATAGGCCATCTCTGTTT 7800
Db 7741 CTACTCCCAACCGATGAACGGGGAGCTAAACACTCCAGGCCCAATAGGCCATCTCTGTTT 7800
QY 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
Db 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
QY 7861 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
Db 7861 TTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
QY 7921 TAGCTGTGAAGGTCCTGTAGCCGCTTGAAGTGTGAGAGAGTGTGATCTGCTCTCTCTG 7980
Db 7921 TAGCTGTGAAGGTCCTGTAGCCGCTTGAAGTGTGAGAGAGTGTGATCTGCTCTCTCTG 7980
QY 7981 AGATCAAGTACT 7992
Db 7981 AGATCAAGTACT 7992

RESULT 14

ADP86271
ID ADP86271 standard; DNA; 11313 BP.

AC ADP86271;

XX 23-SEP-2004 (first entry)

DE Hepatitis C virus Con-1 replicon I377/NS3-3' derived plasmid DNA, pZS10.

XX Hepatitis C virus; HCV; anti-HCV agent; HCV infection; therapy; plasmid;
KW ds.

XX Hepatitis C virus.

OS WO2004055216-A2.

XX 01-JUL-2004.

XX 12-DEC-2003; 2003WO-US039722.

XX 13-DEC-2002; 2002US-0433303P.

XX (FOXC-) FOX CHASE CANCER CENT.
PA Zhu Q, Guo J, Seeger C;
XX WPI; 2004-488079/46.
XX New cell-line that replicates hepatitis C virus (HCV), where the cell
PT line is selected from a non-human cell line and a human non-hepatic cell
PT line, useful for identifying anti-HCV agents for treating HCV infections.
XX Example III; SEQ ID NO 8; 130pp; English.
XX The present invention provides hepatitis C virus (HCV) replication cells
CC and cell lines derived from human non-hepatic cells or non-human cells.
CC The invention is useful for identifying anti-HCV agents for treating HCV
CC infections. The present sequence is hepatitis C virus Con-1 replicon
CC I377/NS3-3' derived plasmid DNA.
XX Sequence 11313 BP; 2346 A; 3334 C; 3153 G; 2480 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 7988.8; DB 12; Length 11313;
Best Local Similarity 100.0%; Pred No. 0;
Matches 7990; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCCAGCCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTGTAGGAACTACTG 60
Db 1 GCCAGCCCCCGATTGGGGGCGACACTCCACATAGATCACTCCCTGTAGGAACTACTG 60
QY 61 TCTTACGAGAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGACGCTCCAGGAC 120
Db 61 TCTTACGAGAGAAAGCGTCTAGCCATGGCGTTAGTATGATGTCGTGACGCTCCAGGAC 120
QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTCTCGGAAACCGGTGAGTACACCGAAATGCGAG 180
Db 121 CCCCCCTCCCGGAGAGCCATAGTGTCTCTCGGAAACCGGTGAGTACACCGAAATGCGAG 180
QY 181 GAGCACCGGTCTCTTTTGGATCAACCCGCTCAATGCTGAGATTTGGCGGTGCCCC 240
Db 181 GAGCACCGGTCTCTTTTGGATCAACCCGCTCAATGCTGAGATTTGGCGGTGCCCC 240
QY 241 GCAGACTGTACCGAGTAGTGTGGTTCGCAAGAGCCCTTGTGTACTGCTCTGATAGG 300
Db 241 GCAGACTGTACCGAGTAGTGTGGTTCGCAAGAGCCCTTGTGTACTGCTCTGATAGG 300
QY 301 GTGCTTCGAGTGTCCCGGAGGTCTCTGAGACCGTGCACCATGAGCAAGATCTTAAC 360
Db 301 GTGCTTCGAGTGTCCCGGAGGTCTCTGAGACCGTGCACCATGAGCAAGATCTTAAC 360
QY 361 CTCAAGAAAAAACAAGAGGCGGCCATGATTTGAACAAAGATGGATTTCACGCGAGTTCTC 420
Db 361 CTCAAGAAAAAACAAGAGGCGGCCATGATTTGAACAAAGATGGATTTCACGCGAGTTCTC 420
QY 421 CGGCGGCTTGGGTGGAGAGGTATTCGGCTATGATGCGGACACACACATCGGTGCT 480
Db 421 CGGCGGCTTGGGTGGAGAGGTATTCGGCTATGATGCGGACACACACATCGGTGCT 480
QY 481 CTGATGCGCGGTGTTCCGGCTGTACGCGAGGGGCGCCCGGTTCCTTTTGTCAAGACCG 540
Db 481 CTGATGCGCGGTGTTCCGGCTGTACGCGAGGGGCGCCCGGTTCCTTTTGTCAAGACCG 540
QY 541 ACCTGTCCGTGCGCTGAATGAATGAACTGAGGAGGCGGCTATCGTGGTGGCCA 600
Db 541 ACCTGTCCGTGCGCTGAATGAATGAACTGAGGAGGCGGCTATCGTGGTGGCCA 600
QY 601 CGAGCGGCTTCCCTTGGCGAGGTCTGCTGACAGTGTCTACCTGAAGCGGAGGACTGCG 660
Db 601 CGAGCGGCTTCCCTTGGCGAGGTCTGCTGACAGTGTCTACCTGAAGCGGAGGACTGCG 660
QY 661 TGCTATTGGGCGAAGTGTCCGGGGCAGGATCTCTCTGTCTCTCTCTCTCTCTCTCTCT 720
Db 661 TGCTATTGGGCGAAGTGTCCGGGGCAGGATCTCTCTGTCTCTCTCTCTCTCTCTCTCT 720

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|------|---|------|------|--|------|
| 2881 | AAAGGGGGGAGGACACCTCATTTTCTGCCATTCCAGAGAAATGTGATGAGCTCGCGCGG | 2940 | 4021 | TGGAATTTTCATCAGCGGGATACAAATATTTAGCAGGTTGTCTCACTCTGCTGTCGCAACCCC | 4080 |
| 2941 | AAAGTCTCGGGCTCGGACTCAATGCTGTAGCATATTACGGGGCCCTTGTATGATCCGTC | 3000 | 4021 | TGGAATTTTCATCAGCGGGATACAAATATTTAGCAGGTTGTCTCACTCTGCTGTCGCAACCCC | 4080 |
| 2941 | AAAGTCTCGGGCTCGGACTCAATGCTGTAGCATATTACGGGGCCCTTGTATGATCCGTC | 3000 | 4081 | GGGATGAGTCACTGATGCAATTCACAGCTCTATCAGCAGCCGCTCACCACCCAAACAT | 4140 |
| 3001 | ATACCAACTAGCGGAGACGTCATTGCTGTAGCAACGGAGCGCTCAATGACGGGCTTTACC | 3060 | 4081 | GGGATGAGTCACTGATGCAATTCACAGCTCTATCAGCAGCCGCTCACCACCCAAACAT | 4140 |
| 3001 | ATACCAACTAGCGGAGACGTCATTGCTGTAGCAACGGAGCGCTCAATGACGGGCTTTACC | 3060 | 4141 | ACCTCTCTGTTTAAACATCTGGGGGATGGGTGGCGCCCAACTTGTCTCTCTCCAGCGCT | 4200 |
| 3061 | GGCGATTTGCACTCAGTGTGAGTCACTGCAATACATGTGTCAACCAGACAGTCGATTCAGC | 3120 | 4141 | ACCTCTCTGTTTAAACATCTGGGGGATGGGTGGCGCCCAACTTGTCTCTCTCCAGCGCT | 4200 |
| 3061 | GGCGATTTGCACTCAGTGTGAGTCACTGCAATACATGTGTCAACCAGACAGTCGATTCAGC | 3120 | 4201 | GCTTCTGCTTTTGGTAGCGCCGACATCGCTGGAGCGGCTGTGGGAGCATAGAGCTTTGGG | 4260 |
| 3121 | CTGGACCCGACCTTACCATTTAGACGACACCGTGCCCAAGACGGGTGTCAACGCTCG | 3180 | 4201 | GCTTCTGCTTTTGGTAGCGCCGACATCGCTGGAGCGGCTGTGGGAGCATAGAGCTTTGGG | 4260 |
| 3121 | CTGGACCCGACCTTACCATTTAGACGACACCGTGCCCAAGACGGGTGTCAACGCTCG | 3180 | 4261 | AGGTGCTTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGGCTCTGTGGCC | 4320 |
| 3181 | CAGCGCGAGGACGAGTGTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA | 3240 | 4261 | AGGTGCTTGTGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGCGGCTCTGTGGCC | 4320 |
| 3181 | CAGCGCGAGGACGAGTGTGTAGGGGAGGATGGGCAATTTACAGGTTTGTGACTCCAGGA | 3240 | 4321 | TTTAAAGTCAATGAGCGGCGAGATGCCCTCCACGAGGACCTGTGTAACTTCTCCCTGCT | 4380 |
| 3241 | GAACGGCCCTCGGGCATGTTTCGATTCCTCGGTTCTGTGCGAGTGTATGACGGGGCTGT | 3300 | 4321 | TTTAAAGTCAATGAGCGGCGAGATGCCCTCCACGAGGACCTGTGTAACTTCTCCCTGCT | 4380 |
| 3241 | GAACGGCCCTCGGGCATGTTTCGATTCCTCGGTTCTGTGCGAGTGTATGACGGGGCTGT | 3300 | 4381 | ATCCTCTCCCTCGGCGCCCTAGTGTGTCGGGCTGTGTGCGCAGGATCTGCTCGGCAC | 4440 |
| 3301 | GCTTGTGACAGCTCAGCCCGCGGACACTCAGTTAGTTGCGGGCTTACCTAAACACA | 3360 | 4381 | ATCCTCTCCCTCGGCGCCCTAGTGTGTCGGGCTGTGTGCGCAGGATCTGCTCGGCAC | 4440 |
| 3301 | GCTTGTGACAGCTCAGCCCGCGGACACTCAGTTAGTTGCGGGCTTACCTAAACACA | 3360 | 4441 | GTGGGCCAGGGAGGGGGCTGTGTCAGTGTGATGAAACCGGCTGTAGGTTTCTGCTGCGG | 4500 |
| 3361 | CCAGGGTTGCGGCTGCCAGGACCATCTGGAGTTCTGGGAGAGCGTCTTTACAGGCTTC | 3420 | 4441 | GTGGGCCAGGGAGGGGGCTGTGTCAGTGTGATGAAACCGGCTGTAGGTTTCTGCTGCGG | 4500 |
| 3361 | CCAGGGTTGCGGCTGCCAGGACCATCTGGAGTTCTGGGAGAGCGTCTTTACAGGCTTC | 3420 | 4501 | GGTAAACACACTCTCCCGCCACGCACTATGTGCTGAGAGCGCTGTGAGCAGCTGTCACT | 4560 |
| 3421 | ACCCACATAGACGCCATTTCTTGTCCAGACTAAGCAGGCGAGGACAACTTCCCGCTAC | 3480 | 4501 | GGTAAACACACTCTCCCGCCACGCACTATGTGCTGAGAGCGCTGTGAGCAGCTGTCACT | 4560 |
| 3421 | ACCCACATAGACGCCATTTCTTGTCCAGACTAAGCAGGCGAGGACAACTTCCCGCTAC | 3480 | 4561 | CAGATCCTCTCTAGTCTTACCATCACTCAGTGTCTGTAAGAGGCTTCCACGATGATCAAC | 4620 |
| 3481 | CTGCTAGCATACAGGCTAGGTTGTGCGCAGGGCTCAGGCTCCACCTCCATCTGTGGAC | 3540 | 4561 | CAGATCCTCTCTAGTCTTACCATCACTCAGTGTCTGTAAGAGGCTTCCACGATGATCAAC | 4620 |
| 3481 | CTGCTAGCATACAGGCTAGGTTGTGCGCAGGGCTCAGGCTCCACCTCCATCTGTGGAC | 3540 | 4621 | GAGGACTGCTCCAGCGCATGCTCGGCTCTGTTGGCTTAAGAGATGTTTGGGATGATATGC | 4680 |
| 3481 | CTGCTAGCATACAGGCTAGGTTGTGCGCAGGGCTCAGGCTCCACCTCCATCTGTGGAC | 3540 | 4681 | ACGGTGTGACTGATTTTCAAGACCTGCTCCAGTCCAAAGCTCTCTGCGCGATTGCCGGA | 4740 |
| 3541 | CAAAATGGAAGTGTCTCATACGGCTTAAAGCTACGCTGCAAGCGGCAAGCGCCCTGCTG | 3600 | 4681 | ACGGTGTGACTGATTTTCAAGACCTGCTCCAGTCCAAAGCTCTCTGCGCGATTGCCGGA | 4740 |
| 3541 | CAAAATGGAAGTGTCTCATACGGCTTAAAGCTACGCTGCAAGCGGCAAGCGCCCTGCTG | 3600 | 4741 | GTCCCTCTTCTCATGTCAAACGTTGGGTAACAGGGAGTCTGGCGGGGCGAGCGATCATG | 4800 |
| 3601 | TATAGGCTGGAGCGGTTTCAAAAAGGTTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA | 3660 | 4741 | GTCCCTCTTCTCATGTCAAACGTTGGGTAACAGGGAGTCTGGCGGGGCGAGCGATCATG | 4800 |
| 3601 | TATAGGCTGGAGCGGTTTCAAAAAGGTTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA | 3660 | 4801 | CAAAACACCTGCCCCATGTCAGCGGCTCCCGCGCGCAATTTATTTAGGCGCTGTGGGGTG | 4980 |
| 3661 | ATGCGATGCTGCGGCTGACCTGAGTGTGTCAGGACCTGCGGCTGCTGCTGCTGCTGCTG | 3720 | 4801 | CAAAACACCTGCCCCATGTCAGCGGCTCCCGCGCGCAATTTATTTAGGCGCTGTGGGGTG | 4980 |
| 3661 | ATGCGATGCTGCGGCTGACCTGAGTGTGTCAGGACCTGCGGCTGCTGCTGCTGCTGCTG | 3720 | 4861 | ATCCTGGGGCTTAGGACTGCTGTAGTAAACAGCTGGCATGGAACATTTCCCATTTAAGCGCTAC | 4920 |
| 3721 | GTCCTAGCAGCTCTGGCGCGTATTGCTGCAACAGGACGCTGCTGCTGCTGCTGCTGCTG | 3780 | 4861 | ATCCTGGGGCTTAGGACTGCTGTAGTAAACAGCTGGCATGGAACATTTCCCATTTAAGCGCTAC | 4920 |
| 3721 | GTCCTAGCAGCTCTGGCGCGTATTGCTGCAACAGGACGCTGCTGCTGCTGCTGCTGCTG | 3780 | 4921 | ACCAAGGCGCTTCCGACGCTTCCCGCGCGCAATTTATTTAGGCGCTGTGGGGTG | 4980 |
| 3781 | ATCATCTTGTCCGAAAGCGGCTTCAAAAAGGTTTAAAGCTTAAAGCTTAAAGCTTAAAG | 3840 | 4921 | ACCAAGGCGCTTCCGACGCTTCCCGCGCGCAATTTATTTAGGCGCTGTGGGGTG | 4980 |
| 3781 | ATCATCTTGTCCGAAAGCGGCTTCAAAAAGGTTTAAAGCTTAAAGCTTAAAGCTTAAAG | 3840 | 4981 | GCTGCTAGGAGTACGTGGAGTACCGCGGTGGGGGATTTCCACTACGTGACGGGCTG | 5040 |
| 3841 | GATGAGTGGAGAGTGGCTGACCTGAGTGTGTCAGGACCTGCGGCTGCTGCTGCTGCTG | 3900 | 4981 | GCTGCTAGGAGTACGTGGAGTACCGCGGTGGGGGATTTCCACTACGTGACGGGCTG | 5040 |
| 3841 | GATGAGTGGAGAGTGGCTGACCTGAGTGTGTCAGGACCTGCGGCTGCTGCTGCTGCTG | 3900 | 5041 | ACCACTGCAACAGTAAAGTGTGTCAGGTTCCGCGCCCGGAAATTTCTTACAGAGTG | 5100 |
| 3901 | GAACAAATTAACAGAGGCAATCGGTTGCTGCAACAGGACGCAACCAAGCGGAGGCT | 3960 | 5041 | ACCACTGCAACAGTAAAGTGTGTCAGGTTCCGCGCCCGGAAATTTCTTACAGAGTG | 5100 |
| 3901 | GAACAAATTAACAGAGGCAATCGGTTGCTGCAACAGGACGCAACCAAGCGGAGGCT | 3960 | | | |
| 3961 | GCTGCTCCGTTGGATCCAGTGGGAGGCTTCCAGGCTTCTGCGGAGCATATG | 4020 | | | |
| 3961 | GCTGCTCCGTTGGATCCAGTGGGAGGCTTCCAGGCTTCTGCGGAGCATATG | 4020 | | | |

| | | | |
|----|------|---|------|
| QY | 5101 | GATGGGTGCGGTGACAGGTACGTCCAGCGTGAACCCCTCCTACGGGAGGAGTC | 5160 |
| Db | 5101 | GATGGGTGCGGTGACAGGTACGTCCAGCGTGAACCCCTCCTACGGGAGGAGTC | 5160 |
| QY | 5161 | ACATTCCTGTCGGGCTCAATCAATACCTGGTTCAGCTCCATCCGAGCCCGGAA | 5220 |
| Db | 5161 | ACATTCCTGTCGGGCTCAATCAATACCTGGTTCAGCTCCATCCGAGCCCGGAA | 5220 |
| QY | 5221 | CGGAGGTAGCAGTGTCTCATCTGCTCACCGACCCCTCCACATTAAGCGGAGAGC | 5280 |
| Db | 5221 | CGGAGGTAGCAGTGTCTCATCTGCTCACCGACCCCTCCACATTAAGCGGAGAGC | 5280 |
| QY | 5281 | GCTAAGCTAGGTGTCGCGAGGAGATCTCCCTCCTCTGCGCAGCTCATCAGTAGCCAG | 5340 |
| Db | 5281 | GCTAAGCTAGGTGTCGCGAGGAGATCTCCCTCCTCTGCGCAGCTCATCAGTAGCCAG | 5340 |
| QY | 5341 | CTGTCTCGCCCTTCTTTGAAGGCAACATGCACTACCCGTATGACTCCCGCGAGCGTGAC | 5400 |
| Db | 5341 | CTGTCTCGCCCTTCTTTGAAGGCAACATGCACTACCCGTATGACTCCCGCGAGCGTGAC | 5400 |
| QY | 5401 | CTCATCGAGGCCAACCTCTCTGTGGCGGAGAGATGGCGGGAACATCACCCGCTGGAG | 5460 |
| Db | 5401 | CTCATCGAGGCCAACCTCTCTGTGGCGGAGAGATGGCGGGAACATCACCCGCTGGAG | 5460 |
| QY | 5461 | TCAGAAATTAAGTAGTAATTTTGGACTCTTTCGAGCGCTCCAGCGGAGGATGAG | 5520 |
| Db | 5461 | TCAGAAATTAAGTAGTAATTTTGGACTCTTTCGAGCGCTCCAGCGGAGGATGAG | 5520 |
| QY | 5521 | AGGGAAGTATCCGTTCCGCGGAGATCCCTGCGGAGGTCCAGAAATTCCTCGAGGATG | 5580 |
| Db | 5521 | AGGGAAGTATCCGTTCCGCGGAGATCCCTGCGGAGGTCCAGAAATTCCTCGAGGATG | 5580 |
| QY | 5581 | CCCATATGGGACGCGCGGATTAACACCTCTGTTAGAGTCTCTGGAAGACCCGAC | 5640 |
| Db | 5581 | CCCATATGGGACGCGCGGATTAACACCTCTGTTAGAGTCTCTGGAAGACCCGAC | 5640 |
| QY | 5641 | TACGTCCCTCAGTGGTACAGGGTGTCCATGTCGCGCTGCAAGCCCTCCGATACCA | 5700 |
| Db | 5641 | TACGTCCCTCAGTGGTACAGGGTGTCCATGTCGCGCTGCAAGCCCTCCGATACCA | 5700 |
| QY | 5701 | CCTCCACGAGGAGAGAGCGGTCTCTGTCAGAACTCTACGTCCTCTGCTTGGG | 5760 |
| Db | 5701 | CCTCCACGAGGAGAGAGCGGTCTCTGTCAGAACTCTACGTCCTCTGCTTGGG | 5760 |
| QY | 5761 | GAGTTCGCCACAAAGACCTTCGGCAGCTCCGAGCTCGAAGCGGACGCA | 5820 |
| Db | 5761 | GAGTTCGCCACAAAGACCTTCGGCAGCTCCGAGCTCGAAGCGGACGCA | 5820 |
| QY | 5821 | ACGGCTCTCTGACCAAGCCCTCCGACGAGCGGACGCGGATCCGATCGATCGTAC | 5880 |
| Db | 5821 | ACGGCTCTCTGACCAAGCCCTCCGACGAGCGGACGCGGATCCGATCGATCGTAC | 5880 |
| QY | 5881 | TCCTCCATGCCCCCTTGAAGGGAGCGGGGATCCCGATCTCAGGACGGGTCTTGG | 5940 |
| Db | 5881 | TCCTCCATGCCCCCTTGAAGGGAGCGGGGATCCCGATCTCAGGACGGGTCTTGG | 5940 |
| QY | 5941 | TCTACCGTAAGCAGGAGGTAGTGAGGACGTCTGCTGCTGCTGCTCTACACATGG | 6000 |
| Db | 5941 | TCTACCGTAAGCAGGAGGTAGTGAGGACGTCTGCTGCTGCTCTACACATGG | 6000 |
| QY | 6001 | ACAGGCGCTGATCAACCGATGCGCTCGGAGGAAACCAAGCTGCCATCAATGCACTG | 6060 |
| Db | 6001 | ACAGGCGCTGATCAACCGATGCGCTCGGAGGAAACCAAGCTGCCATCAATGCACTG | 6060 |
| QY | 6061 | AGCAACTCTTTGCTCCGTCACCAACTTGTCTATGCTAACAATCTCGAGCGCAAGC | 6120 |
| Db | 6061 | AGCAACTCTTTGCTCCGTCACCAACTTGTCTATGCTAACAATCTCGAGCGCAAGC | 6120 |
| QY | 6121 | CTCGGCGAAGAAAGGTCACTTTGACAGCTGCGAGTCTTGGACGACCACTACCGGAC | 6180 |
| Db | 6121 | CTCGGCGAAGAAAGGTCACTTTGACAGCTGCGAGTCTTGGACGACCACTACCGGAC | 6180 |
| QY | 6181 | GTGCTCAAGGAGATGAAGGCGAAGCGGTCCAGTTAAGGCTAAACTTCTATCCGTGGAG | 6240 |

| | | | |
|----|------|--|------|
| Db | 6181 | GTGCTCAAGGAGATGAAGGCGAAGCGTCCACAGTTAAGCTAAACTTCTATCCGTGGAG | 6240 |
| QY | 6241 | GAAGCTCTAAGCTGACGCCCCACATTCGGCCAGATCTAAATTTGGCTATGGGCAAG | 6300 |
| Db | 6241 | GAAGCTCTAAGCTGACGCCCCACATTCGGCCAGATCTAAATTTGGCTATGGGCAAG | 6300 |
| QY | 6301 | GACGTCGGAACTTATCCAGCAAGGCGGTAAACCATCCGCTCCGTGGAGGAGCTTG | 6360 |
| Db | 6301 | GACGTCGGAACTTATCCAGCAAGGCGGTAAACCATCCGCTCCGTGGAGGAGCTTG | 6360 |
| QY | 6361 | CTGGAAGACACTGAGACACCAATTGACACACCATCATCGCAAAATAGAGTTTCTGC | 6420 |
| Db | 6361 | CTGGAAGACACTGAGACACCAATTGACACACCATCATCGCAAAATAGAGTTTCTGC | 6420 |
| QY | 6421 | GTCCAAACAGAAAGGCGGCGCAGCTCGCTTATCGTATTCAGATTTGGGG | 6480 |
| Db | 6421 | GTCCAAACAGAAAGGCGGCGCAGCTCGCTTATCGTATTCAGATTTGGGG | 6480 |
| QY | 6481 | GTTCTGTGTGCGAATAATGGCCCTTTACGATGTGCTCCACCTCCCTCAGGCCGTG | 6540 |
| Db | 6481 | GTTCTGTGTGCGAATAATGGCCCTTTACGATGTGCTCCACCTCCCTCAGGCCGTG | 6540 |
| QY | 6541 | ATGGGCTCTTCAATCGGATTCCTCAATCTCTCTGACAGCGGTGAGTTCTGTTGAAT | 6600 |
| Db | 6541 | ATGGGCTCTTCAATCGGATTCCTCAATCTCTCTGACAGCGGTGAGTTCTGTTGAAT | 6600 |
| QY | 6601 | GCCTGAAAGCAAAATGCGCTTATGGCTTCGATATGACACCGCTGTTTGACTCA | 6660 |
| Db | 6601 | GCCTGAAAGCAAAATGCGCTTATGGCTTCGATATGACACCGCTGTTTGACTCA | 6660 |
| QY | 6661 | ACGTCACCTGAGAAATGACATCCGTTGAGGAGTCAATCTACCAATGTTGACTGGCC | 6720 |
| Db | 6661 | ACGTCACCTGAGAAATGACATCCGTTGAGGAGTCAATCTACCAATGTTGACTGGCC | 6720 |
| QY | 6721 | CCGGAAGCAGACAGGCCATTAAGTCTGCTCAGAGCGCTTTTACATGGGGCCCCCTG | 6780 |
| Db | 6721 | CCGGAAGCAGACAGGCCATTAAGTCTGCTCAGAGCGCTTTTACATGGGGCCCCCTG | 6780 |
| QY | 6781 | ACTAATTTAAAGGCGAAGCTGCGGTATCGCGGTATCGCGGTGCGCGCGAGCGTACGAG | 6840 |
| Db | 6781 | ACTAATTTAAAGGCGAAGCTGCGGTATCGCGGTATCGCGGTGCGCGCGAGCGTACGAG | 6840 |
| QY | 6841 | ACGAGTCGGGTATACCTCAGATGTTACTTGAAGGCGCTGCGGCTGTCGAGCTGG | 6900 |
| Db | 6841 | ACGAGTCGGGTATACCTCAGATGTTACTTGAAGGCGCTGCGGCTGTCGAGCTGG | 6900 |
| QY | 6901 | AAGTCTCAGGACTGACGATGCTGATGCGGAGACGACCTTGTGCTTATCTGTAAGAC | 6960 |
| Db | 6901 | AAGTCTCAGGACTGACGATGCTGATGCGGAGACGACCTTGTGCTTATCTGTAAGAC | 6960 |
| QY | 6961 | CGGGGACCCAGAGGACGAGCGGAGCTACGGGCTTTCAGGAGGCTATGACTAGATAC | 7020 |
| Db | 6961 | CGGGGACCCAGAGGACGAGCGGAGCTACGGGCTTTCAGGAGGCTATGACTAGATAC | 7020 |
| QY | 7021 | TCTGCCCCCTGCGGACCCCAACAGAAATGAGTTGAGTTCGATTAACATCATGCG | 7080 |
| Db | 7021 | TCTGCCCCCTGCGGACCCCAACAGAAATGAGTTGAGTTCGATTAACATCATGCG | 7080 |
| QY | 7081 | TCCTTCCAAATGTCAGTCTGCGCAGATGCTCTGGCAAAAGGGTGTACTCTCACCCGT | 7140 |
| Db | 7081 | TCCTTCCAAATGTCAGTCTGCGCAGATGCTCTGGCAAAAGGGTGTACTCTCACCCGT | 7140 |
| QY | 7141 | GACCCACCCCTTGGCGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAAT | 7200 |
| Db | 7141 | GACCCACCCCTTGGCGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAAT | 7200 |
| QY | 7201 | TCCTGGCTAGGCAACATCATGTCGCGCCACCTTGTGGGCAAGATGATCCTGATG | 7260 |
| Db | 7201 | TCCTGGCTAGGCAACATCATGTCGCGCCACCTTGTGGGCAAGATGATCCTGATG | 7260 |
| QY | 7261 | ACTCATTTCTTCTCCATCTTCTAGCTCAGGAACTTGAAGGCGCTTCTATCCGTGGAG | 7320 |

Db 7261 ACTCATTTCTTCCATCTCTTAGCTCAGAACAACTTGAAGAGCCCTAGATTCTCAG 7320
 QY 7321 ATCTAGGGGCGCTGTTTACTCCATTGAGCCACTTGACCTACCTCAGATCATTTCAACGACTC 7380
 Db 7321 ATCTAGGGGCGCTGTTTACTCCATTGAGCCACTTGACCTACCTCAGATCATTTCAACGACTC 7380
 QY 7381 CATGGCCTTAGCGCATTTTCACTCCATAGTATTCTCTCCAGGTGAGATCAATAGGGTGGCT 7440
 Db 7381 CATGGCCTTAGCGCATTTTCACTCCATAGTATTCTCTCCAGGTGAGATCAATAGGGTGGCT 7440
 QY 7441 TCATGGCCTCAGGAACTTGGGGTACCGCCCTTCGAGTCTGCGAGATCGGGGCCAAGT 7500
 Db 7441 TCATGGCCTCAGGAACTTGGGGTACCGCCCTTCGAGTCTGCGAGATCGGGGCCAAGT 7500
 QY 7501 GTCCGGCTAGGCTACTGTCAGGGGGGGGAGGGCTGCCACTTGTGCAAGTACCTCTTC 7560
 Db 7501 GTCCGGCTAGGCTACTGTCAGGGGGGGGAGGGCTGCCACTTGTGCAAGTACCTCTTC 7560
 QY 7561 AACTGGGCACTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTCGTCCCAAGTTGGAT 7620
 Db 7561 AACTGGGCACTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTCGTCCCAAGTTGGAT 7620
 QY 7621 TTATCCAGCTGGTTCGTGTTTACAGCGGGGAGACATATATACAGCCCTGTCTCGT 7680
 Db 7621 TTATCCAGCTGGTTCGTGTTTACAGCGGGGAGACATATATACAGCCCTGTCTCGT 7680
 QY 7681 GCCCGACCCCGCTGTTTCACTGCTGCTACTCTCTACTTCTGTAGGGGTAGGCATCTAT 7740
 Db 7681 GCCCGACCCCGCTGTTTCACTGCTGCTACTCTCTACTTCTGTAGGGGTAGGCATCTAT 7740
 QY 7741 CTACTCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTTT 7800
 Db 7741 CTACTCCCAACCGATGAACGGGAGCTAAACACTCCAGGCCAATAGGCCATCTGTTTT 7800
 QY 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
 Db 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
 QY 7861 TTTTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 7920
 Db 7861 TTTTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 7920
 QY 7921 TAGCTGTGAAGGTCCTGAGCGCTTGACTGACGAGAGTCTGATACCTGCTCTCTGTC 7980
 Db 7921 TAGCTGTGAAGGTCCTGAGCGCTTGACTGACGAGAGTCTGATACCTGCTCTCTGTC 7980
 QY 7981 AGATCAAGTACT 7992
 Db 7981 AGATCAAGTACT 7992

RESULT 15

AAD25322 standard; cDNA; 7989 BP.
 XX ID AAD25322 standard; cDNA; 7989 BP.
 AC AAD25322;
 XX DT 12-MAR-2002 (first entry)
 XX DE Hepatitis C virus (HCV) replBartMan/Avall cDNA.
 XX KW Hepatitis C virus; HCV; transfection; infection; virus neutralisation;
 KW gene therapy; vaccine; immunoprotection; hepatotropic; virucide; liver;
 KW SS.
 XX OS Hepatitis C virus.
 XX FH Key Location/Qualifiers
 XX CDS /tag= a
 FT /product= "HCVreplBartMan polyprotein"
 FT 7766
 FT misc_feature /tag= b

/note= "Nucleotide creating Availi site"

WO200189364-A2.

29-NOV-2001.

23-MAY-2001; 2001WO-US016822.

23-MAY-2000; 2000US-00576989.

(UNIW) UNIV WASHINGTON.

Rice CM, Blight KJ;

WPI: 2002-066755/09.

P-PSDB; AAE15717.

Hepatitis C virus variants having greater transfection efficiency and ability to survive subpassage, useful as a vaccine for immunizing primate to the virus, comprise non-naturally occurring viral sequences.

Claim 44; Page 69-71; 174pp; English.

The invention relates to Hepatitis C virus (HCV) variants which include polynucleotides comprising non-naturally occurring HCV sequence and HCV variants that have a transfection efficiency and ability to survive subpassage greater than HCV that have wild-type polypeptide coding regions. The polynucleotides of the invention are useful for identifying a cell line that is permissive for infection with HCV and detecting replication of HCV in cells of the cell line. They are also useful for testing a compound for anti-viral properties and for inhibiting HCV infection. They are also useful for the generation of defined HCV virus stocks to develop in vitro and in vivo assays for virus neutralisation, attachment, penetration and entry, structure/function studies on HCV proteins and RNA elements and identification of new antiviral targets, a systematic survey of cell culture systems and conditions to identify those that support wild-type and variant HCV RNA replication and particle release, production of adaptive HCV variants capable of more efficient replication in cell culture, production of HCV variants with altered tissue or species tropism, establishment of alternative animal models for inhibitor evaluation including those supporting HCV variant replication, development of cell-free HCV replication assays, production of immunogenic HCV particles for vaccination, engineering of attenuated HCV derivatives as possible vaccine candidates, engineering of attenuated or defective HCV derivatives for expression of heterologous gene products for gene therapy and vaccine applications and for utilisation of the HCV glycoproteins for targeted delivery of therapeutic agents to the liver or other cell types with appropriate receptors. Vaccine comprising these sequences is useful for inducing immunoprotection to HCV in a primate. The present sequence is Hepatitis C virus (HCV) replBartMan/Avall cDNA

Sequence 7989 BP; 1647 A; 2369 C; 2242 G; 1731 T; 0 U; 0 Other;

Query Match 99.9%; Score 7987.4; DB 6; Length 7989;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 7988; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GCCAGCCCCCGATGGGGGCGACACTCCACATAGACTCCTCCCTGTGAGAACTACTG 60
 Db 1 GCCAGCCCCCGATGGGGGCGACACTCCACATAGACTCCTCCCTGTGAGAACTACTG 60
 QY 61 TCTTACGCGAAGAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGAGCTCCAGGAC 120
 Db 61 TCTTACGCGAAGAGCGTCTAGCCATGGCGTCTAGTATGAGTGTCTGAGCTCCAGGAC 120
 QY 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGAAATGCCAG 180
 Db 121 CCCCCCTCCCGGAGAGCCATAGTGTCTGCGGAACCGGTGAGTACACCGAAATGCCAG 180
 QY 181 GACGACCGGGTCTTTCTTTGGATCAACCCCGCTCAATGCTCTGAGATTTGGCGTGCCTCC 240
 Db 181 GACGACCGGGTCTTTCTTTGGATCAACCCCGCTCAATGCTCTGAGATTTGGCGTGCCTCC 240

QY 241 GCAGACTGCTAGCCAGTAGTGTGGTCCGAAAGGCCCTGTGTGCTACTGCTGATAGG 300
DB 241 GCAGACTGCTAGCCAGTAGTGTGGTCCGAAAGGCCCTGTGTGCTACTGCTGATAGG 300
QY 301 GTCTTTGCGAGTCCCGCGGAGTCTCGTAGACGGTGCACCATGAGCAGCAATCTTAAC 360
DB 301 GTCTTTGCGAGTCCCGCGGAGTCTCGTAGACGGTGCACCATGAGCAGCAATCTTAAC 360
QY 361 CTCAAAGAAACAAAGGCGGCCCATGATTAACAAGATGATTTGACGAGGTTCTC 420
DB 361 CTCAAAGAAACAAAGGCGGCCCATGATTAACAAGATGATTTGACGAGGTTCTC 420
QY 421 CGGCCCTTTGGTGGAGAGCTATTCCGCTATGACTGGGCAACAGCAATCCGCTGCT 480
DB 421 CGGCCCTTTGGTGGAGAGCTATTCCGCTATGACTGGGCAACAGCAATCCGCTGCT 480
QY 481 CTGATGCCCGCTGTTCCGCTGTGACGCGAGGGGCGCCGGTCTTTTGTCAAGCCG 540
DB 481 CTGATGCCCGCTGTTCCGCTGTGACGCGAGGGGCGCCGGTCTTTTGTCAAGCCG 540
QY 541 ACCTGTCCGCTGCTGATGAATGAACTGACGAGGAGCGCGGCTATCGTGGCTGGCA 600
DB 541 ACCTGTCCGCTGCTGATGAATGAACTGACGAGGAGCGCGGCTATCGTGGCTGGCA 600
QY 601 CGACGGCGTTCTTGGCGAGTGTCTCGAGTGTCTCACTGAAGCGGAAAGGACTGGC 660
DB 601 CGACGGCGTTCTTGGCGAGTGTCTCGAGTGTCTCACTGAAGCGGAAAGGACTGGC 660
QY 661 TCGTATTGGCGAAGTCCCGGGCAGGATCTCTGTCACTACCTTGTCTCGCGAGA 720
DB 661 TCGTATTGGCGAAGTCCCGGGCAGGATCTCTGTCACTACCTTGTCTCGCGAGA 720
QY 721 AAGTATCCATCATGCTGATGCAATGCGCGGCTGCTACGCTTGATCCGCTACTCGC 780
DB 721 AAGTATCCATCATGCTGATGCAATGCGCGGCTGCTACGCTTGATCCGCTACTCGC 780
QY 781 CATTCGACCAAGCGGAAACATCGCATCGAGCGAGCAGTACTCGGATGGAAGCGGTC 840
DB 781 CATTCGACCAAGCGGAAACATCGCATCGAGCGAGCAGTACTCGGATGGAAGCGGTC 840
QY 841 TTGTCGATCAGATCATCTGACGAGAGCAGTACAGGGCTCCGCGAGCGCACTGTTCG 900
DB 841 TTGTCGATCAGATCATCTGACGAGAGCAGTACAGGGCTCCGCGAGCGCACTGTTCG 900
QY 901 CCAGSCTCAAGCGCGCATGCCGACGCGAGGATCTCGTGTGACCCATGCGCATGCT 960
DB 901 CCAGSCTCAAGCGCGCATGCCGACGCGAGGATCTCGTGTGACCCATGCGCATGCT 960
QY 961 GCTTCCGAAATATCATGTTGAAATGCGCGCTTTCTGGATTATCGACTGTGCGCGC 1020
DB 961 GCTTCCGAAATATCATGTTGAAATGCGCGCTTTCTGGATTATCGACTGTGCGCGC 1020
QY 1021 TGGGTGTCGCGACCGCTATCAGGACATAGGTTGGCTACCGTGATATGCTGAAGAGC 1080
DB 1021 TGGGTGTCGCGACCGCTATCAGGACATAGGTTGGCTACCGTGATATGCTGAAGAGC 1080
QY 1081 TTGGCGGGAATGSGCTGACCGCTTCCTCGCTTTACGGTATCGCGCTCCCGATTGCG 1140
DB 1081 TTGGCGGGAATGSGCTGACCGCTTCCTCGCTTTACGGTATCGCGCTCCCGATTGCG 1140
QY 1141 AGCGCATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAACG 1200
DB 1141 AGCGCATCGCTTCTATCGCTTCTTGACGAGTCTTCTGAGTTTAAACAGACCAACG 1200
QY 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCGCGCTTAAACAGACCAACG 1260
DB 1201 GTTTCCTCTAGCGGATCAATTCGCGCTCTCCCTCGCGCTTAAACAGACCAACG 1260
QY 1261 CGAAGCCGCTTGGAAATAGCGGCTGTGCTGTGTCTATATGTTATTTCCACCATATG 1320
DB 1261 CGAAGCCGCTTGGAAATAGCGGCTGTGCTGTGTCTATATGTTATTTCCACCATATG 1320
QY 1321 CCGTCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGTCTTTGACGAGCATTCCT 1380

DB 1321 CCGTCTTTTGGCAATGTGAGGCGCGGAAACCTGGCCCTGTCTTCTTGACGATTCCT 1380
QY 1381 AGGGGTCTTTCCCTCTCCGCCAAAGGAATGCAAGGTCTGTGAATGTCTGTAAGGAAGCA 1440
DB 1381 AGGGGTCTTTCCCTCTCCGCCAAAGGAATGCAAGGTCTGTGAATGTCTGTAAGGAAGCA 1440
QY 1441 GTTCCTCTGGAAGCTTTCTTGAAGACAAACAACTGTGTAGCGACCTTTGACGCGCGG 1500
DB 1441 GTTCCTCTGGAAGCTTTCTTGAAGACAAACAACTGTGTAGCGACCTTTGACGCGCGG 1500
QY 1501 AACCCGCCACCTGGCGACAGGTCCTCTCGGCCAAAGCAACGCTGTATAAGATACACCT 1560
DB 1501 AACCCGCCACCTGGCGACAGGTCCTCTCGGCCAAAGCAACGCTGTATAAGATACACCT 1560
QY 1561 GCAAGGCGGCAACACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAGAGTCAAA 1620
DB 1561 GCAAGGCGGCAACACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAGAGTCAAA 1620
QY 1621 TGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATGCCAGAAAGTACCCCATTTG 1680
DB 1621 TGGCTCTCTCAAGCGTATTCAACAGGGGCTGAAGGATGCCAGAAAGTACCCCATTTG 1680
QY 1681 ATGGGATCTGATCTGGGCTCTCGGTGCACATGCTTTACATGTGTTAGTCGAGGTTAAA 1740
DB 1681 ATGGGATCTGATCTGGGCTCTCGGTGCACATGCTTTACATGTGTTAGTCGAGGTTAAA 1740
QY 1741 AACGTCTAGGCCCCCGAAACACAGGGGAGTGTGTTTTTCCCTTTGAAAAACACGATATAC 1800
DB 1741 AACGTCTAGGCCCCCGAAACACAGGGGAGTGTGTTTTTCCCTTTGAAAAACACGATATAC 1800
QY 1801 ATGGCGCTATTACGGCTACTTCCCAACAGCGGAGGCTCAAGTGTCTCCACCGCA 1860
DB 1801 ATGGCGCTATTACGGCTACTTCCCAACAGCGGAGGCTCAAGTGTCTCCACCGCA 1860
QY 1861 AGCCTCACAGGCGCGGACAGGAACACAGTCCAGGGGAGGTCACAGTGTCTCCACCGCA 1920
DB 1861 AGCCTCACAGGCGCGGACAGGAACACAGTCCAGGGGAGGTCACAGTGTCTCCACCGCA 1920
QY 1921 ACACAAATCTTCTGGCGACCTGCTCAATGGCTGTGTGGACTGTCTATCATGCTGC 1980
DB 1921 ACACAAATCTTCTGGCGACCTGCTCAATGGCTGTGTGGACTGTCTATCATGCTGC 1980
QY 1981 GGCTCAAGAGCCCTTGGCGGCCCAAGGCCCAATCAACCAATGTACCAATGTGAC 2040
DB 1981 GGCTCAAGAGCCCTTGGCGGCCCAAGGCCCAATCAACCAATGTACCAATGTGAC 2040
QY 2041 CAGGACCTCGTGGCTGGCAAGCGCCCGCGGGCGCTTCCCTGACACCATGCACTGC 2100
DB 2041 CAGGACCTCGTGGCTGGCAAGCGCCCGCGGGCGCTTCCCTGACACCATGCACTGC 2100
QY 2101 GGCAGCTCGGACCTTTACTTGGTCAAGGAGATGCCGATGTCAATCCCGTGGCGCGCGG 2160
DB 2101 GGCAGCTCGGACCTTTACTTGGTCAAGGAGATGCCGATGTCAATCCCGTGGCGCGCGG 2160
QY 2161 GGCACAGCAGGCGGAGCTACTCTCCCGAGGCGGCTCTCTACTTGAAGGCTCTTCG 2220
DB 2161 GGCACAGCAGGCGGAGCTACTCTCCCGAGGCGGCTCTCTACTTGAAGGCTCTTCG 2220
QY 2221 GCGGCTCCACTGTCTGCGCTCGGGGACGCTGTGGGCACTTTCCGGCTCGCGTGTGC 2280
DB 2221 GCGGCTCCACTGTCTGCGCTCGGGGACGCTGTGGGCACTTTCCGGCTCGCGTGTGC 2280
QY 2281 ACCGAGGGTGTGGAAGGGGTGGACTTTGTACCCGCTCGAGTCTATGGAACCACTATG 2340
DB 2281 ACCGAGGGTGTGGAAGGGGTGGACTTTGTACCCGCTCGAGTCTATGGAACCACTATG 2340
QY 2341 CGGTCCCGGCTTTCACGGAACACTGCTCCCTCCCGCGGTACCGCAGACATTCAGGTG 2400
DB 2341 CGGTCCCGGCTTTCACGGAACACTGCTCCCTCCCGCGGTACCGCAGACATTCAGGTG 2400
QY 2401 GCCCATCTACAGCCCTTCTGTTAGGCGGCAAGGACATAGGTGCGCGCTGCGTATGCA 2460

| | | | |
|----|------|--|------|
| Db | 2401 | GCCATCTACAGCCCTTACTGTAGCGGCAAGACACTAAAGTGCCTGCGGTGCGTATGCA | 2460 |
| Qy | 2461 | GCCCAAGGGTATAGGTGCTTGTCTGAACCCCTCGTTCGCGCCGACCTTAGTTCGGG | 2520 |
| Db | 2461 | GCCCAAGGGTATAGGTGCTTGTCTGAACCCCTCGTTCGCGCCGACCTTAGTTCGGG | 2520 |
| Qy | 2521 | GCGTATATGCTTAAGGCACATGTATCGACCCCTAAACATCAGAACCGGGGTAAAGAACCATC | 2580 |
| Db | 2521 | GCGTATATGCTTAAGGCACATGTATCGACCCCTAAACATCAGAACCGGGGTAAAGAACCATC | 2580 |
| Qy | 2581 | ACCACGGGTGCCCCATACGTACTACCATATGCGGAAGTTTCTTGCCGACGGTGTGCTG | 2640 |
| Db | 2581 | ACCACGGGTGCCCCATACGTACTACCATATGCGGAAGTTTCTTGCCGACGGTGTGCTG | 2640 |
| Qy | 2641 | TCTGGGGGCCCTATGACATCATATATGATGAGTGCCACTCAACTGACTCGACCACT | 2700 |
| Db | 2641 | TCTGGGGGCCCTATGACATCATATATGATGAGTGCCACTCAACTGACTCGACCACT | 2700 |
| Qy | 2701 | ATCTGGGCATCGGCACAGTCTTGACCAAGCGGAGACGGCTGGAGCGGCACTCGTCGTG | 2760 |
| Db | 2701 | ATCTGGGCATCGGCACAGTCTTGACCAAGCGGAGACGGCTGGAGCGGCACTCGTCGTG | 2760 |
| Qy | 2761 | CTGCCACCGCTACGCCCTCGGGATCGGTCAACCGTGCACATCCAAACATCGAGAGGTG | 2820 |
| Db | 2761 | CTGCCACCGCTACGCCCTCGGGATCGGTCAACCGTGCACATCCAAACATCGAGAGGTG | 2820 |
| Qy | 2821 | GCTCTGTCCAGCACTGAGAAATCCCTTTTATGGCAAGCCATCCCCATCGACACCATC | 2880 |
| Db | 2821 | GCTCTGTCCAGCACTGAGAAATCCCTTTTATGGCAAGCCATCCCCATCGACACCATC | 2880 |
| Qy | 2881 | AAGGGGGGAGGACCTCATTTTCTGCGCATTCCTCAAGAGAAATGTAGTCTGCCGCG | 2940 |
| Db | 2881 | AAGGGGGGAGGACCTCATTTTCTGCGCATTCCTCAAGAGAAATGTAGTCTGCCGCG | 2940 |
| Qy | 2941 | AAGCTGTCCGGCTCGGACTCAATGTCTGATAGCATATTACCGGGGCTTGTATTCGCTC | 3000 |
| Db | 2941 | AAGCTGTCCGGCTCGGACTCAATGTCTGATAGCATATTACCGGGGCTTGTATTCGCTC | 3000 |
| Qy | 3001 | ATACCAACTAGCGAGAGCTCATTTGCTAGCAAGGAGCTCTAATGACGGGCTTTACC | 3060 |
| Db | 3001 | ATACCAACTAGCGAGAGCTCATTTGCTAGCAAGGAGCTCTAATGACGGGCTTTACC | 3060 |
| Qy | 3061 | GGCGATTCGACTCAGTGCATGCAATGCAATGCTGTCTCAACCGAGACAGTCTCAGC | 3120 |
| Db | 3061 | GGCGATTCGACTCAGTGCATGCAATGCTGTCTCAACCGAGACAGTCTCAGC | 3120 |
| Qy | 3121 | CTGACCCGACCTTACCATTTGAGAGAGACCGTGCACAGAGCGGCTGTCAGCTCG | 3180 |
| Db | 3121 | CTGACCCGACCTTACCATTTGAGAGAGACCGTGCACAGAGCGGCTGTCAGCTCG | 3180 |
| Qy | 3181 | CAGCGGCGAGGACGAGCTGGTAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGGA | 3240 |
| Db | 3181 | CAGCGGCGAGGACGAGCTGGTAGGGGAGGATGGGCAATTTACAGTTTGTGACTCCAGGA | 3240 |
| Qy | 3241 | GAAAGGGCCCTCGGGCATGTCGATTCCTCGGTTCTGTGCGAGTGTCTATGACGCGGCTGT | 3300 |
| Db | 3241 | GAAAGGGCCCTCGGGCATGTCGATTCCTCGGTTCTGTGCGAGTGTCTATGACGCGGCTGT | 3300 |
| Qy | 3301 | GCTTGGTACGAGCTCAGCGCCGCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACA | 3360 |
| Db | 3301 | GCTTGGTACGAGCTCAGCGCCGCGAGACCTCAGTTAGTTGCGGGCTTACCTAAACACA | 3360 |
| Qy | 3361 | CCAGGGTTCGCGCTGCGCAGGACCATCTGGAGTTCTGGAGAGCTTTTACAGGCTC | 3420 |
| Db | 3361 | CCAGGGTTCGCGCTGCGCAGGACCATCTGGAGTTCTGGAGAGCTTTTACAGGCTC | 3420 |
| Qy | 3421 | ACCCACATAGAGCCCATTTCTTGTCCAGACTTAAGAGGCGAGGAGACAATTCCTCCTAC | 3480 |
| Db | 3421 | ACCCACATAGAGCCCATTTCTTGTCCAGACTTAAGAGGCGAGGAGACAATTCCTCCTAC | 3480 |
| Qy | 3481 | CTGGTAGCATACAGCTACGGTGTGCGCCAGGGGCTCAGGCTCCACCTCCATCGTGGGAC | 3540 |
| Db | 3481 | CTGGTAGCATACAGCTACGGTGTGCGCCAGGGGCTCAGGCTCCACCTCCATCGTGGGAC | 3540 |
| Qy | 3541 | CRAATCTGGAAGTGTCTCATACGGCTAAAGCTTACGCTGACGCGGCCAACGCCCTGCTG | 3600 |
| Db | 3541 | CRAATCTGGAAGTGTCTCATACGGCTAAAGCTTACGCTGACGCGGCCAACGCCCTGCTG | 3600 |
| Qy | 3601 | TATAGCTGAGAGCCGTTCAAACGAGGTACTACACACACACCCCAATACCAATATACATC | 3660 |
| Db | 3601 | TATAGCTGAGAGCCGTTCAAACGAGGTACTACACACACACCCCAATACCAATATACATC | 3660 |
| Qy | 3661 | ATGCGATGATGTCGGTGCCTGACCTGGAGGTCTGTCAACGAGCACTGGGTGCTGAGCGGA | 3720 |
| Db | 3661 | ATGCGATGATGTCGGTGCCTGACCTGGAGGTCTGTCAACGAGCACTGGGTGCTGAGCGGA | 3720 |
| Qy | 3721 | GTCTTAGCAGCTCTGCGCGGTATGCTTCAACAGGAGCGTGTCTATTTGGGCGAG | 3780 |
| Db | 3721 | GTCTTAGCAGCTCTGCGCGGTATGCTTCAACAGGAGCGTGTCTATTTGGGCGAG | 3780 |
| Qy | 3781 | ATCATCTTGTCCGAAAGCGCGGCATCATTCCCGACAGGGAAGTCTTTTACCGGAGTTC | 3840 |
| Db | 3781 | ATCATCTTGTCCGAAAGCGCGGCATCATTCCCGACAGGGAAGTCTTTTACCGGAGTTC | 3840 |
| Qy | 3841 | GATGAGATGGAAGTGCCTCACACCTCCCTTATCATCGAAACAGGGAATGCACTCGCC | 3900 |
| Db | 3841 | GATGAGATGGAAGTGCCTCACACCTCCCTTATCATCGAAACAGGGAATGCACTCGCC | 3900 |
| Qy | 3901 | GAACAATTCAAACAGAGGCAATCGGTTGCTGCAAAACAGCCACCAAGCAAGCGAGGCT | 3960 |
| Db | 3901 | GAACAATTCAAACAGAGGCAATCGGTTGCTGCAAAACAGCCACCAAGCAAGCGAGGCT | 3960 |
| Qy | 3961 | GCTGCTCCGCTGGTGGATCCAGTGGCGGACCTCGAAGCTTCTCGGGCGAAGCATATG | 4020 |
| Db | 3961 | GCTGCTCCGCTGGTGGATCCAGTGGCGGACCTCGAAGCTTCTCGGGCGAAGCATATG | 4020 |
| Qy | 4021 | TGGAATTTTCATCAGCGGGATACAATATTTAGCAGGCTTGTTCACCTGCTCGGCAACCCC | 4080 |
| Db | 4021 | TGGAATTTTCATCAGCGGGATACAATATTTAGCAGGCTTGTTCACCTGCTCGGCAACCCC | 4080 |
| Qy | 4081 | GCGATAGCATCATGTATGGCATTCACAGCCTCTATACAGCCCGCTCACACCCCAACAT | 4140 |
| Db | 4081 | GCGATAGCATCATGTATGGCATTCACAGCCTCTATACAGCCCGCTCACACCCCAACAT | 4140 |
| Qy | 4141 | ACCTCTCTGTTTAAACATCTCGGGGGGATGGGTGCGCGCCCACTGCTCTCCAGCGCT | 4200 |
| Db | 4141 | ACCTCTCTGTTTAAACATCTCGGGGGGATGGGTGCGCGCCCACTGCTCTCCAGCGCT | 4200 |
| Qy | 4201 | GCTTCTGCTTTCTGAGGCGCGGATCGTGGAGCGGCTGTTGGCAGCATAGGCTTGGG | 4260 |
| Db | 4201 | GCTTCTGCTTTCTGAGGCGCGGATCGTGGAGCGGCTGTTGGCAGCATAGGCTTGGG | 4260 |
| Qy | 4261 | AAGTGTCTGTGGATATTTTGGCAGGTTATGGAGCGGGTGGCAGGCGCTCGTGCC | 4320 |
| Db | 4261 | AAGTGTCTGTGGATATTTTGGCAGGTTATGGAGCGGGTGGCAGGCGCTCGTGCC | 4320 |
| Qy | 4321 | TTTAAAGTTCATGAGCGGAGATGCCCTCCACCGAGGACCTGGTTAACTACTCCTGCT | 4380 |
| Db | 4321 | TTTAAAGTTCATGAGCGGAGATGCCCTCCACCGAGGACCTGGTTAACTACTCCTGCT | 4380 |
| Qy | 4381 | ATCCTCTCCCTGCGCGCTTAGTCTGCGGGTCTGTGTCGAGCGGATACTGGTCTGGGAC | 4440 |
| Db | 4381 | ATCCTCTCCCTGCGCGCTTAGTCTGCGGGTCTGTGTCGAGCGGATACTGGTCTGGGAC | 4440 |
| Qy | 4441 | GTGGGCCACAGGGGAGGGGCTGTGAGTGAGTAAACCGGCTGATAGCGTTCGCTTCGGG | 4500 |
| Db | 4441 | GTGGGCCACAGGGGAGGGGCTGTGAGTGAGTAAACCGGCTGATAGCGTTCGCTTCGGG | 4500 |
| Qy | 4501 | GGTAAACAGCTCTCCCGACGACCTATGTGCTGAGAGCGCTGACGAGCGTGTCACT | 4560 |
| Db | 4501 | GGTAAACAGCTCTCCCGACGACCTATGTGCTGAGAGCGCTGACGAGCGTGTCACT | 4560 |
| Qy | 4561 | CAGATCTCTCTAGTCTTTACCATCACTCAGTGTGTGAAGAGGCTTCAACAGTGGATCAAC | 4620 |
| Db | 4561 | CAGATCTCTCTAGTCTTTACCATCACTCAGTGTGTGAAGAGGCTTCAACAGTGGATCAAC | 4620 |

Db 6781 ACTAATTTCTAAAGGCGAAGACTGGCGCTATGCGCGGTGCCGCGAGCGGCTGTAAGG 6840
Qy 6841 ACCAGCTGCGGTAAATACCTTACATGTTACTTGAAGCGCGCTGCGGCTGTGAGAGTGGG 6900
Db 6841 ACCAGCTGCGGTAAATACCTTACATGTTACTTGAAGCGCGCTGCGGCTGTGAGAGTGGG 6900
Qy 6901 AAGCTCCAGGACTGCGAGTGTGATGCGGAGACGACCTTGTGCTTAATCTGTGAAAGC 6960
Db 6901 AAGCTCCAGGACTGCGAGTGTGATGCGGAGACGACCTTGTGCTTAATCTGTGAAAGC 6960
Qy 6961 GCGGGACCCAAAGAGGAGGCGAGCTAGCGGCTTACGGAGGCTATGACTAGATAC 7020
Db 6961 GCGGGACCCAAAGAGGAGGCGAGCTAGCGGCTTACGGAGGCTATGACTAGATAC 7020
Qy 7021 TCTGCCCGCCCTGGGGACCCGCCCAACAGATACGACTTGGAGTTGATAACATCATGC 7080
Db 7021 TCTGCCCGCCCTGGGGACCCGCCCAACAGATACGACTTGGAGTTGATAACATCATGC 7080
Qy 7081 TCTTCCAATGTGTCAGTGGGACGATGCAATCTGGCAAAAGGTTGTAATCTCAACCGT 7140
Db 7081 TCTTCCAATGTGTCAGTGGGACGATGCAATCTGGCAAAAGGTTGTAATCTCAACCGT 7140
Qy 7141 GACCCACACCCCTTGGCGGCTGCGGAGACGCTAGACACCTCCAGTCAAT 7200
Db 7141 GACCCACACCCCTTGGCGGCTGCGGAGACGCTAGACACCTCCAGTCAAT 7200
Qy 7201 TCTGGCTAGGCAACATCATGATATGCGCCACCTTGTGGGCAAGGATGATCCTGATG 7260
Db 7201 TCTGGCTAGGCAACATCATGATATGCGCCACCTTGTGGGCAAGGATGATCCTGATG 7260
Qy 7261 ACTCAATTTCTTCCATCTTCTAGCTCAGGAACAACCTTGAAAGCCCTAGATTGTGAG 7320
Db 7261 ACTCAATTTCTTCCATCTTCTAGCTCAGGAACAACCTTGAAAGCCCTAGATTGTGAG 7320
Qy 7321 ATCTACGGGCGCTGTACTCCATTGAGCCTTACCTCAGATCATTTCAACGACTC 7380
Db 7321 ATCTACGGGCGCTGTACTCCATTGAGCCTTACCTCAGATCATTTCAACGACTC 7380
Qy 7381 CATGGCCTTAGGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGTTGGCT 7440
Db 7381 CATGGCCTTAGGCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGTTGGCT 7440
Qy 7441 TCATGCTCAGGAACCTTGGGTTACCGCTTGGAGTCTGGAGACATCGGCGCAGAAAT 7500
Db 7441 TCATGCTCAGGAACCTTGGGTTACCGCTTGGAGTCTGGAGACATCGGCGCAGAAAT 7500
Qy 7501 GTCCGCGTAGGCTACTGTCCAGGGGGAGGCTGCCACTTCTGCAAGTACTCTTC 7560
Db 7501 GTCCGCGTAGGCTACTGTCCAGGGGGAGGCTGCCACTTCTGCAAGTACTCTTC 7560
Qy 7561 AACTGGGCGAGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCCCTCCAGTTGGAT 7620
Db 7561 AACTGGGCGAGTAAGGACCAAGCTCAAACTCACTCCAAATCCCGGCTGCCCTCCAGTTGGAT 7620
Qy 7621 TTATCCAGCTGCTTGTGTTGTTAGCGGGGAGACATATACAGCCTGTCTCGT 7680
Db 7621 TTATCCAGCTGCTTGTGTTGTTAGCGGGGAGACATATACAGCCTGTCTCGT 7680
Qy 7681 GCGCGACCCCGCTGGTTCAATGTTGCTACTCTCTACTTCTGTAGGGGTAGGCATCTAT 7740
Db 7681 GCGCGACCCCGCTGGTTCAATGTTGCTACTCTCTACTTCTGTAGGGGTAGGCATCTAT 7740
Qy 7741 CTACTCCCAACCGATGAAGCGGAGCTAAACACTCCAGGCGCAATAGGCCATCTGTTTT 7800
Db 7741 CTACTCCCAACCGATGAAGCGGAGCTAAACACTCCAGGCGCAATAGGCCATCTGTTTT 7800
Qy 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
Db 7801 TTTCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7860
Qy 7861 TTTTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920
Db 7861 TTTTTCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 7920

Qy 7921 TAGCTGTGAAAGGTCCGTGAGCCGCTTGACTGCGAGAGTCTGTGATACTGCGCCTCTCTGC 7980
Db 7921 TAGCTGTGAAAGGTCCGTGAGCCGCTTGACTGCGAGAGTCTGTGATACTGCGCCTCTCTGC 7980
Qy 7981 AGATCAAGT 7989
Db 7981 AGATCAAGT 7989

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